GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 09:47:20 ; Search time 196 Seconds
(without alignments)
30.326 Million cell updates/sec

Title: US-10-062-257A-10
Perfect score: 30
Sequence: 1 TFXXXXXXLXDXX 13

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	30	100.0	13	4	AAG68082	Aag68082 Antitumou
2	30	100.0	13	4	AAG68084	Aag68084 Antitumou
3	30	100.0	13	4	AAG68081	Aag68081 Antitumou
4	30	100.0	13	4	AAG68083	Aag68083 Antitumou
5	30	100.0	13	4	AAB73126	Aab73126 Tumour an
6	30	100.0	13	4	AAB73147	Aab73147 Tumour an
7	30	100.0	13	4	AAB73145	Aab73145 Tumour an
8	30	100.0	13	4	AAB73148	Aab73148 Tumour an
9	30	100.0	13	4	AAB73146	Aab73146 Tumour an
10	30	100.0	13	4	AAB73151	Aab73151 Tumour an
11	30	100.0	13	4	AAB73150	Aab73150 Tumour an
12	30	100.0	13	4	AAB73149	Aab73149 Tumour an
13	30	100.0	13	4	AAB73144	Aab73144 Tumour an
14	30	100.0	13	7	ADM75342	Adm75342 Potential
15	30	100.0	14	7	ADD23350	Add23350 Breast ca
16	30	100.0	16	6	ABR63280	Abr63280 Peptide #
17	30	100.0	16	7	ADD35548	Add35548 Affinity
18	30	100.0	16	7	AAO27568	Aao27568 Bovine BS
19	30	100.0	16	7	AEA78908	Aea78908 Bovine Se
20	30	100.0	16	7	AEA79083	Aea79083 Bovine Se
21	30	100.0	16	7	AEA78834	Aea78834 Bovine Se
22	30	100.0	16	8	ADH11188	Adh11188 MALDI-MS
23	30	100.0	16	8	ADJ78034	Adj78034 Peptide,
24	30	100.0	16	8	ADJ78050	Adj78050 Peptide,
25	30	100.0	16	9	ADZ86402	Adz86402 Protein q
26	30	100.0	17	7	ADD35547	Add35547 Bovine al
27	30	100.0	18	2	AAW65655	Aaw65655 Peptide #
28	30	100.0	18	5	ABG95997	Abg95997 Cysteine-
29	30	100.0	18	9	ADV95854	Adv95854 Bovine se
30	30	100.0	19	7	AEA78835	Aea78835 Bovine Se
31	30	100.0	20	6	ABO14117	Abo14117 Novel hum
32	30	100.0	20	8	ADG78512	Adg78512 Human sec
33	30	100.0	20	8	ADN60815	Adn60815 Human sec
34	30	100.0	21	2	AAY06544	Aay06544 Hepatocel
35	30	100.0	21	5	AAU89862	Aau89862 Insulin/i
36	30	100.0	21	5	AAU89785	Aau89785 Insulin/i
37	30	100.0	21	7	ADE01174	Ade01174 Bovine Se
38	30	100.0	25	2	AAW22187	Aaw22187 Endogenou
39	30	100.0	25	9	ADW97006	Adw97006 Human gra
40	30	100.0	25	9	ADZ69775	Adz69775 Botulinum
41	30	100.0	26	4	AAB91264	Aab91264 Secretin
42	30	100.0	26	8	ADR84082	Adr84082 S. pyogen
43	30	100.0	27	1	AAP20383	Aap20383 Protected
44	30	100.0	27	1	AAP20398	Aap20398 Secretin
45	30	100.0	27	1	AAP30021	Aap30021 Synthetic
46	30	100.0	27	1	AAP30014	Aap30014 27-Desami
47	30	100.0	27	1	AAP30038	Aap30038 Pig Secre
48	30	100.0	27	1	AAP30551	Aap30551 Sequence
49	30	100.0	27	1	AAP30049	Aap30049 Intermedi
50	30	100.0	27	2	AAW37796	Aaw37796 Porcine s
51	30	100.0	27	2	AAW37793	Aaw37793 Porcine s
52	30	100.0	27	2	AAW71676	Aaw71676 Secretin-
53	30	100.0	27	2	AAY50236	Aay50236 Neutrophi
54	30	100.0	27	4	AAB70901	Aab70901 Porcine s
55	30	100.0	27	4	AAB91262	Aab91262 Secretin
56	30	100.0	27	4	AAB91263	Aab91263 Secretin
57	30	100.0	27	4	AAB50844	Aab50844 Pig prote
58	30	100.0	27	5	AAE23673	Aae23673 Heptacosi
59	30	100.0	27	5	ABB06679	Abb06679 Mammalian
60	30	100.0	27	5	AAE23659	Aae23659 Heptacosi
61	30	100.0	27	5	ABB08014	Abb08014 Human sec
62	30	100.0	27	5	ABB04453	Abb04453 Secretin
63	30	100.0	27	5	ABB81203	Abb81203 Secretin
64	30	100.0	27	6	ABR40226	Abr40226 Porcine s
65	30	100.0	27	6	ABP56898	Abp56898 Secretin
66	30	100.0	27	7	ADD69986	Add69986 Vasoactiv
67	30	100.0	27	8	ADP74185	Adp74185 Secretin
68	30	100.0	27	9	ADU74133	Adu74133 Porcine s
69	30	100.0	27	9	ADW91706	Adw91706 Human VIP
70	30	100.0	27	9	ADZ60126	Adz60126 Secretin
71	30	100.0	28	1	AAP30063	Aap30063 Recombina
72	30	100.0	28	1	AAP30062	Aap30062 27-desami
73	30	100.0	28	4	AAU14782	Aau14782 Novel bon
74	30	100.0	30	1	AAP81564	Aap81564 Human ins
75	30	100.0	32	4	AAB82887	Aab82887 Mouse T c
76	30	100.0	32	8	ADU04520	Adu04520 Protein t
77	30	100.0	33	1	AAP70421	Aap70421 Sequence
78	30	100.0	33	4	ABB40034	Abb40034 Peptide #
79	30	100.0	33	4	AAM33655	Aam33655 Peptide #
80	30	100.0	33	4	AAM73457	Aam73457 Human bon
81	30	100.0	33	4	AAM60783	Aam60783 Human bra
82	30	100.0	33	4	ABG55180	Abg55180 Human liv
83	30	100.0	33	4	ABG08414	Abg08414 Novel hum
84	30	100.0	33	5	ABG43316	Abg43316 Human pep
85	30	100.0	36	5	ADJ33828	Adj33828 Peptide o
86	30	100.0	41	7	ADE78243	Ade78243 Endometri
87	30	100.0	42	4	AAM90201	Aam90201 Human imm
88	30	100.0	44	8	ADS07740	Ads07740 Staphyloc
89	30	100.0	45	4	ABB11306	Abb11306 Human sec
90	30	100.0	46	4	AAO12027	Aao12027 Human pol
91	30	100.0	46	6	ABU44233	Abu44233 Protein e
92	30	100.0	49	4	ABG52332	Abg52332 Human liv
93	30	100.0	49	4	AAM06070	Aam06070 Peptide #
94	30	100.0	51	7	ADJ99951	Adj99951 Plant tra
95	30	100.0	51	8	ADU04355	Adu04355 Synechocy
96	30	100.0	51	8	ADU04353	Adu04353 Unidentif

97	30	100.0	51	9	ADX69981	Adx69981 R1 revers
98	30	100.0	52	4	AAM20412	Aam20412 Peptide #
99	30	100.0	52	4	ABB41124	Abb41124 Peptide #
100	30	100.0	52	4	AAM34900	Aam34900 Peptide #

ALIGNMENTS

RESULT 1
AAG68082
ID AAG68082 standard; peptide; 13 AA.
XX
AC AAG68082;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antitumour peptide yes 508-520.
XX
KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
KW cyclophilin B gene; HLA-A2402.
XX
OS Homo sapiens.
XX
PN JP2001245675-A.
XX
PD 11-SEP-2001.
XX
PF 25-DEC-2000; 2000JP-00393047.
XX
PR 28-DEC-1999; 99JP-00374322.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2001-610076/70.
XX
PT New peptides for recognizing cancer cells with tumor specific cytotoxic T
PT lymphocytes and for treating cancer.
XX
PS Claim 8; Page 2; 14pp; Japanese.
XX
CC The present invention describes peptides recognising cancer cells with
CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
CC the above mentioned sequences; and (4) peptides with one or more deleted,
CC substituted, added or inserted amino acid(s) of the above mentioned
CC sequences, particularly those having recognising property due to HLA-
CC A2402 binding CTL, especially having at least 5 amino acids, used for
CC medicine, particularly anticancer agents, derived from antitumour
CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
CC genes. The antitumour peptides have cytostatic activities. The peptides
CC are used for the treatment of cancer. The peptides cause activation of
CC CTL in cancer patients. The present sequence represents a peptide from
CC the present invention
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 30; DB 4; Length 13;
Best Local Similarity 30.8%; Pred. No. 2.2e+02;
Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TFXXXXXXLXDXX 13
              ||:::::|:|::
Db          1 TFEYIQSFLEDYF 13
```

RESULT 2
AAG68084
ID AAG68084 standard; peptide; 13 AA.
XX
AC AAG68084;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antitumour peptide blk 482-494.
XX
KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
KW cyclophilin B gene; HLA-A2402.
XX
OS Homo sapiens.
XX
PN JP2001245675-A.
XX
PD 11-SEP-2001.
XX
PF 25-DEC-2000; 2000JP-00393047.
XX
PR 28-DEC-1999; 99JP-00374322.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2001-610076/70.
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PT New peptides for recognizing cancer cells with tumor specific cytotoxic T
PT lymphocytes and for treating cancer.
XX
PS Claim 8; Page 2; 14pp; Japanese.
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CC The present invention describes peptides recognising cancer cells with
CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
CC the above mentioned sequences; and (4) peptides with one or more deleted,
CC substituted, added or inserted amino acid(s) of the above mentioned
CC sequences, particularly those having recognising property due to HLA-
CC A2402 binding CTL, especially having at least 5 amino acids, used for
CC medicine, particularly anticancer agents, derived from antitumour
CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
CC genes. The antitumour peptides have cytostatic activities. The peptides
CC are used for the treatment of cancer. The peptides cause activation of
CC CTL in cancer patients. The present sequence represents a peptide from
CC the present invention
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 30; DB 4; Length 13;
Best Local Similarity 30.8%; Pred. No. 2.2e+02;
Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TFXXXXXXLXDXX 13
              ||:::::|:|::
Db          1 TFEFLQSVLEDFY 13
```

RESULT 3
AAG68081
ID AAG68081 standard; peptide; 13 AA.
XX
AC AAG68081;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antitumour peptide src 511-523.
XX
KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
KW cyclophilin B gene; HLA-A2402.
XX
OS Homo sapiens.
XX
PN JP2001245675-A.

XX
PD 11-SEP-2001.
XX
PF 25-DEC-2000; 2000JP-00393047.
XX
PR 28-DEC-1999; 99JP-00374322.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2001-610076/70.
XX
PT New peptides for recognizing cancer cells with tumor specific cytotoxic T
PT lymphocytes and for treating cancer.
XX
PS Claim 8; Page 2; 14pp; Japanese.
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CC The present invention describes peptides recognising cancer cells with
CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
CC the above mentioned sequences; and (4) peptides with one or more deleted,
CC substituted, added or inserted amino acid(s) of the above mentioned
CC sequences, particularly those having recognising property due to HLA-
CC A2402 binding CTL, especially having at least 5 amino acids, used for
CC medicine, particularly anticancer agents, derived from antitumour
CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
CC genes. The antitumour peptides have cytostatic activities. The peptides
CC are used for the treatment of cancer. The peptides cause activation of
CC CTL in cancer patients. The present sequence represents a peptide from
CC the present invention
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 30; DB 4; Length 13;
Best Local Similarity 30.8%; Pred. No. 2.2e+02;
Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFXXXXXXLXDXX 13
||::::::|:|::
Db 1 TFEYLQAFLEDYF 13

RESULT 4
AAG68083
ID AAG68083 standard; peptide; 13 AA.
XX
AC AAG68083;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antitumour peptide hck 503-515.
XX
KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
KW cyclophilin B gene; HLA-A2402.
XX
OS Homo sapiens.
XX
PN JP2001245675-A.
XX
PD 11-SEP-2001.
XX
PF 25-DEC-2000; 2000JP-00393047.
XX
PR 28-DEC-1999; 99JP-00374322.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2001-610076/70.
XX
PT New peptides for recognizing cancer cells with tumor specific cytotoxic T
PT lymphocytes and for treating cancer.
XX
PS Claim 8; Page 2; 14pp; Japanese.
XX
CC The present invention describes peptides recognising cancer cells with
CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
CC the above mentioned sequences; and (4) peptides with one or more deleted,
CC substituted, added or inserted amino acid(s) of the above mentioned
CC sequences, particularly those having recognising property due to HLA-
CC A2402 binding CTL, especially having at least 5 amino acids, used for
CC medicine, particularly anticancer agents, derived from antitumour
CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
CC genes. The antitumour peptides have cytostatic activities. The peptides
CC are used for the treatment of cancer. The peptides cause activation of
CC CTL in cancer patients. The present sequence represents a peptide from
CC the present invention
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 30; DB 4; Length 13;
Best Local Similarity 30.8%; Pred. No. 2.2e+02;
Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFXXXXXXLXDXX 13
||::::::|:|::
Db 1 TFEYIQSVLDDFY 13

RESULT 5
AAB73126
ID AAB73126 standard; peptide; 13 AA.
XX
AC AAB73126;
XX
DT 09-MAY-2001 (first entry)
XX
DE Tumour antigen peptide #10.
XX
KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS Homo sapiens.
XX
PN WO200111044-A1.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-JP005220.
XX
PR 05-AUG-1999; 99JP-00222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT polynucleotides encoding them for treatment of cancer.
XX
PS Claim 2; Page 46; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 30; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TFXXXXXXLXDXX 13
              |||||||||||||
Db          1 TFXXXXXXLXDXX 13
```

RESULT 6
AAB73147
ID AAB73147 standard; peptide; 13 AA.
XX
AC AAB73147;
XX
DT 09-MAY-2001 (first entry)
XX
DE Tumour antigen peptide #31.
XX
KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS Homo sapiens.
XX
PN WO200111044-A1.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-JP005220.
XX
PR 05-AUG-1999; 99JP-00222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT polynucleotides encoding them for treatment of cancer.
XX
PS Example 6; Page 36; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are.useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 30; DB 4; Length 13;
Best Local Similarity 30.8%; Pred. No. 2.2e+02;
Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          1 TFEYLQSFLEDFF 13
```

RESULT 7
AAB73145
ID AAB73145 standard; peptide; 13 AA.
XX
AC AAB73145;
XX
DT 09-MAY-2001 (first entry)
XX
DE Tumour antigen peptide #29.
XX
KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS Homo sapiens.
XX
PN WO200111044-A1.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-JP005220.
XX
PR 05-AUG-1999; 99JP-00222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT polynucleotides encoding them for treatment of cancer.
XX
PS Example 6; Page 36; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 30; DB 4; Length 13;
Best Local Similarity 30.8%; Pred. No. 2.2e+02;
Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          1 TFEYLQAFLEDYF 13
```

RESULT 8
AAB73148
ID AAB73148 standard; peptide; 13 AA.
XX
AC AAB73148;
XX
DT 09-MAY-2001 (first entry)
XX
DE Tumour antigen peptide #32.
XX
KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS Homo sapiens.
XX
PN WO200111044-A1.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-JP005220.
XX
PR 05-AUG-1999; 99JP-00222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT polynucleotides encoding them for treatment of cancer.
XX
PS Example 6; Page 36; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 30; DB 4; Length 13;
Best Local Similarity 30.8%; Pred. No. 2.2e+02;

```
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          1 TFEYLQSFLEDYF 13


RESULT 9
AAB73146
ID   AAB73146 standard; peptide; 13 AA.
XX
AC   AAB73146;
XX
DT   09-MAY-2001  (first entry)
XX
DE   Tumour antigen peptide #30.
XX
KW   Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS   Homo sapiens.
XX
PN   WO200111044-A1.
XX
PD   15-FEB-2001.
XX
PF   03-AUG-2000; 2000WO-JP005220.
XX
PR   05-AUG-1999;   99JP-00222101.
XX
PA   (ITOH/) ITOH K.
XX
PI   Itoh K;
XX
DR   WPI; 2001-191541/19.
XX
PT   Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT   polynucleotides encoding them for treatment of cancer.
XX
PS   Example 6; Page 36; 75pp; Japanese.
XX
CC   The present invention relates to peptides which are partial sequences of
CC   src/lck family proteins. The present sequence is one such peptide. The
CC   peptides are useful for producing vaccines for the treatment of cancer,
CC   including colon cancer and small-cell lung cancer
XX
SQ   Sequence 13 AA;

  Query Match             100.0%;  Score 30;  DB 4;  Length 13;
  Best Local Similarity   30.8%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          1 TFEYIQSFLEDYF 13


RESULT 10
AAB73151
ID   AAB73151 standard; peptide; 13 AA.
XX
AC   AAB73151;
XX
DT   09-MAY-2001  (first entry)
XX
DE   Tumour antigen peptide #35.
XX
KW   Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS   Homo sapiens.
XX
PN   WO200111044-A1.
XX
PD   15-FEB-2001.
XX
PF   03-AUG-2000; 2000WO-JP005220.
XX
PR   05-AUG-1999;   99JP-00222101.
XX
PA   (ITOH/) ITOH K.
XX
PI   Itoh K;
XX
DR   WPI; 2001-191541/19.
XX
PT   Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT   polynucleotides encoding them for treatment of cancer.
XX
PS   Example 6; Page 36; 75pp; Japanese.
XX
CC   The present invention relates to peptides which are partial sequences of
CC   src/lck family proteins. The present sequence is one such peptide. The
CC   peptides are useful for producing vaccines for the treatment of cancer,
CC   including colon cancer and small-cell lung cancer
XX
SQ   Sequence 13 AA;

  Query Match             100.0%;  Score 30;  DB 4;  Length 13;
  Best Local Similarity   30.8%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          1 TFEFLQSVLEDFY 13


RESULT 11
AAB73150
ID   AAB73150 standard; peptide; 13 AA.
XX
AC   AAB73150;
XX
DT   09-MAY-2001  (first entry)
XX
DE   Tumour antigen peptide #34.
XX
KW   Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS   Homo sapiens.
XX
PN   WO200111044-A1.
XX
PD   15-FEB-2001.
XX
PF   03-AUG-2000; 2000WO-JP005220.
XX
PR   05-AUG-1999;   99JP-00222101.
XX
PA   (ITOH/) ITOH K.
XX
PI   Itoh K;
XX
DR   WPI; 2001-191541/19.
XX
PT   Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT   polynucleotides encoding them for treatment of cancer.
XX
PS   Example 6; Page 36; 75pp; Japanese.
XX
CC   The present invention relates to peptides which are partial sequences of
CC   src/lck family proteins. The present sequence is one such peptide. The
CC   peptides are useful for producing vaccines for the treatment of cancer,
CC   including colon cancer and small-cell lung cancer
XX
SQ   Sequence 13 AA;

  Query Match             100.0%;  Score 30;  DB 4;  Length 13;
```

```
  Best Local Similarity   30.8%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::|:|::
Db          1 TFEYIQSVLDDFY 13


RESULT 12
AAB73149
ID   AAB73149 standard; peptide; 13 AA.
XX
AC   AAB73149;
XX
DT   09-MAY-2001  (first entry)
XX
DE   Tumour antigen peptide #33.
XX
KW   Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS   Homo sapiens.
XX
PN   WO200111044-A1.
XX
PD   15-FEB-2001.
XX
PF   03-AUG-2000; 2000WO-JP005220.
XX
PR   05-AUG-1999;   99JP-00222101.
XX
PA   (ITOH/) ITOH K.
XX
PI   Itoh K;
XX
DR   WPI; 2001-191541/19.
XX
PT   Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT   polynucleotides encoding them for treatment of cancer.
XX
PS   Example 6; Page 36; 75pp; Japanese.
XX
CC   The present invention relates to peptides which are partial sequences of
CC   src/lck family proteins. The present sequence is one such peptide. The
CC   peptides are useful for producing vaccines for the treatment of cancer,
CC   including colon cancer and small-cell lung cancer
XX
SQ   Sequence 13 AA;

  Query Match             100.0%;  Score 30;  DB 4;  Length 13;
  Best Local Similarity   30.8%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::|:|::
Db          1 TFDYLQSVLDDFY 13


RESULT 13
AAB73144
ID   AAB73144 standard; peptide; 13 AA.
XX
AC   AAB73144;
XX
DT   09-MAY-2001  (first entry)
XX
DE   Tumour antigen peptide #28.
XX
KW   Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS   Homo sapiens.
XX
PN   WO200111044-A1.
XX
PD   15-FEB-2001.
XX
PF   03-AUG-2000; 2000WO-JP005220.
XX
PR   05-AUG-1999;   99JP-00222101.
XX
PA   (ITOH/) ITOH K.
XX
PI   Itoh K;
XX
DR   WPI; 2001-191541/19.
XX
PT   Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT   polynucleotides encoding them for treatment of cancer.
XX
PS   Example 6; Page 36; 75pp; Japanese.
XX
CC   The present invention relates to peptides which are partial sequences of
CC   src/lck family proteins. The present sequence is one such peptide. The
CC   peptides are useful for producing vaccines for the treatment of cancer,
CC   including colon cancer and small-cell lung cancer
XX
SQ   Sequence 13 AA;

  Query Match             100.0%;  Score 30;  DB 4;  Length 13;
  Best Local Similarity   30.8%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::|:|::
Db          1 TFDYLRSVLEDFF 13


RESULT 14
ADM75342
ID   ADM75342 standard; peptide; 13 AA.
XX
AC   ADM75342;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Potential human MHC class II binding human Factor VIII peptide #562.
XX
KW   human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
KW   MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.
XX
OS   Homo sapiens.
XX
PN   WO2003087161-A1.
XX
PD   23-OCT-2003.
XX
PF   17-APR-2003; 2003WO-EP004063.
XX
PR   18-APR-2002; 2002EP-00008712.
PR   24-MAR-2003; 2003EP-00006554.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Jones T,  Baker M,  Carr FJ;
XX
DR   WPI; 2003-845307/78.
XX
PT   New modified human Factor VIII molecule being substantially non-
PT   immunogenic or less immunogenic than non-modified human Factor VIII,
PT   useful in preparing a composition for treating e.g., Gaucher's disease.
XX
PS   Disclosure; Fig 1; 68pp; English.
XX
CC   The invention relates to a novel modified human Factor VIII molecule. The
CC   modified human Factor VIII molecule being substantially non-immunogenic
CC   or less immunogenic than a non-modified human Factor VIII and having
CC   essentially the same biological specificity and activity when used in
```

CC vivo. The modified human Factor VIII molecule comprises specifically
CC altered amino acid residues compared with the non-modified parental
CC molecule, where the altered amino acid residues cause a reduction or an
CC elimination of one or more of the T-cell epitopes, which act in the
CC parental non-modified molecule as MHC class II binding ligands and
CC stimulate T-cells. The potential MHC class I1 binding activity peptide is
CC useful for the manufacture of the modified Factor VIII molecule or a
CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.
CC The modified Factor VIII molecule is useful in preparing a composition
CC for treating e.g., Gaucher's disease. This sequence represents a human
CC Factor VIII peptide with potential human MHC class II binding activity of
CC the invention.
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 30; DB 7; Length 13;
Best Local Similarity 30.8%; Pred. No. 2.2e+02;
Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          1 TFLTAQTLLMDLG 13
```

RESULT 15
ADD23350
ID ADD23350 standard; peptide; 14 AA.
XX
AC ADD23350;
XX
DT 15-JAN-2004 (first entry)
XX
DE Breast cancer membrane protein (BCMP) peptide SEQ ID NO:120.
XX
KW breast cancer; screening; diagnosis; breast cancer therapy;
KW breast cancer membrane protein; BCMP; cytostatic; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003087831-A2.
XX
PD 23-OCT-2003.
XX
PF 10-APR-2003; 2003WO-GB001559.
XX
PR 11-APR-2002; 2002GB-00008331.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Hudson LJ, Stamps AC, Terrett JA;
XX
DR WPI; 2003-845381/78.
XX
PT Screening, diagnosing and/or treating breast cancer by detecting a change
PT in expression or activity of a breast cancer membrane protein (BCMP)
PT polypeptide or encoding nucleic acid molecule.
XX
PS Claim 1; SEQ ID NO 120; 81pp; English.
XX
CC The present invention describes a method of screening for and/or
CC diagnosing breast cancer in a subject, and/or monitoring the
CC effectiveness of breast cancer therapy. The method comprises detecting
CC and/or quantifying in a biological sample obtained from the subject a
CC breast cancer membrane protein (BCMP) polypeptide and a nucleic acid
CC molecule. Also described: (1) an antibody, its functionally-active
CC fragment, derivative or analogue, that specifically binds to one or more
CC of the BCMP polypeptide; (2) a diagnostic kit comprising a capture
CC reagent specific for an BCMP polypeptide, reagents and instructions for
CC use; (3) a method for screening for anti-breast cancer agents that
CC interact with the BCMP polypeptide, comprising contacting the polypeptide
CC with a candidate agent, and determining whether or not the candidate
CC agent interacts with the polypeptide; (4) a method for screening for anti
CC -breast cancer agents that modulate the expression or activity of an BCMP
CC polypeptide or the nucleic acid molecule cited above, comprising
CC comparing the expression or activity of the polypeptide or nucleic acid
CC molecule, in the presence and absence of a candidate agent or in the
CC presence of a control agent, and determining whether the candidate agent
CC causes the expression or activity of the polypeptide or nucleic acid
CC molecule to change; and (5) an agent identified by the method of (3) or
CC (4), which interacts with the polypeptide or causes the expression or
CC activity of the polypeptide, or the expression of the nucleic acid
CC molecule to change. BCMPs have cytostatic activities, and can be used in
CC vaccines. The BCMP polypeptide, nucleic acid molecule, antibody, agent or
CC their derivatives, are useful in the manufacture of a medicament for the
CC treatment of breast cancer, where the composition is a vaccine. The
CC present sequence represents a BCMP peptide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 30; DB 7; Length 14;
Best Local Similarity 30.8%; Pred. No. 2.4e+02;
Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          2 TFNHLTTWLEDAR 14
```

RESULT 16
ABR63280
ID ABR63280 standard; peptide; 16 AA.
XX
AC ABR63280;
XX
DT 10-OCT-2003 (first entry)
XX
DE Peptide #10 used during reagent labeling.
XX
KW Isotope; intelligent data acquisition; reverse phase chromatography;
KW reagent labeling.
XX
OS Synthetic.
XX
PN WO2003027682-A2.
XX
PD 03-APR-2003.
XX
PF 27-SEP-2002; 2002WO-US030742.
XX
PR 27-SEP-2001; 2001US-0325335P.
XX
PA (PURD) PURDUE RES FOUND.
PA (REGN/) REGNIER F E.
PA (ZHAN/) ZHANG R.
PA (CHAK/) CHAKRABORTY A B.
XX
PI Regnier FE, Zhang R, Chakraborty AB;
XX
DR WPI; 2003-402986/38.
XX
PT Isotope coding agent useful in proteomics comprises functional group and
PT isotopic linker containing at least three heavy non-deuterium isotopes.
XX
PS Example 2; Page 66; 58pp; English.
XX
CC The present invention relates to an isotope coding agent, used in
CC proteomics for controlling or eliminating isotope effects during
CC fractionation of chemically equivalent but isotopically distinct
CC compounds. The isotope facilitates intelligent data acquisition, also the
CC isotope effect is reduced by eliminating deuterium from. The present
CC sequence represents a peptide used in the exemplification of the
CC specification, used to compare the resolution caused by reagents
XX
SQ Sequence 16 AA;

```
  Query Match             100.0%;  Score 30;  DB 6;  Length 16;
  Best Local Similarity   30.8%;  Pred. No. 2.9e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::::|:|::
Db          3 TFHADICTLPDTE 15


RESULT 17
ADD35548
ID   ADD35548 standard; peptide; 16 AA.
XX
AC   ADD35548;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Affinity marker peptide #1.
XX
KW   affinity tag; N-phenylene-thio urea; ICAT; isotope coded affinity tag.
XX
OS   Unidentified.
XX
PN   WO2003040093-A2.
XX
PD   15-MAY-2003.
XX
PF   30-OCT-2002; 2002WO-EP012106.
XX
PR   09-NOV-2001; 2001DE-01054753.
PR   29-JUL-2002; 2002DE-01034416.
XX
PA   (FARB ) BAYER AG.
XX
PI   Lerchen H,  Lockhoff O,  Immler D,  Siegmund H;
XX
DR   WPI; 2003-513527/48.
XX
PT   New, preferably isotopically labeled affinity tag compounds, useful in
PT   analyzing proteins by mass spectrometry, comprise affinity ligand,
PT   protein reactive group and acid-cleavable thiourea derivative linker.
XX
PS   Disclosure; Page 46; 65pp; German.
XX
CC   This invention describes novel affinity tag compounds (preferably
CC   isotopically labelled with carbon-13 and optionally nitrogen-15)
CC   consisting of an affinity ligand residue covalently bonded to a protein
CC   reactive group via a linking group. The linking group contains an acid-
CC   cleavable N-phenylene-thio urea derivative group. The use of the novel
CC   tag, in isotopically labelled form, is claimed as a reagent for the mass
CC   spectrometric analysis of proteins, especially for identifying proteins
CC   or protein functions in samples containing one or more proteins. The
CC   affinity tag can also be used to determine the relative protein
CC   expression levels in samples containing one or more proteins.
CC   Isotopically labelled tags are designated 'ICAT's' (isotope coded
CC   affinity tags). An acid-labile group can serve as a pre-determined
CC   cleavage site for acid-induced cleavage of the affinity label, e.g. to
CC   facilitate release on an affinity column to make the residue attached to
CC   the protein smaller and/or make the processing more efficient. The tags
CC   remaining on the protein fragments after acidolysis have a markedly
CC   reduced molecular weight and higher isotope density. The affinity tags
CC   also have higher solubility than prior art analogs. This sequence
CC   represents a marker peptide which is used in the method of the invention.
XX
SQ   Sequence 16 AA;

  Query Match             100.0%;  Score 30;  DB 7;  Length 16;
  Best Local Similarity   30.8%;  Pred. No. 2.9e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::::|:|::
Db          3 TFHADICTLPDTE 15


RESULT 18
AAO27568
ID   AAO27568 standard; peptide; 16 AA.
XX
AC   AAO27568;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Bovine BSA peptide fragment.
XX
KW   CA; peptide sequencing; mutation identification; carbonic anhydrase II;
KW   bovine serum albumin; BSA; ubiquitin; UB; superoxide dismutase; SOD.
XX
OS   Bos sp.
XX
PN   WO2003078584-A2.
XX
PD   25-SEP-2003.
XX
PF   11-MAR-2003; 2003WO-US007637.
XX
PR   11-MAR-2002; 2002US-0363647P.
XX
PA   (THER-) THERMO FINNIGAN LLC.
XX
PI   Maroto FM;
XX
DR   WPI; 2003-757000/71.
XX
PT   Method for identifying modifications in a polypeptide, based on
PT   sequencing peptides to define a tag and comparing this with candidate
PT   sequences.
XX
PS   Example; Fig 6; 0pp; English.
XX
CC   The invention relates to identifying a modification in a polypeptide by a
CC   method involving peptide sequencing. The method involves (a) identifying
CC   a set of one or more candidate sequences including sequence information
CC   potentially corresponding to an unmodified variant of the polypeptide of
CC   known sequence; (b) sequencing at least a portion of one or more peptides
CC   derived from the polypeptide to identify a sequence tag in a peptide; (c)
CC   comparing the identified sequence tag with sequence information for the
CC   set of candidate sequences to identify a candidate sequence containing
CC   the identified sequence tag; and (d) calculating the difference between
CC   at least one subsequence mass of the peptide and at least one subsequence
CC   mass of the identified candidate sequence. Modifications that may be
CC   identified include mutations, additions, deletions, and posttranslational
CC   modifications. Possible sample materials include cells, body fluids, and
CC   environmental samples such as soil, water and air samples. Sequences
CC   AAO27541-603 represent peptide fragments from bovine carbonic anhydrase
CC   (CA) II, bovine serum albumin (BSA), ubiquitin (UB) and superoxide
CC   dismutase (SOD), identified in an exemplary experiment
XX
SQ   Sequence 16 AA;

  Query Match             100.0%;  Score 30;  DB 7;  Length 16;
  Best Local Similarity   30.8%;  Pred. No. 2.9e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::::|:|::
Db          3 TFHADICTLPDTE 15


RESULT 19
AEA78908
ID   AEA78908 standard; peptide; 16 AA.
XX
AC   AEA78908;
XX
DT   11-AUG-2005  (first entry)
```

XX
DE Bovine Serum Albumin indexed peptide database peptide #124.
XX
KW mass spectrometry; peptide index; protein identification;
KW protein quantitation; protease; high-resolution mass spectrometry;
KW proteomics; genomics; bioinformatics; Bovine Serum Albumin.
XX
OS Bos sp.
XX
PN WO2003054549-A2.
XX
PD 03-JUL-2003.
XX
PF 09-DEC-2002; 2002WO-GB005571.
XX
PR 08-DEC-2001; 2001US-0340460P.
PR 14-MAR-2002; 2002US-0364847P.
XX
PA (MICR-) MICROMASS LTD.
XX
PI Geromanos S, Dongre A, Opiteck G, Silva J;
XX
DR WPI; 2003-569290/53.
XX
PT A method of mass spectrometry, useful in protein identification and
PT quantitation, by mass analyzing the first molecules in the first mixture
PT and accurately determining the mass to charge ratio of the first
PT molecules in the first mixture.
XX
PS Disclosure; Fig 8B; 123pp; English.
XX
CC The invention relates to a novel method of mass spectrometry. The method
CC comprises mass analysing the first molecules in a first mixture and
CC accurately determining the mass to charge ratio of the first molecules in
CC the first mixture. The invention further relates to: generating an index
CC for use in identifying molecules of biological origin by mass
CC spectrometry by accurately determining the masses or mass to charge
CC ratios of molecules comprising peptides resulting from the digestion or
CC fragmentation of a polypeptide or protein; determining a first physico-
CC chemical property other than mass or mass to charge ratio of the
CC molecules comprising peptides; and optionally determining a second,
CC third, fourth and/or fifth physico-chemical property of the molecules
CC comprising peptides; and a mass spectrometer comprising a mass analyser
CC for accurately determining the mass to charge ratio of the first
CC molecules, and means for identifying the first molecules of the basis of
CC at least the first physico-chemical property and the accurately
CC determined mass to charge ratio of the first molecules and optionally on
CC the basis of the second, third, fourth and/or fifth physico-chemical
CC property. The method and spectrometer are useful in protein
CC identification, protein quantitation, proteases, high-resolution mass
CC spectrometry, proteomics, genomics and bioinformatics. This sequence
CC represents a peptide from an indexed peptide database created by the
CC novel mass spectrometry method of the invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 30; DB 7; Length 16;
Best Local Similarity 30.8%; Pred. No. 2.9e+02;
Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFXXXXXXLXDXX 13
||:::::|:|::
Db 3 TFHADICTLPDTE 15

RESULT 20
AEA79083
ID AEA79083 standard; peptide; 16 AA.
XX
AC AEA79083;
XX
DT 11-AUG-2005 (first entry)
XX
DE Bovine Serum Albumin indexed peptide database peptide #299.
XX
KW mass spectrometry; peptide index; protein identification;
KW protein quantitation; protease; high-resolution mass spectrometry;
KW proteomics; genomics; bioinformatics; Bovine Serum Albumin.
XX
OS Bos sp.
XX
PN WO2003054549-A2.
XX
PD 03-JUL-2003.
XX
PF 09-DEC-2002; 2002WO-GB005571.
XX
PR 08-DEC-2001; 2001US-0340460P.
PR 14-MAR-2002; 2002US-0364847P.
XX
PA (MICR-) MICROMASS LTD.
XX
PI Geromanos S, Dongre A, Opiteck G, Silva J;
XX
DR WPI; 2003-569290/53.
XX
PT A method of mass spectrometry, useful in protein identification and
PT quantitation, by mass analyzing the first molecules in the first mixture
PT and accurately determining the mass to charge ratio of the first
PT molecules in the first mixture.
XX
PS Disclosure; Fig 9M; 123pp; English.
XX
CC The invention relates to a novel method of mass spectrometry. The method
CC comprises mass analysing the first molecules in a first mixture and
CC accurately determining the mass to charge ratio of the first molecules in
CC the first mixture. The invention further relates to: generating an index
CC for use in identifying molecules of biological origin by mass
CC spectrometry by accurately determining the masses or mass to charge
CC ratios of molecules comprising peptides resulting from the digestion or
CC fragmentation of a polypeptide or protein; determining a first physico-
CC chemical property other than mass or mass to charge ratio of the
CC molecules comprising peptides; and optionally determining a second,
CC third, fourth and/or fifth physico-chemical property of the molecules
CC comprising peptides; and a mass spectrometer comprising a mass analyser
CC for accurately determining the mass to charge ratio of the first
CC molecules, and means for identifying the first molecules of the basis of
CC at least the first physico-chemical property and the accurately
CC determined mass to charge ratio of the first molecules and optionally on
CC the basis of the second, third, fourth and/or fifth physico-chemical
CC property. The method and spectrometer are useful in protein
CC identification, protein quantitation, proteases, high-resolution mass
CC spectrometry, proteomics, genomics and bioinformatics. This sequence
CC represents a peptide from an indexed peptide database created by the
CC novel mass spectrometry method of the invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 30; DB 7; Length 16;
Best Local Similarity 30.8%; Pred. No. 2.9e+02;
Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFXXXXXXLXDXX 13
||:::::|:|::
Db 3 TFHADICTLPDTE 15

RESULT 21
AEA78834
ID AEA78834 standard; peptide; 16 AA.
XX
AC AEA78834;
XX
DT 11-AUG-2005 (first entry)
XX
DE Bovine Serum Albumin indexed peptide database peptide #49.

XX
KW mass spectrometry; peptide index; protein identification;
KW protein quantitation; protease; high-resolution mass spectrometry;
KW proteomics; genomics; bioinformatics; Bovine Serum Albumin.
XX
OS Bos sp.
XX
PN WO2003054549-A2.
XX
PD 03-JUL-2003.
XX
PF 09-DEC-2002; 2002WO-GB005571.
XX
PR 08-DEC-2001; 2001US-0340460P.
PR 14-MAR-2002; 2002US-0364847P.
XX
PA (MICR-) MICROMASS LTD.
XX
PI Geromanos S, Dongre A, Opiteck G, Silva J;
XX
DR WPI; 2003-569290/53.
XX
PT A method of mass spectrometry, useful in protein identification and
PT quantitation, by mass analyzing the first molecules in the first mixture
PT and accurately determining the mass to charge ratio of the first
PT molecules in the first mixture.
XX
PS Disclosure; Fig 7B; 123pp; English.
XX
CC The invention relates to a novel method of mass spectrometry. The method
CC comprises mass analysing the first molecules in a first mixture and
CC accurately determining the mass to charge ratio of the first molecules in
CC the first mixture. The invention further relates to: generating an index
CC for use in identifying molecules of biological origin by mass
CC spectrometry by accurately determining the masses or mass to charge
CC ratios of molecules comprising peptides resulting from the digestion or
CC fragmentation of a polypeptide or protein; determining a first physico-
CC chemical property other than mass or mass to charge ratio of the
CC molecules comprising peptides; and optionally determining a second,
CC third, fourth and/or fifth physico-chemical property of the molecules
CC comprising peptides; and a mass spectrometer comprising a mass analyser
CC for accurately determining the mass to charge ratio of the first
CC molecules, and means for identifying the first molecules of the basis of
CC at least the first physico-chemical property and the accurately
CC determined mass to charge ratio of the first molecules and optionally on
CC the basis of the second, third, fourth and/or fifth physico-chemical
CC property. The method and spectrometer are useful in protein
CC identification, protein quantitation, proteases, high-resolution mass
CC spectrometry, proteomics, genomics and bioinformatics. This sequence
CC represents a peptide from an indexed peptide database created by the
CC novel mass spectrometry method of the invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 30; DB 7; Length 16;
Best Local Similarity 30.8%; Pred. No. 2.9e+02;
Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFXXXXXXLXDXX 13
||:::::|:|::
Db 3 TFHADICTLPDTE 15

RESULT 22
ADH11188
ID ADH11188 standard; peptide; 16 AA.
XX
AC ADH11188;
XX
DT 11-MAR-2004 (first entry)
XX
DE MALDI-MS tryptic peptide #28.
XX
KW biopolymer; proteome; peptidome.
XX
OS Unidentified.
XX
PN WO2003096021-A1.
XX
PD 20-NOV-2003.
XX
PF 09-MAY-2003; 2003WO-EP004878.
XX
PR 10-MAY-2002; 2002DE-01020804.
PR 10-MAY-2002; 2002EP-00010555.
XX
PA (PROT-) PROTEOME FACTORY AG.
XX
PI Scheler C, Essmann F, Thies S;
XX
DR WPI; 2004-034708/03.
XX
PT Analyzing complex mixtures of polypeptides, useful e.g. for proteome
PT analysis, by fragmentation, immobilization, selective release, labeling
PT and characterization.
XX
PS Example; Fig 2; 64pp; German.
XX
CC This invention describes a novel method of analysing complex mixtures of
CC biopolymers that contain peptide bonds by fragmentation, immobilisation,
CC selective release of bound fragments, labelling, separation of labelled
CC fragments according to physicochemical properties and detecting the
CC label. The biopolymers are peptides, proteins, peptide nucleic acids
CC (PNA), lipo- or glyco-peptides or -proteins, or their derivatives; and
CC the binding fragments are amino acids, (lipo- or glyco-)peptides, PNA or
CC their derivatives. Typical enzymes for used in the method are
CC (chymo)trypsin, caspase and factor Xa, and typical chemical cleaving
CC reagents are hydrochloric and formic acids and cyanogen bromide. Agents
CC for coupling to the linker depend on the nature of the terminal amino
CC acid, e.g. thiols are reacted through dithiols; Glu and Asp are reacted
CC with a carbodimide; Arg is reacted with glyoxal and Met is converted to
CC homoserine lactone with cyanogen bromide and this coupled to amino in the
CC linker. Reagents for blocking specific monomers are e.g. acid anhydrides
CC or chlorides, aldehydes etc., most preferably acetyl chloride or
CC citraconic anhydride, and the most preferred linker is 1,4-di-
CC isothiocyanatobenzene. The method is used in proteome and peptidome
CC analysis. The method allows a significant reduction in the number of
CC components that need to be characterised (and thus saves time and money),
CC without a significant loss of information. ADH11161-ADH11216 represent
CC tryptic peptides used in the method of the invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 30; DB 8; Length 16;
Best Local Similarity 30.8%; Pred. No. 2.9e+02;
Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFXXXXXXLXDXX 13
||:::::|:|::
Db 3 TFHADICTLPDTE 15

RESULT 23
ADJ78034
ID ADJ78034 standard; peptide; 16 AA.
XX
AC ADJ78034;
XX
DT 06-MAY-2004 (first entry)
XX
DE Peptide, SEQ ID 53, for analysing cysteine-containing protein expression.
XX
KW Protein expression analysis; protease cleavage site.
XX
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Modified-site 9
FT /note= "Peptag-modified cysteine residue"
XX
PN WO2004013636-A2.
XX
PD 12-FEB-2004.
XX
PF 28-JUL-2003; 2003WO-IB003863.
XX
PR 01-AUG-2002; 2002US-00212628.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Haynes P, Wei J, Yates J, Andon N;
XX
DR WPI; 2004-169365/16.
XX
PT Novel reagent for simultaneously identifying and determining levels of
PT expression of cysteine-containing proteins in normal and perturbed cells.
XX
PS Example 2; SEQ ID NO 53; 183pp; English.
XX
CC The present invention relates to reagent compounds (C1) for identifying
CC and determining the levels of expression of cysteine-containing proteins
CC in normal and perturbed cells. The reagent compounds have the formula:
CC immobilisation site-cleavage site-link, where the immobilisation site is
CC selected from the group consisting of an epitope tag, a linker to a solid
CC surface, a metal chelating site, and a magnetic site, or a combination
CC thereof, and the cleavage site is selected from the group consisting of a
CC protease cleavage site (ADJ77982), a photocleavable linker, a restriction
CC site, a chemical cleavage site and a thermal cleavage site, or a
CC combination thereof. The present sequence was used to illustrate the
CC invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 30; DB 8; Length 16;
Best Local Similarity 38.5%; Pred. No. 2.9e+02;
Matches 5; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFXXXXXXLXDXX 13
||:::::|:|:|::
Db 3 TFHADIXTLPDTE 15

RESULT 24
ADJ78050
ID ADJ78050 standard; peptide; 16 AA.
XX
AC ADJ78050;
XX
DT 06-MAY-2004 (first entry)
XX
DE Peptide, SEQ ID 69, for analysing cysteine-containing protein expression.
XX
KW Protein expression analysis; protease cleavage site; bovine; albumin.
XX
OS Bos taurus.
XX
FH Key Location/Qualifiers
FT Modified-site 9
FT /note= "Peptag-modified cysteine residue"
XX
PN WO2004013636-A2.
XX
PD 12-FEB-2004.
XX
PF 28-JUL-2003; 2003WO-IB003863.
XX
PR 01-AUG-2002; 2002US-00212628.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Haynes P, Wei J, Yates J, Andon N;
XX
DR WPI; 2004-169365/16.
XX
PT Novel reagent for simultaneously identifying and determining levels of
PT expression of cysteine-containing proteins in normal and perturbed cells.
XX
PS Example 11; SEQ ID NO 69; 183pp; English.
XX
CC The present invention relates to reagent compounds (C1) for identifying
CC and determining the levels of expression of cysteine-containing proteins
CC in normal and perturbed cells. The reagent compounds have the formula:
CC immobilisation site-cleavage site-link, where the immobilisation site is
CC selected from the group consisting of an epitope tag, a linker to a solid
CC surface, a metal chelating site, and a magnetic site, or a combination
CC thereof, and the cleavage site is selected from the group consisting of a
CC protease cleavage site (ADJ77982), a photocleavable linker, a restriction
CC site, a chemical cleavage site and a thermal cleavage site, or a
CC combination thereof. The present bovine albumin peptide was used to
CC illustrate the invention.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 30; DB 8; Length 16;
Best Local Similarity 30.8%; Pred. No. 2.9e+02;
Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFXXXXXXLXDXX 13
||::::::|:|::
Db 3 TFHADICTLPDTE 15

RESULT 25
ADZ86402
ID ADZ86402 standard; peptide; 16 AA.
XX
AC ADZ86402;
XX
DT 14-JUL-2005 (first entry)
XX
DE Protein quantitative analysis method related tagged BSA peptide #4.
XX
KW quantitative analysis; HPLC; electrospray ionization; mass spectroscopy;
KW proteomics.
XX
OS Unidentified.
XX
PN JP2005121380-A.
XX
PD 12-MAY-2005.
XX
PF 14-OCT-2003; 2003JP-00353574.
XX
PR 14-OCT-2003; 2003JP-00353574.
XX
PA (SUMU) SUMITOMO SEIYAKU KK.
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
DR WPI; 2005-349932/36.
XX
PT Quantitative analysis of protein, by hydrolyzing test sample and control
PT in water containing labeled oxygen, mixing hydrolyzed substance and
PT subjecting liquid mixture to liquid chromatography/electrospray
PT ionization-mass spectrometry.
XX
PS Example 3; Page; 13pp; Japanese.
XX
CC The invention relates to a novel method for the quantitative analysis of
CC a protein. The method involves hydrolyzing a first test sample in water
CC containing 90% or more of 18-O (an isotopic labeling element),
CC hydrolyzing a second sample in water containing 90% or more of 16-O,
CC mixing the hydrolyzed substance of the first and second samples, and

```
CC   carrying out quantitative analysis of the liquid mixture by liquid
CC   chromatography/electrospray ionization-mass spectrometry (LC/ESI-MS). The
CC   method enables the quantification of proteins in large-scale proteomics,
CC   and trace amount of proteins present in an organism can be quantified
CC   accurately and efficiently. This sequence represents a peptide fragment
CC   used in the protein quantitative analysis method of the invention.
XX
SQ   Sequence 16 AA;

  Query Match             100.0%;  Score 30;  DB 9;  Length 16;
  Best Local Similarity   30.8%;  Pred. No. 2.9e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          3 TFHADICTLPDTE 15


RESULT 26
ADD35547
ID   ADD35547 standard; peptide; 17 AA.
XX
AC   ADD35547;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Bovine albumin fragment.
XX
KW   affinity tag; N-phenylene-thio urea; ICAT; isotope coded affinity tag;
KW   bovine; albumin.
XX
OS   Bos taurus.
XX
PN   WO2003040093-A2.
XX
PD   15-MAY-2003.
XX
PF   30-OCT-2002; 2002WO-EP012106.
XX
PR   09-NOV-2001; 2001DE-01054753.
PR   29-JUL-2002; 2002DE-01034416.
XX
PA   (FARB ) BAYER AG.
XX
PI   Lerchen H,  Lockhoff O,  Immler D,  Siegmund H;
XX
DR   WPI; 2003-513527/48.
XX
PT   New, preferably isotopically labeled affinity tag compounds, useful in
PT   analyzing proteins by mass spectrometry, comprise affinity ligand,
PT   protein reactive group and acid-cleavable thiourea derivative linker.
XX
PS   Disclosure; Page 45; 65pp; German.
XX
CC   This invention describes novel affinity tag compounds (preferably
CC   isotopically labelled with carbon-13 and optionally nitrogen-15)
CC   consisting of an affinity ligand residue covalently bonded to a protein
CC   reactive group via a linking group. The linking group contains an acid-
CC   cleavable N-phenylene-thio urea derivative group. The use of the novel
CC   tag, in isotopically labelled form, is claimed as a reagent for the mass
CC   spectrometric analysis of proteins, especially for identifying proteins
CC   or protein functions in samples containing one or more proteins. The
CC   affinity tag can also be used to determine the relative protein
CC   expression levels in samples containing one or more proteins.
CC   Isotopically labelled tags are designated 'ICAT's' (isotope coded
CC   affinity tags). An acid-labile group can serve as a pre-determined
CC   cleavage site for acid-induced cleavage of the affinity label, e.g. to
CC   facilitate release on an affinity column to make the residue attached to
CC   the protein smaller and/or make the processing more efficient. The tags
CC   remaining on the protein fragments after acidolysis have a markedly
CC   reduced molecular weight and higher isotope density. The affinity tags
CC   also have higher solubility than prior art analogs. This sequence
CC   represents a fragment of bovine albumin which is used in the method of
CC   the invention.
XX
SQ   Sequence 17 AA;

  Query Match             100.0%;  Score 30;  DB 7;  Length 17;
  Best Local Similarity   30.8%;  Pred. No. 3.1e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          3 TFHADICTLPDTE 15


RESULT 27
AAW65655
ID   AAW65655 standard; peptide; 18 AA.
XX
AC   AAW65655;
XX
DT   23-OCT-1998  (first entry)
XX
DE   Peptide #14 derived from the CKD of the insulin receptor beta chain.
XX
KW   Insulin receptor beta chain; cytoplasmic kinase domain; modulator;
KW   insulin activation; glucose; conformation; diabetes; CKD.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9832017-A2.
XX
PD   23-JUL-1998.
XX
PF   15-JAN-1998;   98WO-US000801.
XX
PR   15-JAN-1997;   97US-00784854.
PR   15-JAN-1997;   97US-00784855.
PR   15-JAN-1997;   97US-00784857.
PR   27-MAR-1997;   97US-00825269.
PR   21-AUG-1997;   97US-00916088.
XX
PA   (TERR-) TERRAPIN TECHNOLOGIES INC.
XX
PI   Kauvar LM,  Sportsman R,  Villar HO,  Spevak WR,  Kohanski RA;
PI   Satyam A,  Koehler R;
XX
DR   WPI; 1998-414253/35.
XX
PT   Identifying materials which modulate insulin receptor kinase activity -
PT   useful for screening for compounds which can enhance glucose uptake in
PT   cells or lower blood glucose levels.
XX
PS   Example 7; Page 38; 77pp; English.
XX
CC   The invention relates to methods for identification of compounds which
CC   interact with the insulin receptor beta chain at specific loci; and/or
CC   alter the conformation of the cytoplasmic kinase domain (CKD). In
CC   addition the invention relates to simple non-peptide compounds that
CC   behave as agonists for the insulin receptor and enhance the effect of
CC   insulin on this receptor. The processes may be used for identification of
CC   compounds which can stimulate the uptake of glucose in cells or lower
CC   blood glucose levels. The identified compounds can be used in the
CC   treatment of, e.g., diabetes. In order to identify additional regions of
CC   the CKD to which a compound (TER16998) binds, a series of 14 peptides
CC   ("ryan peptides", AAW65642-55) were synthesised. These peptides were
CC   chosen to correspond to distinct surface elements of the CKD made evident
CC   by the X-ray structure. Collectively, these 14 peptides cover 85 per cent
CC   of the surface-exposed residues. These peptides were tested for their
CC   ability to inhibit the activation of insulin receptor by TER16998
XX
SQ   Sequence 18 AA;

  Query Match             100.0%;  Score 30;  DB 2;  Length 18;
```

```
  Best Local Similarity   30.8%;  Pred. No. 3.3e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          3 TFLEIVNLLKDDL 15


RESULT 28
ABG95997
ID   ABG95997 standard; peptide; 18 AA.
XX
AC   ABG95997;
XX
DT   11-DEC-2002  (first entry)
XX
DE   Cysteine-containing peptide isolated from BSA, #17.
XX
KW   Rabbit; bovine; analytical reagent; trifunctional; peptide mixture;
KW   enrichment; immobilisation site; cleavage site; link; epitope tag;
KW   protease; cysteine-containing; perturbed cell; mass spectrometry;
KW   peptide tag; BSA; bovine serum albumin; PEPTag; APEPTag; IPEPTag;
KW   affinity peptide encoded tag; immobilised peptide encoded tag; chicken;
KW   beta-lactogobulin; GAPDH; glyceraldehyde-3-phosphate dehydrogenase;
KW   a-lactalbumin; ovalbumin; yeast.
XX
OS   Bos taurus.
XX
PN   WO200259144-A2.
XX
PD   01-AUG-2002.
XX
PF   25-JAN-2002; 2002WO-US002487.
XX
PR   26-JAN-2001; 2001US-0264576P.
PR   13-JUL-2001; 2001US-0305232P.
XX
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI   Haynes P,  Wei J,  Yates J,  Andon N;
XX
DR   WPI; 2002-599760/64.
XX
PT   Novel trifunctional synthetic reagents for labeling peptides at specific
PT   amino acid residue and selectively enriching only those peptides
PT   containing labeled amino acid, useful for proteomic analysis.
XX
PS   Disclosure; Page 44; 79pp; English.
XX
CC   The invention discloses analytical reagents (e.g. trifunctional synthetic
CC   reagents) which can be used for reducing the complexity of peptide
CC   mixtures. The method labels peptides at a specific amino acid residue and
CC   then selectively enriches only those peptides containing the labelled
CC   amino acid. The compound have the formula of immobilisation site-cleavage
CC   site-link. The immobilisation site is chosen from an epitope tag, a
CC   linker to a solid surface, a metal chelating site, a magnetic site and a
CC   specific oligonucleotide sequence, or their combination, the cleavage
CC   site is chosen from a protease cleavage site, a photocleavable linker, a
CC   restriction enzyme cleavage site, a chemical cleavage site and a thermal
CC   cleavage site, or their combination and the link is chosen from an amino
CC   acid reactive site and a mass variance site, or their combination. The
CC   compounds are useful for simultaneously identifying and determining the
CC   levels of expression of cysteine-containing proteins in normal and
CC   perturbed cells. The advantage is that these reagents allow rapid and
CC   quantitative analysis of proteins or protein function in mixtures of
CC   proteins. By preparing the reagent in two forms with detectably different
CC   masses, accurate relative quantification of peptide amounts using mass
CC   spectrometry, can be achieved. The sequences given in ABG95935-ABG96244
CC   are examples of the peptide tags used to isolate cysteine-containing
CC   proteins, the target sequences tested and the peptides isolated using the
CC   peptide tags
XX
SQ   Sequence 18 AA;

  Query Match             100.0%;  Score 30;  DB 5;  Length 18;
  Best Local Similarity   30.8%;  Pred. No. 3.3e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          4 TFHADICTLPDTE 16


RESULT 29
ADV95854
ID   ADV95854 standard; peptide; 18 AA.
XX
AC   ADV95854;
XX
DT   10-MAR-2005  (first entry)
XX
DE   Bovine serum albumin peptide fragment #28.
XX
KW   arthritis; antiarthritic; antiinflammatory; immunosuppressive;
KW   musculoskeletal disease; degeneration; bovine serum albumin.
XX
OS   Bos taurus.
XX
PN   WO2004110475-A1.
XX
PD   23-DEC-2004.
XX
PF   17-JUN-2004; 2004WO-AU000788.
XX
PR   17-JUN-2003; 2003AU-00903037.
XX
PA   (NUTR-) INST NUTRACEUTICAL RES PTY LTD.
XX
PI   Ghosh P;
XX
DR   WPI; 2005-039981/04.
XX
PT   Pharmaceutical composition for treating or preventing arthritis or other
PT   degenerative disease in an individual, comprises a polypeptide comprising
PT   a collagen type IX alpha 1 chain NC4 domain.
XX
PS   Disclosure; Fig 5; 92pp; English.
XX
CC   This invention describes a novel pharmaceutical composition for treating
CC   or preventing arthritis or other degenerative disease which comprises a
CC   polypeptide a collagen type IX alpha 1 chain NC4 domain or a biologically
CC   active fragment having antiarthritic, antiinflammatory and
CC   immunosuppressive activity in combination with a carrier. The invention
CC   describes two methods for recovering a polypeptide having anti-arthritic
CC   or anti-inflammatory activity. The first method comprises isolating a
CC   mixture comprising a GAG-peptide and a polypeptide having a molecular
CC   weight of less than 30000 Da by autolysis from connective tissue,
CC   separating the GAG-peptide from the polypeptide, and recovering the
CC   polypeptide. The second method comprises incubating connective tissue in
CC   an autolysis medium that provides a buffered pH range of 2.5-8.5 for a
CC   time and under conditions sufficient to release a GAG-peptide and a
CC   polypeptide having a molecular weight of less than 30000 Da, recovering a
CC   mixture comprising the GAG-peptide and polypeptide from the autolysis
CC   medium, separating the polypeptide from the GAG-peptide, and recovering
CC   the polypeptide having a molecular weight of less than 30000 Da. The
CC   recovered anti-arthritic or anti-inflammatory polypeptides are useful for
CC   inducing cartilage formation or for preparing a medicament for the
CC   treatment or prevention of arthritis or other musculoskeletal
CC   degenerative condition or for tolerizing an individual to at least one
CC   antigenic component of cartilage. This sequence represents a fragment of
CC   bovine serum albumin.
XX
SQ   Sequence 18 AA;

  Query Match             100.0%;  Score 30;  DB 9;  Length 18;
  Best Local Similarity   30.8%;  Pred. No. 3.3e+02;
```

Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          4 TFHADICTLPDTE 16
```

RESULT 30
AEA78835
ID AEA78835 standard; peptide; 19 AA.
XX
AC AEA78835;
XX
DT 11-AUG-2005 (first entry)
XX
DE Bovine Serum Albumin indexed peptide database peptide #50.
XX
KW mass spectrometry; peptide index; protein identification;
KW protein quantitation; protease; high-resolution mass spectrometry;
KW proteomics; genomics; bioinformatics; Bovine Serum Albumin.
XX
OS Bos sp.
XX
PN WO2003054549-A2.
XX
PD 03-JUL-2003.
XX
PF 09-DEC-2002; 2002WO-GB005571.
XX
PR 08-DEC-2001; 2001US-0340460P.
PR 14-MAR-2002; 2002US-0364847P.
XX
PA (MICR-) MICROMASS LTD.
XX
PI Geromanos S, Dongre A, Opiteck G, Silva J;
XX
DR WPI; 2003-569290/53.
XX
PT A method of mass spectrometry, useful in protein identification and
PT quantitation, by mass analyzing the first molecules in the first mixture
PT and accurately determining the mass to charge ratio of the first
PT molecules in the first mixture.
XX
PS Disclosure; Fig 7B; 123pp; English.
XX
CC The invention relates to a novel method of mass spectrometry. The method
CC comprises mass analysing the first molecules in a first mixture and
CC accurately determining the mass to charge ratio of the first molecules in
CC the first mixture. The invention further relates to: generating an index
CC for use in identifying molecules of biological origin by mass
CC spectrometry by accurately determining the masses or mass to charge
CC ratios of molecules comprising peptides resulting from the digestion or
CC fragmentation of a polypeptide or protein; determining a first physico-
CC chemical property other than mass or mass to charge ratio of the
CC molecules comprising peptides; and optionally determining a second,
CC third, fourth and/or fifth physico-chemical property of the molecules
CC comprising peptides; and a mass spectrometer comprising a mass analyser
CC for accurately determining the mass to charge ratio of the first
CC molecules, and means for identifying the first molecules of the basis of
CC at least the first physico-chemical property and the accurately
CC determined mass to charge ratio of the first molecules and optionally on
CC the basis of the second, third, fourth and/or fifth physico-chemical
CC property. The method and spectrometer are useful in protein
CC identification, protein quantitation, proteases, high-resolution mass
CC spectrometry, proteomics, genomics and bioinformatics. This sequence
CC represents a peptide from an indexed peptide database created by the
CC novel mass spectrometry method of the invention.
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 30; DB 7; Length 19;
Best Local Similarity 30.8%; Pred. No. 3.6e+02;
Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          3 TFHADICTLPDTE 15
```

Search completed: June 29, 2006, 09:51:06
Job time : 201 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 09:47:59 ; Search time 295 Seconds
(without alignments)
40.763 Million cell updates/sec

Title: US-10-062-257A-10
Perfect score: 30
Sequence: 1 TFXXXXXXLXDXX 13

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	30	100.0	25	2	Q7YXI3_9BILA	Q7yxi3 ancylostoma
2	30	100.0	27	1	SECR_BOVIN	P63296 bos taurus
3	30	100.0	27	1	SECR_CAVPO	P63297 cavia porce
4	30	100.0	27	1	SECR_SHEEP	P31299 ovis aries
5	30	100.0	27	2	Q6JDH7_CANFA	Q6jdh7 canis famil
6	30	100.0	27	2	Q900E5_9HIV1	Q900e5 human immun
7	30	100.0	31	2	Q4S2T4_TETNG	Q4s2t4 tetraodon n
8	30	100.0	33	2	Q9GYZ8_TRYCR	Q9gyz8 trypanosoma
9	30	100.0	36	2	Q9H3W9_HUMAN	Q9h3w9 homo sapien
10	30	100.0	38	2	Q2KKH4_9BILA	Q2kkh4 trichostron
11	30	100.0	38	2	Q3YN35_BACTK	Q3yn35 bacillus th
12	30	100.0	39	2	Q8DT72_STRMU	Q8dt72 streptococc
13	30	100.0	42	2	Q3WGH1_9ACTO	Q3wgh1 frankia sp.
14	30	100.0	43	2	O80797_ARATH	O80797 arabidopsis
15	30	100.0	43	2	Q87GK5_VIBPA	Q87gk5 vibrio para
16	30	100.0	45	2	Q8J052_9EURO	Q8j052 penicillium
17	30	100.0	45	2	Q8J160_9EURO	Q8j160 penicillium
18	30	100.0	45	2	Q8J161_9EURO	Q8j161 penicillium
19	30	100.0	45	2	Q8J162_9EURO	Q8j162 penicillium
20	30	100.0	45	2	Q8J163_9EURO	Q8j163 penicillium
21	30	100.0	45	2	Q8J164_9EURO	Q8j164 eupenicilli
22	30	100.0	45	2	Q8J165_9EURO	Q8j165 penicillium
23	30	100.0	45	2	Q58MQ3_9CAUD	Q58mq3 cyanophage
24	30	100.0	45	2	Q3JLT1_BURP1	Q3jlt1 burkholderi
25	30	100.0	46	2	Q91FG1_IRV6	Q91fg1 chilo iride
26	30	100.0	47	2	Q3IBR9_9BACT	Q3ibr9 uncultured
27	30	100.0	49	2	Q8MJA7_MACMU	Q8mja7 macaca mula
28	30	100.0	49	2	Q87QM2_VIBPA	Q87qm2 vibrio para
29	30	100.0	50	2	Q7UH49_RHOBA	Q7uh49 rhodopirell
30	30	100.0	54	2	Q4N2A0_THEPA	Q4n2a0 theileria p
31	30	100.0	56	2	Q5U3C6_BRARE	Q5u3c6 brachydanio
32	30	100.0	57	2	Q5VZE0_HUMAN	Q5vze0 homo sapien
33	30	100.0	60	2	Q3DCJ3_STRAG	Q3dcj3 streptococc
34	30	100.0	60	2	Q3DP28_STRAG	Q3dp28 streptococc
35	30	100.0	60	2	Q7VAG3_PROMA	Q7vag3 prochloroco
36	30	100.0	60	2	Q8RBV5_THETN	Q8rbv5 thermoanaer
37	30	100.0	60	2	Q4KSD4_9VIRU	Q4ksd4 orange-spot
38	30	100.0	60	2	Q5YF66_9VIRU	Q5yf66 rock bream
39	30	100.0	61	2	O76363_CAEEL	O76363 caenorhabdi
40	30	100.0	61	2	Q54PU6_DICDI	Q54pu6 dictyosteli
41	30	100.0	62	2	Q8QUU0_9VIRU	Q8quu0 infectious
42	30	100.0	63	2	Q8WMJ2_MACMU	Q8wmj2 macaca mula
43	30	100.0	63	2	Q3QT01_9RHOB	Q3qt01 silicibacte
44	30	100.0	63	2	Q9PSQ1_CHICK	Q9psq1 gallus gall
45	30	100.0	64	2	Q3THF1_MOUSE	Q3thf1 mus musculu
46	30	100.0	64	2	Q52UN3_ANAPL	Q52un3 anas platyr
47	30	100.0	66	2	Q5F6D5_NEIG1	Q5f6d5 neisseria g
48	30	100.0	67	2	Q3FZ66_9DELT	Q3fz66 pelobacter
49	30	100.0	67	2	Q441L9_SOLUS	Q441l9 solibacter
50	30	100.0	67	2	Q46H01_PROMT	Q46h01 prochloroco
51	30	100.0	67	2	Q6MX20_MYCTU	Q6mx20 mycobacteri
52	30	100.0	67	2	Q7TXG9_MYCBO	Q7txg9 mycobacteri
53	30	100.0	68	2	Q71UK5_HUMAN	Q71uk5 homo sapien
54	30	100.0	68	2	Q84FK2_ENTAG	Q84fk2 enterobacte
55	30	100.0	68	2	Q8FKT9_ECOL6	Q8fkt9 escherichia
56	30	100.0	68	2	Q788Z2_CHICK	Q788z2 gallus gall
57	30	100.0	68	2	Q91978_COTCO	Q91978 coturnix co
58	30	100.0	69	2	Q98A03_RHILO	Q98a03 rhizobium l
59	30	100.0	70	1	YITO_BACSU	O06750 bacillus su
60	30	100.0	70	2	Q5BTL7_SCHJA	Q5btl7 schistosoma
61	30	100.0	70	2	Q6D381_ERWCT	Q6d381 erwinia car
62	30	100.0	70	2	O41424_9HIV1	O41424 human immun
63	30	100.0	71	2	Q9H3I8_HUMAN	Q9h3i8 homo sapien
64	30	100.0	72	2	Q6NE51_9PROT	Q6ne51 magnetospir
65	30	100.0	73	2	Q97HU6_CLOAB	Q97hu6 clostridium
66	30	100.0	73	2	Q4VAF8_MOUSE	Q4vaf8 mus musculu
67	30	100.0	74	2	Q86JA2_DICDI	Q86ja2 dictyosteli
68	30	100.0	74	2	Q4FLV6_PELUB	Q4flv6 pelagibacte
69	30	100.0	75	2	Q5XUM9_HUMAN	Q5xum9 homo sapien
70	30	100.0	75	2	Q9P1H8_HUMAN	Q9p1h8 homo sapien
71	30	100.0	75	2	Q54AU5_DICDI	Q54au5 dictyosteli
72	30	100.0	76	1	YRHC_BACSU	O05395 bacillus su
73	30	100.0	76	2	O02709_MONDO	O02709 monodelphis
74	30	100.0	76	2	Q4BQ11_BURVI	Q4bq11 burkholderi
75	30	100.0	76	2	Q8VLH3_MICAE	Q8vlh3 microcystis
76	30	100.0	76	2	Q8VLJ4_MICAE	Q8vlj4 microcystis
77	30	100.0	76	2	Q8VLJ8_9CHRO	Q8vlj8 microcystis
78	30	100.0	76	2	Q8VLJ9_MICAE	Q8vlj9 microcystis
79	30	100.0	76	2	Q8VW27_9CHRO	Q8vw27 microcystis
80	30	100.0	76	2	Q8VW28_MICAE	Q8vw28 microcystis
81	30	100.0	76	2	Q8VW30_9CHRO	Q8vw30 microcystis
82	30	100.0	76	2	Q8VW33_9CHRO	Q8vw33 microcystis
83	30	100.0	76	2	Q8VW36_9CHRO	Q8vw36 microcystis
84	30	100.0	76	2	Q2L9E8_9HERP	Q2l9e8 tortoise he
85	30	100.0	76	2	Q2L9F0_9HERP	Q2l9f0 tortoise he
86	30	100.0	77	2	Q3S087_RALME	Q3s087 ralstonia m
87	30	100.0	77	2	Q45CC8_9BURK	Q45cc8 burkholderi
88	30	100.0	77	2	Q4LXN2_9BURK	Q4lxn2 burkholderi
89	30	100.0	77	2	Q5F0K6_9CYAN	Q5f0k6 lyngbya aer
90	30	100.0	77	2	Q5F0L4_9CYAN	Q5f014 phormidium
91	30	100.0	77	2	Q5HXG7_GLUOX	Q5hxg7 gluconobact
92	30	100.0	78	1	VHED_BPPF3	P03672 bacteriopha
93	30	100.0	78	2	Q4YDD3_PLABE	Q4ydd3 plasmodium
94	30	100.0	78	2	Q563D9_9CYAN	Q563d9 uncultured
95	30	100.0	78	2	Q9F506_ECOLI	Q9f506 escherichia
96	30	100.0	78	2	Q6Q0X9_MICAE	Q6q0x9 microcystis
97	30	100.0	79	1	DCOR_PARBR	Q92445 paracoccidi
98	30	100.0	79	2	Q9V6X4_DROME	Q9v6x4 drosophila
99	30	100.0	79	2	Q30QU7_THIDN	Q30qu7 thiomicrosp
100	30	100.0	79	2	Q4NBG7_9MICC	Q4nbg7 arthrobacte

ALIGNMENTS

```
RESULT 1
Q7YXI3_9BILA
ID   Q7YXI3_9BILA   PRELIMINARY;   PRT;    25 AA.
AC   Q7YXI3;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Beta tubulin (Fragment).
OS   Ancylostoma duodenale.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC   Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
OX   NCBI_TaxID=51022;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15003848; DOI=10.1016/j.molbiopara.2003.12.008;
RA   Albonico M., Wright V., Bickle Q.;
RT   "Molecular analysis of the beta-tubulin gene of human hookworms as a
RT   basis for possible benzimidazole resistance on Pemba Island.";
RL   Mol. Biochem. Parasitol. 134:281-284(2004).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF453525; AAQ01173.1; -; Genomic_DNA.
DR   GO; GO:0005874; C:microtubule; IEA.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR002453; Beta_tubulin.
DR   InterPro; IPR000217; Tubulin.
DR   InterPro; IPR003008; Tubulin_FtsZ.
DR   PANTHER; PTHR11588:SF9; Beta_tubulin; 1.
DR   PANTHER; PTHR11588; Tubulin; 1.
DR   Pfam; PF00091; Tubulin; 1.
KW   GTP-binding; Nucleotide-binding.
FT   NON_TER       1      1
FT   NON_TER      25     25
SQ   SEQUENCE   25 AA;  2936 MW;  554CF1ECB60AEF4B CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 25;
  Best Local Similarity   30.8%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          3 TFCIDNEALYDIC 15


RESULT 2
SECR_BOVIN
ID   SECR_BOVIN     STANDARD;      PRT;    27 AA.
AC   P63296; P01279; Q9TR13;
DT   21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT   11-OCT-2004, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Secretin.
GN   Name=SCT;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=81237102; PubMed=7250377; DOI=10.1016/0014-5793(81)80343-2;
RA   Carlquist M., Joernvall H., Mutt V.;
RT   "Isolation and amino acid sequence of bovine secretin.";
RL   FEBS Lett. 127:71-74(1981).
CC   -!- FUNCTION: Stimulates formation of NaHCO(3)-rich pancreatic juice
CC       and secretion of NaHCO(3)-rich bile and inhibits HCl production by
CC       the stomach.
CC   -!- SUBCELLULAR LOCATION: Secreted protein.
CC   -!- SIMILARITY: Belongs to the glucagon family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   InterPro; IPR000532; Glucagon.
DR   Pfam; PF00123; Hormone_2; 1.
DR   SMART; SM00070; GLUCA; 1.
DR   PROSITE; PS00260; GLUCAGON; 1.
KW   Amidation; Direct protein sequencing; Hormone.
FT   PEPTIDE       1     27       Secretin.
FT                                /FTId=PRO_0000043933.
FT   MOD_RES      27     27       Valine amide.
SQ   SEQUENCE   27 AA;  3056 MW;  2D4015814ED05B78 CRC64;

  Query Match             100.0%;  Score 30;  DB 1;  Length 27;
  Best Local Similarity   30.8%;  Pred. No. 5e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          5 TFTSELSRLRDSA 17


RESULT 3
SECR_CAVPO
ID   SECR_CAVPO     STANDARD;      PRT;    27 AA.
AC   P63297; P01279; Q9TR13;
DT   21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT   11-OCT-2004, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Secretin.
GN   Name=SCT;
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC   Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Small intestine;
RX   MEDLINE=90254163; PubMed=2340294; DOI=10.1016/0167-4838(90)90248-E;
RA   Buscail L., Cauvin A., Gourlet P., Gossen D., de Neef P., Rathe J.,
RA   Robberecht P., Vandermeers-Piret M.-C., Vandermeers A., Christophe J.;
RT   "Purification and amino acid sequence of vasoactive intestinal
RT   peptide, peptide histidine isoleucinamide (1-27) and secretin from the
RT   small intestine of guinea pig.";
RL   Biochim. Biophys. Acta 1038:355-359(1990).
CC   -!- FUNCTION: Stimulates formation of NaHCO(3)-rich pancreatic juice
CC       and secretion of NaHCO(3)-rich bile and inhibits HCl production by
CC       the stomach.
CC   -!- SUBCELLULAR LOCATION: Secreted protein.
CC   -!- SIMILARITY: Belongs to the glucagon family.
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CC   ---------------------------------------------------------------------
DR   InterPro; IPR000532; Glucagon.
DR   Pfam; PF00123; Hormone_2; 1.
DR   SMART; SM00070; GLUCA; 1.
DR   PROSITE; PS00260; GLUCAGON; 1.
KW   Amidation; Direct protein sequencing; Hormone.
FT   PEPTIDE       1     27       Secretin.
FT                                /FTId=PRO_0000043935.
FT   MOD_RES      27     27       Valine amide.
SQ   SEQUENCE   27 AA;  3056 MW;  2D4015814ED05B78 CRC64;

  Query Match             100.0%;  Score 30;  DB 1;  Length 27;
  Best Local Similarity   30.8%;  Pred. No. 5e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
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              ||:::::::|:|::
Db          5 TFTSELSRLRDSA 17


RESULT 4
SECR_SHEEP
ID   SECR_SHEEP     STANDARD;      PRT;    27 AA.
AC   P31299;
DT   01-JUL-1993, integrated into UniProtKB/Swiss-Prot.
DT   01-JUL-1993, sequence version 1.
DT   07-FEB-2006, entry version 33.
DE   Secretin.
GN   Name=SCT;
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Small intestine;
RX   MEDLINE=91239834; PubMed=2034821; DOI=10.1016/0167-0115(91)90044-H;
RA   Bounjoua Y., Vandermeers A., Robberecht P., Vandermeers-Piret M.C.,
RA   Christophe J.;
RT   "Purification and amino acid sequence of vasoactive intestinal
RT   peptide, peptide histidine isoleucinamide and secretin from the ovine
RT   small intestine.";
RL   Regul. Pept. 32:169-179(1991).
CC   -!- FUNCTION: Stimulates formation of NaHCO(3)-rich pancreatic juice
CC       and secretion of NaHCO(3)-rich bile and inhibits HCl production by
CC       the stomach.
CC   -!- SUBCELLULAR LOCATION: Secreted protein.
CC   -!- SIMILARITY: Belongs to the glucagon family.
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CC   ---------------------------------------------------------------------
DR   PIR; C60072; SESH.
DR   InterPro; IPR000532; Glucagon.
DR   Pfam; PF00123; Hormone_2; 1.
DR   SMART; SM00070; GLUCA; 1.
DR   PROSITE; PS00260; GLUCAGON; 1.
KW   Amidation; Direct protein sequencing; Hormone.
FT   PEPTIDE       1     27       Secretin.
FT                                /FTId=PRO_0000043937.
FT   MOD_RES      27     27       Valine amide.
SQ   SEQUENCE   27 AA;  3056 MW;  2D4015814ED05B78 CRC64;

  Query Match             100.0%;  Score 30;  DB 1;  Length 27;
  Best Local Similarity   30.8%;  Pred. No. 5e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::::|:|::
Db          5 TFTSELSRLRDSA 17


RESULT 5
Q6JDH7_CANFA
ID   Q6JDH7_CANFA   PRELIMINARY;   PRT;    27 AA.
AC   Q6JDH7;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   RAS oncogene family member RAB2 (Fragment).
GN   Name=RAB2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15233990; DOI=10.1016/j.ygeno.2004.04.001;
RA   Housley D.J.E., Ritzert E., Venta P.J.;
RT   "Comparative radiation hybrid map of canine chromosome 1 (CFA1)
RT   incorporating SNP and indel polymorphisms.";
RL   Genomics 84:248-264(2004).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY514756; AAT44586.1; -; Genomic_DNA.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR   InterPro; IPR001806; Ras_trnsfrmng.
DR   Pfam; PF00071; Ras; 1.
KW   GTP-binding; Nucleotide-binding.
FT   NON_TER       1      1
FT   NON_TER      27     27
SQ   SEQUENCE   27 AA;  3119 MW;  14D5E56B1C5C4731 CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 27;
  Best Local Similarity   30.8%;  Pred. No. 5e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::::|:|::
Db         15 TFNHLTTWLEDAR 27


RESULT 6
Q900E5_9HIV1
ID   Q900E5_9HIV1   PRELIMINARY;   PRT;    27 AA.
AC   Q900E5;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Envelope glycoprotein (Fragment).
GN   Name=env;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC   Lentivirus; Primate lentivirus group.
OX   NCBI_TaxID=11676;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole saliva;
RX   MEDLINE=21211648; PubMed=11312368;
RX   DOI=10.1128/JVI.75.10.4936-4940.2001;
RA   Freel S.A., Williams J.M., Nelson J.A., Patton L.L., Fiscus S.A.,
RA   Swanstrom R., Shugars D.C.;
RT   "Characterization of human immunodeficiency virus type 1 in saliva and
RT   blood plasma by V3-specific heteroduplex tracking assay and genotype
RT   analyses.";
RL   J. Virol. 75:4936-4940(2001).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF362885; AAK52012.1; -; Genomic_RNA.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120; 1.
KW   Envelope protein.
FT   NON_TER       1      1
FT   NON_TER      27     27
SQ   SEQUENCE   27 AA;  3039 MW;  91F798FB14EF05D7 CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 27;
  Best Local Similarity   30.8%;  Pred. No. 5e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::::|:|::
Db         15 TFYATGDILGDIR 27
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RESULT 7
Q4S2T4_TETNG
ID   Q4S2T4_TETNG   PRELIMINARY;   PRT;    31 AA.
AC   Q4S2T4;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Chromosome 17 SCAF14760, whole genome shotgun sequence.
GN   ORFNames=GSTENG00024943001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
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CC   ---------------------------------------------------------------------
DR   EMBL; CAAE01014760; CAG05048.1; -; Genomic_DNA.
SQ   SEQUENCE   31 AA;  3414 MW;  780B92E08D35B525 CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 31;
  Best Local Similarity   30.8%;  Pred. No. 5.9e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          6 TFMKNVQVLLDAA 18


RESULT 8
Q9GYZ8_TRYCR
ID   Q9GYZ8_TRYCR   PRELIMINARY;   PRT;    33 AA.
AC   Q9GYZ8;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Sm-D3 (Fragment).
GN   Name=Sm-D3;
OS   Trypanosoma cruzi.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
OC   Schizotrypanum.
OX   NCBI_TaxID=5693;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20381320; PubMed=10900267; DOI=10.1073/pnas.150236097;
RA   Palfi Z., Luecke S., Lahm H.-W., Lane W.S., Kruft V.,
RA   Bragado-Nilsson E., Seraphin B., Bindereif A.;
RT   "The spliceosomal snRNP core complex of Trypanosoma brucei: cloning
RT   and functional analysis reveals seven Sm protein constituents.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:8967-8972(2000).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF280390; AAG00464.1; -; mRNA.
FT   NON_TER      33     33
SQ   SEQUENCE   33 AA;  3519 MW;  CB8FE375E0704065 CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 33;
  Best Local Similarity   30.8%;  Pred. No. 6.3e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          3 TFSIPLKVLFDAI 15


RESULT 9
Q9H3W9_HUMAN
ID   Q9H3W9_HUMAN   PRELIMINARY;   PRT;    36 AA.
AC   Q9H3W9;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Hypothetical protein DKFZp547I137 (Fragment).
GN   Name=DKFZp547I137;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RG   The German cDNA Consortium;
RA   Ansorge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,
RA   Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AL442076; CAC09442.1; -; mRNA.
DR   Ensembl; ENSG00000103202; Homo sapiens.
KW   Hypothetical protein.
FT   NON_TER      1      1
SQ   SEQUENCE   36 AA;  3628 MW;  8E3135426AA691B5 CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 36;
  Best Local Similarity   30.8%;  Pred. No. 6.9e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db         18 TFPNGVKGLPDFA 30


RESULT 10
Q2KKH4_9BILA
ID   Q2KKH4_9BILA   PRELIMINARY;   PRT;    38 AA.
AC   Q2KKH4;
DT   07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT   07-MAR-2006, sequence version 1.
DT   07-MAR-2006, entry version 1.
DE   Beta tubulin isotype 2 (Fragment).
OS   Trichostrongylus tenuis.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
```

```
OC   Trichostrongyloidea; Trichostrongylidae; Trichostrongylinae;
OC   Trichostrongylus.
OX   NCBI_TaxID=40351;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Webster L.M.I., Johnson P.C.D., Adam A., Keller L.F.;
RT   "Absence of known benzimidazole resistance mutations in
RT   Trichostrongylus tenuis, a nematode parasite of avian hosts.";
RL   Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AY914052; AAX92642.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER      38     38
SQ   SEQUENCE   38 AA;  4406 MW;  AD916C1027FC36E5 CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 38;
  Best Local Similarity   30.8%;  Pred. No. 7.3e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db         18 TFCIDNEALYDIC 30


RESULT 11
Q3YN35_BACTK
ID   Q3YN35_BACTK   PRELIMINARY;   PRT;    38 AA.
AC   Q3YN35;
DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Hypothetical protein.
GN   ORFNames=pAW63_040;
OS   Bacillus thuringiensis subsp. kurstaki.
OG   Plasmid pAW63.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC   Bacillus cereus group.
OX   NCBI_TaxID=29339;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=HD73;
RA   Van der Auwera G.A., Andrup L., Mahillon J.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; DQ025752; AAZ06610.1; -; Genomic_DNA.
KW   Hypothetical protein; Plasmid.
SQ   SEQUENCE   38 AA;  4373 MW;  E77F652ABADDC54F CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 38;
  Best Local Similarity   30.8%;  Pred. No. 7.3e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db         14 TFMVLMILLFDAS 26


RESULT 12
Q8DT72_STRMU
ID   Q8DT72_STRMU   PRELIMINARY;   PRT;    39 AA.
AC   Q8DT72;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   21-FEB-2006, entry version 15.
DE   Hypothetical protein.
GN   ORFNames=SMU_1505c;
OS   Streptococcus mutans.
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=1309;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=UA159 / ATCC 700610 / Serotype c;
RX   MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
RA   Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA   Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RA   Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
RA   Ferretti J.J.;
RT   "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RT   pathogen.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AE014133; AAN59156.1; -; Genomic_DNA.
DR   InterPro; IPR005121; Fdx_antiC_bd.
DR   Pfam; PF03147; FDX-ACB; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   39 AA;  4463 MW;  2DFAA508C2ACE89D CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 39;
  Best Local Similarity   30.8%;  Pred. No. 7.5e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          6 TFQNPNDNLTDEE 18


RESULT 13
Q3WGH1_9ACTO
ID   Q3WGH1_9ACTO   PRELIMINARY;   PRT;    42 AA.
AC   Q3WGH1;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Hypothetical protein.
GN   ORFNames=Franean1DRAFT_6440;
OS   Frankia sp. EAN1pec.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Frankineae; Frankiaceae; Frankia.
OX   NCBI_TaxID=298653;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=EAN1pec;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome and assembly of Frankia sp. EAN1pec.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=EAN1pec;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Frankia sp. EAN1pec.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AAII01000006; EAN17833.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   42 AA;  4726 MW;  F60DC6D007529D17 CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 42;
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  Best Local Similarity   30.8%;  Pred. No. 8.2e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db         19 TFDLKPTPLDDVL 31


RESULT 14
O80797_ARATH
ID   O80797_ARATH   PRELIMINARY;   PRT;    43 AA.
AC   O80797;
DT   01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1998, sequence version 1.
DT   07-FEB-2006, entry version 17.
DE   T8F5.3.
GN   Name=T8F5.3;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Kwan A., Liu S.,
RA   Li J., Araujo R., Au M., Brendel V., Buehler E., Conway A.B.,
RA   Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Y., Palm C.J.,
RA   Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
RA   Theologis A.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Theologis;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AC004512; AAC27136.1; -; Genomic_DNA.
DR   PIR; T02348; T02348.
DR   GO; GO:0005489; F:electron transporter activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006662; Thiored.
DR   PRINTS; PR00421; THIOREDOXIN.
SQ   SEQUENCE   43 AA;  4972 MW;  24F057D87E3D5945 CRC64;

  Query Match            100.0%;  Score 30;  DB 2;  Length 43;
  Best Local Similarity   30.8%;  Pred. No. 8.4e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db         27 TFGSGSSSLGDEV 39


RESULT 15
Q87GK5_VIBPA
ID   Q87GK5_VIBPA   PRELIMINARY;   PRT;    43 AA.
AC   Q87GK5;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Hypothetical protein VPA1310.
GN   OrderedLocusNames=VPA1310;
OS   Vibrio parahaemolyticus.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Vibrio.
OX   NCBI_TaxID=670;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=RIMD 2210633 / Serotype O3:K6;
RX   MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA   Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA   Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA   Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT   "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT   distinct from that of V. cholerae.";
RL   Lancet 361:743-749(2003).
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CC   ---------------------------------------------------------------------
DR   EMBL; BA000032; BAC62653.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   43 AA;  5048 MW;  ABD923038890678F CRC64;

  Query Match            100.0%;  Score 30;  DB 2;  Length 43;
  Best Local Similarity   30.8%;  Pred. No. 8.4e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db         14 TFKKIPFFLQDGN 26


RESULT 16
Q8J052_9EURO
ID   Q8J052_9EURO   PRELIMINARY;   PRT;    45 AA.
AC   Q8J052;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Beta-tubulin (Fragment).
OS   Penicillium boreae.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX   NCBI_TaxID=189054;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NRRL 31002, and NRRL 31401;
RA   Peterson S.W., Sigler L.;
RT   "Four new Penicillium species having Thysanophora-like melanized
RT   conidiophores.";
RL   Mycol. Res. 106:1109-1118(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF481129; AAN86258.1; -; Genomic_DNA.
DR   EMBL; AF481132; AAN86261.1; -; Genomic_DNA.
DR   SMR; Q8J052; 1-45.
DR   GO; GO:0005874; C:microtubule; IEA.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR002453; Beta_tubulin.
DR   InterPro; IPR000217; Tubulin.
DR   InterPro; IPR003008; Tubulin_FtsZ.
DR   PANTHER; PTHR11588:SF9; Beta_tubulin; 1.
DR   PANTHER; PTHR11588; Tubulin; 1.
DR   Pfam; PF00091; Tubulin; 1.
DR   PRINTS; PR01163; BETATUBULIN.
KW   GTP-binding; Nucleotide-binding.
FT   NON_TER       1      1
FT   NON_TER      45     45
SQ   SEQUENCE   45 AA;  5020 MW;  D1E9D443770CB0BA CRC64;

  Query Match            100.0%;  Score 30;  DB 2;  Length 45;
  Best Local Similarity   30.8%;  Pred. No. 8.8e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          6 TFCIDNEALYDIC 18
```

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RESULT 17
Q8J160_9EURO
ID   Q8J160_9EURO   PRELIMINARY;   PRT;    45 AA.
AC   Q8J160;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Beta-tubulin (Fragment).
OS   Penicillium subarcticum.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX   NCBI_TaxID=189057;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NRRL 31108;
RA   Peterson S.W., Sigler L.;
RT   "Four new Penicillium species having Thysanophora-like melanized
RT   conidiophores.";
RL   Mycol. Res. 106:1109-1118(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF481131; AAN86260.1; -; Genomic_DNA.
DR   SMR; Q8J160; 1-45.
DR   GO; GO:0005874; C:microtubule; IEA.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR002453; Beta_tubulin.
DR   InterPro; IPR000217; Tubulin.
DR   InterPro; IPR003008; Tubulin_FtsZ.
DR   PANTHER; PTHR11588:SF9; Beta_tubulin; 1.
DR   PANTHER; PTHR11588; Tubulin; 1.
DR   Pfam; PF00091; Tubulin; 1.
DR   PRINTS; PR01163; BETATUBULIN.
KW   GTP-binding; Nucleotide-binding.
FT   NON_TER       1      1
FT   NON_TER      45     45
SQ   SEQUENCE   45 AA;  5033 MW;  D1E9D44367D6D0BA CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 45;
  Best Local Similarity   30.8%;  Pred. No. 8.8e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          6 TFCIDNEALYDIC 18


RESULT 18
Q8J161_9EURO
ID   Q8J161_9EURO   PRELIMINARY;   PRT;    45 AA.
AC   Q8J161;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Beta-tubulin (Fragment).
OS   Penicillium sp. NRRL 28214.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX   NCBI_TaxID=189052;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NRRL 28214;
RA   Peterson S.W., Sigler L.;
RT   "Four new Penicillium species having Thysanophora-like melanized
RT   conidiophores.";
RL   Mycol. Res. 106:1109-1118(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF481130; AAN86259.1; -; Genomic_DNA.
DR   SMR; Q8J161; 1-45.
DR   GO; GO:0005874; C:microtubule; IEA.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR002453; Beta_tubulin.
DR   InterPro; IPR000217; Tubulin.
DR   InterPro; IPR003008; Tubulin_FtsZ.
DR   PANTHER; PTHR11588:SF9; Beta_tubulin; 1.
DR   PANTHER; PTHR11588; Tubulin; 1.
DR   Pfam; PF00091; Tubulin; 1.
DR   PRINTS; PR01163; BETATUBULIN.
KW   GTP-binding; Nucleotide-binding.
FT   NON_TER       1      1
FT   NON_TER      45     45
SQ   SEQUENCE   45 AA;  5006 MW;  D1E9D443720CE0BA CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 45;
  Best Local Similarity   30.8%;  Pred. No. 8.8e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db          6 TFCIDNEALYDIC 18


RESULT 19
Q8J162_9EURO
ID   Q8J162_9EURO   PRELIMINARY;   PRT;    45 AA.
AC   Q8J162;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Beta-tubulin (Fragment).
OS   Penicillium canariense.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX   NCBI_TaxID=189055;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NRRL 31003;
RA   Peterson S.W., Sigler L.;
RT   "Four new Penicillium species having Thysanophora-like melanized
RT   conidiophores.";
RL   Mycol. Res. 106:1109-1118(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF481128; AAN86257.1; -; Genomic_DNA.
DR   SMR; Q8J162; 1-45.
DR   GO; GO:0005874; C:microtubule; IEA.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR002453; Beta_tubulin.
DR   InterPro; IPR000217; Tubulin.
DR   InterPro; IPR003008; Tubulin_FtsZ.
DR   PANTHER; PTHR11588:SF9; Beta_tubulin; 1.
DR   PANTHER; PTHR11588; Tubulin; 1.
DR   Pfam; PF00091; Tubulin; 1.
DR   PRINTS; PR01163; BETATUBULIN.
KW   GTP-binding; Nucleotide-binding.
FT   NON_TER       1      1
FT   NON_TER      45     45
SQ   SEQUENCE   45 AA;  5020 MW;  D1E9D443770CB0BA CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 45;
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  Best Local Similarity   30.8%;  Pred. No. 8.8e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::::|:|::
Db          6 TFCIDNEALYDIC 18


RESULT 20
Q8J163_9EURO
ID   Q8J163_9EURO   PRELIMINARY;   PRT;    45 AA.
AC   Q8J163;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Beta-tubulin (Fragment).
OS   Penicillium donkii.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX   NCBI_TaxID=69772;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NRRL 5562;
RA   Peterson S.W., Sigler L.;
RT   "Four new Penicillium species having Thysanophora-like melanized
RT   conidiophores.";
RL   Mycol. Res. 106:1109-1118(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF481127; AAN86256.1; -; Genomic_DNA.
DR   SMR; Q8J163; 1-45.
DR   GO; GO:0005874; C:microtubule; IEA.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR002453; Beta_tubulin.
DR   InterPro; IPR000217; Tubulin.
DR   InterPro; IPR003008; Tubulin_FtsZ.
DR   PANTHER; PTHR11588:SF9; Beta_tubulin; 1.
DR   PANTHER; PTHR11588; Tubulin; 1.
DR   Pfam; PF00091; Tubulin; 1.
DR   PRINTS; PR01163; BETATUBULIN.
KW   GTP-binding; Nucleotide-binding.
FT   NON_TER       1      1
FT   NON_TER      45     45
SQ   SEQUENCE   45 AA;  5006 MW;  D1E9D443720CE0BA CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 45;
  Best Local Similarity   30.8%;  Pred. No. 8.8e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::::|:|::
Db          6 TFCIDNEALYDIC 18


RESULT 21
Q8J164_9EURO
ID   Q8J164_9EURO   PRELIMINARY;   PRT;    45 AA.
AC   Q8J164;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Beta-tubulin (Fragment).
OS   Eupenicillium stolkiae.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; Eupenicillium.
OX   NCBI_TaxID=69802;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NRRL 5816;
RA   Peterson S.W., Sigler L.;
RT   "Four new Penicillium species having Thysanophora-like melanized
RT   conidiophores.";
RL   Mycol. Res. 106:1109-1118(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF481126; AAN86255.1; -; Genomic_DNA.
DR   SMR; Q8J164; 1-45.
DR   GO; GO:0005874; C:microtubule; IEA.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR002453; Beta_tubulin.
DR   InterPro; IPR000217; Tubulin.
DR   InterPro; IPR003008; Tubulin_FtsZ.
DR   PANTHER; PTHR11588:SF9; Beta_tubulin; 1.
DR   PANTHER; PTHR11588; Tubulin; 1.
DR   Pfam; PF00091; Tubulin; 1.
DR   PRINTS; PR01163; BETATUBULIN.
KW   GTP-binding; Nucleotide-binding.
FT   NON_TER       1      1
FT   NON_TER      45     45
SQ   SEQUENCE   45 AA;  4979 MW;  D1E9D440C1ECB0BA CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 45;
  Best Local Similarity   30.8%;  Pred. No. 8.8e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::::|:|::
Db          6 TFCIDNEALYDIC 18


RESULT 22
Q8J165_9EURO
ID   Q8J165_9EURO   PRELIMINARY;   PRT;    45 AA.
AC   Q8J165;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Beta-tubulin (Fragment).
OS   Penicillium pullum.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX   NCBI_TaxID=189056;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NRRL 721;
RA   Peterson S.W., Sigler L.;
RT   "Four new Penicillium species having Thysanophora-like melanized
RT   conidiophores.";
RL   Mycol. Res. 106:1109-1118(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF481125; AAN86254.1; -; Genomic_DNA.
DR   SMR; Q8J165; 1-45.
DR   GO; GO:0005874; C:microtubule; IEA.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0007018; P:microtubule-based movement; IEA.
DR   InterPro; IPR002453; Beta_tubulin.
DR   InterPro; IPR000217; Tubulin.
DR   InterPro; IPR003008; Tubulin_FtsZ.
DR   PANTHER; PTHR11588:SF9; Beta_tubulin; 1.
DR   PANTHER; PTHR11588; Tubulin; 1.
DR   Pfam; PF00091; Tubulin; 1.
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DR   PRINTS; PR01163; BETATUBULIN.
KW   GTP-binding; Nucleotide-binding.
FT   NON_TER       1      1
FT   NON_TER      45     45
SQ   SEQUENCE   45 AA;  5020 MW;  D1E9D443770CB0BA CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 45;
  Best Local Similarity   30.8%;  Pred. No. 8.8e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::|:|::
Db          6 TFCIDNEALYDIC 18


RESULT 23
Q58MQ3_9CAUD
ID   Q58MQ3_9CAUD   PRELIMINARY;   PRT;    45 AA.
AC   Q58MQ3;
DT   26-APR-2005, integrated into UniProtKB/TrEMBL.
DT   26-APR-2005, sequence version 1.
DT   07-FEB-2006, entry version 4.
DE   Hypothetical protein.
GN   ORFNames=PSSM2_101;
OS   Cyanophage P-SSM2.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC   T4-like viruses.
OX   NCBI_TaxID=268746;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15828858; DOI=10.1371/journal.pbio.0030144;
RA   Sullivan M.B., Coleman M.L., Weigele P., Rohwer F., Chisholm S.W.;
RT   "Three prochlorococcus cyanophage genomes: signature features and
RT   ecological interpretations.";
RL   PLoS Biol. 3:E144-E144(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Lindell D., Sullivan M.B., Johnson Z.I., Tolonen A.C., Rohwer F.,
RA   Chisholm S.W.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AY939844; AAX44479.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   45 AA;  5197 MW;  6DFCABF3F78E809B CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 45;
  Best Local Similarity   30.8%;  Pred. No. 8.8e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::|:|::
Db          2 TFNRFDDYLTDDA 14


RESULT 24
Q3JLT1_BURP1
ID   Q3JLT1_BURP1   PRELIMINARY;   PRT;    45 AA.
AC   Q3JLT1;
DT   08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT   08-NOV-2005, sequence version 1.
DT   21-FEB-2006, entry version 4.
DE   Hypothetical protein.
GN   OrderedLocusNames=BURPS1710b_A0313;
OS   Burkholderia pseudomallei (strain 1710b).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia; pseudomallei group.
OX   NCBI_TaxID=320372;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA   Woods D.E., Nierman W.C.;
RL   Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; CP000125; ABA51693.1; -; Genomic_DNA.
DR   TIGR; BURPS1710b_A0313; -.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   45 AA;  4619 MW;  01C9B6229185CE49 CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 45;
  Best Local Similarity   30.8%;  Pred. No. 8.8e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::|:|::
Db          3 TFGEPLVALFDGS 15


RESULT 25
Q91FG1_IRV6
ID   Q91FG1_IRV6    PRELIMINARY;   PRT;    46 AA.
AC   Q91FG1;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   363L.
OS   Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
OC   Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
OX   NCBI_TaxID=176652;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99125223; PubMed=9926400; DOI=10.1023/A:1008017820941;
RA   Muller K., Tidona C.A., Bahr U., Darai G.;
RT   "Identification of a thymidylate synthase gene within the genome of
RT   Chilo iridescent virus.";
RL   Virus Genes 17:243-258(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93118242; PubMed=1475907;
RA   Sonntag K.C., Darai G.;
RT   "Characterization of the third origin of DNA replication of the genome
RT   of insect iridescent virus type 6.";
RL   Virus Genes 6:333-342(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=94353641; PubMed=8073636;
RA   Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.;
RT   "Chilo iridescent virus encodes a putative helicase belonging to a
RT   distinct family within the 'DEAD/H' superfamily: implications for the
RT   evolution of large DNA viruses.";
RL   Virus Genes 8:151-158(1994).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=94292906; PubMed=8021587;
RA   Schnitzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J.,
RA   Koonin E.V., Darai G.;
RT   "Insect iridescent virus type 6 encodes a polypeptide related to the
RT   largest subunit of eukaryotic RNA polymerase II.";
RL   J. Gen. Virol. 75:1557-1567(1994).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=95213160; PubMed=7698884;
RA   Sonntag K.C., Schnitzler P., Janssen W., Darai G.;
RT   "Identification of the primary structure and the coding capacity of
RT   the genome of insect iridescent virus type 6 between the genome
RT   coordinates 0.310 and 0.347 (7990 bp).";
RL   Intervirology 37:287-297(1994).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98141693; PubMed=9482589; DOI=10.1023/A:1007932620930;
RA   Bahr U., Tidona C.A., Darai G.;
RT   "The DNA sequence of Chilo iridescent virus between the genome
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RT   coordinates 0.101 and 0.391; similarities in coding strategy between
RT   insect and vertebrate iridoviruses.";
RL   Virus Genes 15:235-245(1997).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RA   Delius H., Darai G., Fluegel R.M.;
RT   "DNA analysis of insect iridescent virus 6: evidence for circular
RT   permutation and terminal redundancy.";
RL   J. Virol. 49:609-614(1984).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86174607; PubMed=3959991;
RA   Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
RT   "Insect iridescent virus type 6 induced toxic degenerative hepatitis
RT   in mice.";
RL   Med. Microbiol. Immunol. 175:43-53(1986).
RN   [9]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87321126; PubMed=2820141;
RA   Schnitzler P., Soltau J.B., Fischer M., Reisner H., Scholz J.,
RA   Delius H., Darai G.;
RT   "Molecular cloning and physical mapping of the genome of insect
RT   iridescent virus type 6: further evidence for circular permutation of
RT   the viral genome.";
RL   Virology 160:66-74(1987).
RN   [10]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=89073752; PubMed=3201750;
RA   Fischer M., Schnitzler P., Delius H., Darai G.;
RT   "Identification and characterization of the repetitive DNA element in
RT   the genome of insect iridescent virus type 6.";
RL   Virology 167:485-496(1988).
RN   [11]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=92196996; PubMed=1549908;
RA   Handermann M., Schnitzler P., Roesen-Wolff A.P., Raab K.,
RA   Sonntag K.C., Darai G.;
RT   "Identification and mapping of origins of DNA replication within the
RT   DNA sequences of the genome of insect iridescent virus type 6.";
RL   Virus Genes 6:19-32(1992).
RN   [12]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93260401; PubMed=8492091;
RA   Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.;
RT   "Identification of the gene encoding the major capsid protein of
RT   insect iridescent virus type 6 by polymerase chain reaction.";
RL   J. Gen. Virol. 74:873-879(1993).
RN   [13]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=94167241; PubMed=8121799;
RA   Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
RA   Delius H., Darai C.;
RT   "Identification of genes encoding zinc finger proteins, non-histone
RT   chromosomal HMG protein homologue, and a putative GTP phosphohydrolase
RT   in the genome of Chilo iridescent virus.";
RL   Nucleic Acids Res. 22:158-166(1994).
RN   [14]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99383793; PubMed=10456793; DOI=10.1023/A:1008072319875;
RA   Muller K., Tidona C.A., Darai G.;
RT   "Identification of a gene cluster within the genome of Chilo
RT   iridescent virus encoding enzymes involved in viral DNA replication
RT   and processing.";
RL   Virus Genes 18:243-264(1999).
RN   [15]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;
RA   Jakob N.J., Mueller K., Bahr U., Darai G.;
RT   "Analysis of the first complete DNA sequence of an invertebrate
RT   iridovirus: coding strategy of the genome of Chilo iridescent virus.";
RL   Virology 286:182-196(2001).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF303741; AAK82223.1; -; Genomic_DNA.
SQ   SEQUENCE   46 AA;  5365 MW;  6D82076DEF12EE14 CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 46;
  Best Local Similarity   30.8%;  Pred. No. 9.1e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::|:|::
Db         12 TFIQLVQLLEDIL 24


RESULT 26
Q3IBR9_9BACT
ID   Q3IBR9_9BACT   PRELIMINARY;   PRT;    47 AA.
AC   Q3IBR9;
DT   08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT   08-NOV-2005, sequence version 1.
DT   07-FEB-2006, entry version 4.
DE   Hypothetical protein.
GN   ORFNames=42c90002;
OS   uncultured sulfate-reducing bacterium.
OC   Bacteria; environmental samples.
OX   NCBI_TaxID=153939;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=16199583; DOI=10.1128/JB.187.20.7126-7137.2005;
RA   Mussmann M., Richter M., Lombardot T., Meyerdierks A., Kuever J.,
RA   Kube M., Gloeckner F.O., Amann R.;
RT   "Clustered Genes Related to Sulfate Respiration in Uncultured
RT   ProkaryotesSupport the Theory of Their Concomitant Horizontal
RT   Transfer.";
RL   J. Bacteriol. 187:7126-7137(2005).
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CC   ---------------------------------------------------------------------
DR   EMBL; CT025834; CAJ31123.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   47 AA;  5403 MW;  94C9D3FBEF349435 CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 47;
  Best Local Similarity   30.8%;  Pred. No. 9.3e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||:::::|:|::
Db          8 TFPIRSSPLNDRI 20


RESULT 27
Q8MJA7_MACMU
ID   Q8MJA7_MACMU   PRELIMINARY;   PRT;    49 AA.
AC   Q8MJA7;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   FRK (Fragment).
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Norgren R.B., Zink M.A., Jia Y., Ojeda S.R., Spindel E.R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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DR   EMBL; AF512352; AAM75335.1; -; Genomic_DNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   49 AA;  6023 MW;  3FAD624A333DD54F CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 49;
  Best Local Similarity   30.8%;  Pred. No. 9.7e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db         23 TFETLHWKLEDYF 35


RESULT 28
Q87QM2_VIBPA
ID   Q87QM2_VIBPA   PRELIMINARY;   PRT;    49 AA.
AC   Q87QM2;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Hypothetical protein VP1127.
GN   OrderedLocusNames=VP1127;
OS   Vibrio parahaemolyticus.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Vibrio.
OX   NCBI_TaxID=670;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=RIMD 2210633 / Serotype O3:K6;
RX   MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA   Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA   Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA   Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT   "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT   distinct from that of V. cholerae.";
RL   Lancet 361:743-749(2003).
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CC   ---------------------------------------------------------------------
DR   EMBL; BA000031; BAC59390.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   49 AA;  5544 MW;  9F4137D4132CAB8E CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 49;
  Best Local Similarity   30.8%;  Pred. No. 9.7e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db         30 TFLVFRSLLRDYS 42


RESULT 29
Q7UH49_RHOBA
ID   Q7UH49_RHOBA   PRELIMINARY;   PRT;    50 AA.
AC   Q7UH49;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   Hypothetical protein.
GN   OrderedLocusNames=RB4844;
OS   Rhodopirellula baltica.
OC   Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC   Planctomycetaceae; Pirellula.
OX   NCBI_TaxID=117;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=1;
RX   MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA   Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA   Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA   Schlesner H., Amann R., Reinhardt R.;
RT   "Complete genome sequence of the marine planctomycete Pirellula sp.
RT   strain 1.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
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CC   ---------------------------------------------------------------------
DR   EMBL; BX294141; CAD78130.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   50 AA;  5444 MW;  4FF2B5333D11FA48 CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 50;
  Best Local Similarity   30.8%;  Pred. No. 9.9e+02;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db         14 TFICYLFGLGDEI 26


RESULT 30
Q4N2A0_THEPA
ID   Q4N2A0_THEPA   PRELIMINARY;   PRT;    54 AA.
AC   Q4N2A0;
DT   02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   02-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Hypothetical protein.
GN   ORFNames=TP04_0452;
OS   Theileria parva.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC   Theileria.
OX   NCBI_TaxID=5875;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Muguga;
RX   PubMed=15994558; DOI=10.1126/science.1110439;
RA   Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA   Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.,
RA   Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA   Jiang L., Lynn J., Weaver B., Shoaibi A., Domingo A.R., Wasawo D.,
RA   Crabtree J., Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C.,
RA   Suh B., Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M.,
RA   Allen J., Nierman W.C., Taracha E.L., Salzberg S.L., White O.R.,
RA   Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;
RT   "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
RT   Lymphocytes.";
RL   Science 309:134-137(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Muguga;
RA   Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA   Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA   Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA   Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA   Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA   Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
RA   Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA   Fraser C.M., Nene V.;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
```

```
CC   ----------------------------------------------------------------------
DR   EMBL; AAGK01000004; EAN31804.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   54 AA;  6238 MW;  8B9494FCD89342FC CRC64;

  Query Match             100.0%;  Score 30;  DB 2;  Length 54;
  Best Local Similarity    30.8%;  Pred. No. 1.1e+03;
  Matches    4;  Conservative    9;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TFXXXXXXLXDXX 13
              ||::::::|:|::
Db         27 TFNSWSFRLADQT 39


Search completed: June 29, 2006, 09:56:07
Job time : 299 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:14 ; Search time 87.8313 Seconds
(without alignments)
46.851 Million cell updates/sec

Title: US-10-062-257A-11
Perfect score: 41
Sequence: 1 LQDNLVIAL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	100.0	9	4	AAB73127	Aab73127 Tumour an
2	41	100.0	126	2	AAW73554	Aaw73554 Lymphoid
3	41	100.0	346	3	AAY76750	Aay76750 Human pro
4	41	100.0	346	4	AAE06208	Aae06208 Human pro
5	41	100.0	346	5	ABB84435	Abb84435 Human pro
6	41	100.0	355	8	ABM82980	Abm82980 Human dia
7	41	100.0	363	6	ABR59690	Abr59690 Human p56
8	41	100.0	363	8	ADP48375	Adp48375 Human lym
9	41	100.0	437	5	ABG79672	Abg79672 Tumour in
10	41	100.0	458	7	ADC99048	Adc99048 Human KPP
11	41	100.0	508	3	AAB37700	Aab37700 Human lym
12	41	100.0	508	7	ADE58802	Ade58802 Human Pro
13	41	100.0	508	7	ADE58799	Ade58799 Human Pro
14	41	100.0	508	7	ADF45072	Adf45072 Human kin
15	41	100.0	508	7	ADL34479	Adl34479 Human lym
16	41	100.0	508	8	ADS88148	Ads88148 Human pro
17	41	100.0	509	3	AAY49420	Aay49420 PKA subst
18	41	100.0	509	6	ABR58699	Abr58699 Human can
19	41	100.0	509	7	ABR56202	Abr56202 Human Lym
20	41	100.0	509	7	ADE40449	Ade40449 Human pro
21	41	100.0	509	8	ADL22907	Adl22907 Human MP2
22	41	100.0	509	8	ADP12458	Adp12458 Protein e
23	41	100.0	509	8	ADP48374	Adp48374 Human lym
24	41	100.0	509	9	ADZ51107	Adz51107 Amino aci
25	41	100.0	509	9	AEA35921	Aea35921 Human Lck
26	41	100.0	539	8	ABM82981	Abm82981 Human dia
27	41	100.0	539	8	ABM82982	Abm82982 Human dia
28	41	100.0	551	4	ABG22264	Abg22264 Novel hum
29	34	82.9	480	10	AEF30109	Aef30109 Lead_Cere
30	33	80.5	761	7	ABM86174	Abm86174 Rice abio
31	33	80.5	769	8	ADJ49264	Adj49264 Oil-assoc
32	32	78.0	61	2	AAR60993	Aar60993 Fragment
33	32	78.0	249	6	ADA34526	Ada34526 Acinetoba
34	32	78.0	466	5	ABP73905	Abp73905 Candida a
35	32	78.0	502	5	AAE21689	Aae21689 Fugu rubr
36	32	78.0	567	5	ABG79673	Abg79673 Tumour in
37	32	78.0	754	9	AEA00731	Aea00731 Brevibaci
38	32	78.0	1377	5	ABP65418	Abp65418 Bifidobac
39	31	75.6	85	8	ABO54831	Abo54831 Human gen
40	31	75.6	270	4	AAB49504	Aab49504 Clone HNT
41	31	75.6	270	5	AAB47950	Aab47950 Human 232
42	31	75.6	270	8	ADJ76359	Adj76359 Marker ge
43	31	75.6	270	9	ADY54291	Ady54291 Human 232
44	31	75.6	317	4	ABB70536	Abb70536 Drosophil
45	31	75.6	329	3	AAB18969	Aab18969 Amino aci
46	31	75.6	329	5	ABB90429	Abb90429 Human pol
47	31	75.6	330	5	ABP69599	Abp69599 Human pol
48	31	75.6	351	4	ABB68045	Abb68045 Drosophil
49	31	75.6	379	3	AAB20902	Aab20902 Drosophil
50	31	75.6	379	3	AAB26430	Aab26430 Drosophil
51	31	75.6	402	7	ADD15292	Add15292 Fruitfly
52	31	75.6	424	9	ABM95606	Abm95606 M. xanthu
53	31	75.6	1017	2	AAY22427	Aay22427 Human bra
54	30	73.2	65	5	ADK35586	Adk35586 Novel hum
55	30	73.2	93	8	ADN99387	Adn99387 Novel hum
56	30	73.2	168	2	AAW06596	Aaw06596 Human end
57	30	73.2	168	3	AAY69674	Aay69674 Human end
58	30	73.2	168	9	ADY37620	Ady37620 EMAP III
59	30	73.2	168	9	ADY58166	Ady58166 Human end
60	30	73.2	178	4	AAB47613	Aab47613 Human Tyr
61	30	73.2	178	5	AAE13489	Aae13489 Human Tyr
62	30	73.2	178	6	ABU72382	Abu72382 Human Tyr
63	30	73.2	192	7	ADF07576	Adf07576 Bacterial
64	30	73.2	265	7	ADH86176	Adh86176 Enterococ
65	30	73.2	301	2	AAW53962	Aaw53962 Monocyte
66	30	73.2	301	8	ADE76967	Ade76967 Human pro
67	30	73.2	301	9	AED20222	Aed20222 Human ova
68	30	73.2	320	8	ADT55550	Adt55550 Plant pol
69	30	73.2	351	9	AED20221	Aed20221 Human ova
70	30	73.2	365	7	ABO62635	Abo62635 Klebsiell
71	30	73.2	365	8	ADS41571	Ads41571 Bacterial
72	30	73.2	403	4	AAG91293	Aag91293 C glutami
73	30	73.2	432	4	AAB79725	Aab79725 Corynebac
74	30	73.2	432	4	AAB79092	Aab79092 Corynebac
75	30	73.2	432	4	AAG91438	Aag91438 C glutami
76	30	73.2	432	7	ADD13439	Add13439 C. glutam
77	30	73.2	432	7	ADD13607	Add13607 C. glutam
78	30	73.2	436	6	ABU34813	Abu34813 Protein e
79	30	73.2	468	7	ABM86189	Abm86189 Rice abio
80	30	73.2	473	8	ADI45165	Adi45165 Rice isop
81	30	73.2	476	8	ADT58335	Adt58335 Plant pol
82	30	73.2	526	8	ADY07792	Ady07792 Plant ful
83	30	73.2	527	7	ABU64299	Abu64299 Human tyr
84	30	73.2	528	7	ADF76697	Adf76697 Novel hum
85	30	73.2	528	8	ADN05830	Adn05830 Antipsori
86	30	73.2	528	8	ADQ65849	Adq65849 Novel hum
87	30	73.2	528	8	ABM80058	Abm80058 Tumour-as
88	30	73.2	528	8	ADP24469	Adp24469 PRO polyp
89	30	73.2	528	9	ADW08740	Adw08740 Human pro
90	30	73.2	528	9	ADY16697	Ady16697 PRO polyp
91	30	73.2	528	9	ADY19754	Ady19754 PRO polyp
92	30	73.2	536	4	AAB47611	Aab47611 Human ful
93	30	73.2	536	5	AAE13487	Aae13487 Human tyr
94	30	73.2	536	6	ABU72380	Abu72380 Human ful
95	30	73.2	696	7	ADJ11548	Adj11548 Rice prot
96	30	73.2	813	8	ADR86362	Adr86362 Aspergill

97	30	73.2	900	6	ABU36857	Abu36857 Protein e
98	30	73.2	3614	4	ABB62664	Abb62664 Drosophil
99	29	70.7	80	5	AAE20614	Aae20614 Protein #
100	29	70.7	80	5	AAE20624	Aae20624 Protein #

ALIGNMENTS

RESULT 1
AAB73127
ID AAB73127 standard; peptide; 9 AA.
XX
AC AAB73127;
XX
DT 09-MAY-2001 (first entry)
XX
DE Tumour antigen peptide #11.
XX
KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS Homo sapiens.
XX
PN WO200111044-A1.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-JP005220.
XX
PR 05-AUG-1999; 99JP-00222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT polynucleotides encoding them for treatment of cancer.
XX
PS Claim 1; Page 69; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|||||||||
Db 1 LQDNLVIAL 9

RESULT 2
AAW73554
ID AAW73554 standard; protein; 126 AA.
XX
AC AAW73554;
XX
DT 08-MAR-1999 (first entry)
XX
DE Lymphoid cell protein-tyrosine kinase SH3 domain.
XX
KW Lymphoid cell protein-tyrosine kinase; Lck; SH3 domain; inhibitor;
KW immune suppressant; autoimmune disease.
XX
OS Unidentified.
XX
PN JP10327864-A.
XX
PD 15-DEC-1998.
XX
PF 28-MAY-1997; 97JP-00138905.
XX
PR 28-MAY-1997; 97JP-00138905.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (MITU) MITSUBISHI CHEM CORP.
XX
DR WPI; 1999-099029/09.
DR N-PSDB; AAV62889.
XX
PT New immunosupressant DNA and protein - useful for inhibition and
PT treatment of autoimmune diseases caused by lymphoid cell protein-tyrosine
PT kinase analogues.
XX
PS Claim 1; Page 4-5; 6pp; Japanese.
XX
CC This sequence is the Lymphoid cell protein-tyrosine kinase (Lck) SH3
CC domain of the invention. The DNA and protein are useful as immune
CC suppressants, and are useful for inhibition and treatment of autoimmune
CC diseases caused by Lck analogues
XX
SQ Sequence 126 AA;

Query Match 100.0%; Score 41; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|||||||||
Db 61 LQDNLVIAL 69

RESULT 3
AAY76750
ID AAY76750 standard; protein; 346 AA.
XX
AC AAY76750;
XX
DT 17-APR-2000 (first entry)
XX
DE Human protein kinase homologue, PKH-3.
XX
KW Protein kinase homologue; human; PKH; diagnosis; therapy; cancer; AIDS;
KW autoimmune disorder; inflammatory disorder; reproductive defect; asthma;
KW diabetes mellitus; infertility; ovulatory defect; endometriosis;
KW polycystic ovary syndrome.
XX
OS Homo sapiens.
XX
PN US6013455-A.
XX
PD 11-JAN-2000.
XX
PF 15-OCT-1998; 98US-00173581.
XX
PR 15-OCT-1998; 98US-00173581.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Hillman JL, Yue H, Yang YT, Corley NC, Gorgone GA, Azimzai Y;
PI Lu DAM, Bandman O, Guegler KJ;
XX
DR WPI; 2000-136321/12.
DR N-PSDB; AAZ86794.
XX
PT Nucleic acids encoding a human protein kinase homolog useful for
PT preventing, diagnosing and treating cancer, autoimmune/inflammatory
PT disorders and reproductive defects.
XX

PS Claim 1; Col 47-50; 38pp; English.
XX
CC This sequence represents a human protein kinase homolog (PKH) of the
CC invention. The PKH sequences may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate PKH expression such
CC as cancers, autoimmune/inflammatory disorders and reproductive defects.
CC They may be used to treat disorders associated with decreased PKH
CC expression such as cancers (e.g. lymphoma, melanoma and cancers of the
CC breast lung and prostate), autoimmune/inflammatory disorders (e.g. AIDS,
CC asthma and diabetes mellitus), and reproductive defects (e.g.
CC infertility, ovulatory defects, endometriosis and polycystic ovary
CC syndrome). The DNA may be administered to treat diseases by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC PKH by expressing inactive proteins or to supplement the patients own
CC production of PKH polypeptides. Additionally, the DNA may be used to
CC produce PKH, according to standard recombinant DNA methodology, by
CC inserting the nucleic acids into a host cell and culturing the cell to
CC express the protein. Conversely, antisense nucleic acid molecules may be
CC administered to down regulate PKH expression by binding with the cells
CC own PKH genes and preventing their expression. The DNA, and antisense
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acid sequences in samples,
CC and hence which patients may be in need of restorative therapy. They may
CC also be used to study the expression and function of PKH polypeptides and
CC their role in metabolism. The PKH polypeptides may be used as antigens in
CC the production of antibodies against PKH and in assays to identify
CC modulators (agonists and antagonists) of PKH expression and activity. The
CC anti-PKH antibodies and PKH antagonists may also be used to down regulate
CC PKH expression and activity. The anti-PKH antibodies may also be used as
CC diagnostic agents for detecting the presence of PKH polypeptides in
CC samples
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 41; DB 3; Length 346;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|||||||||
Db 61 LQDNLVIAL 69

RESULT 4
AAE06208
ID AAE06208 standard; protein; 346 AA.
XX
AC AAE06208;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human protein kinase homolog-3 (PKH-3).
XX
KW Human; protein kinase homolog-3; PKH-3; cytostatic; protein therapy;
KW vaccine; immunosuppressive; antisclerotic; antiabortive; adenocarcinoma;
KW Acquired Immune deficiency Syndrome; AIDS; melanoma; cancer; bone; liver;
KW breast; autoimmune disorder; multiple sclerosis; drug screening; anaemia;
KW Crohn's disease; ectopic pregnancy; tubal disease; inflammatory disorder;
KW reproductive disorder; polycystic ovary syndrome; asthma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 125. .333
FT /note= "Signature sequence"
XX
PN US6264947-B1.
XX
PD 24-JUL-2001.
XX
PF 20-OCT-1999; 99US-00420915.
XX
PR 15-OCT-1998; 98US-00173581.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Bandman O, Tang YT, Hillman JL, Yue H, Guegler KJ, Corley NC;
PI Gorgone GA, Azimzai Y, Lu DAM;
XX
DR WPI; 2001-450728/48.
DR N-PSDB; AAD11845.
XX
PT Human protein kinase proteins and homologs, useful for preventing,
PT diagnosing and treating cancers, autoimmune/inflammatory disorders and
PT reproductive disorders.
XX
PS Claim 1; Col 47-50; 38pp; English.
XX
CC The present sequence is human protein kinase homolog-3 (PKH-3). Human
CC protein kinase homologs (PKH) and their cDNA molecules are used in the
CC prevention, diagnosis and treatment of diseases associated with increased
CC or decreased expression of PKH. Examples of such disorders include,
CC cancer (e.g. adenocarcinoma, melanoma and bone, breast and liver cancer),
CC autoimmune/inflammatory disorders (e.g. Acquired Immune deficiency
CC Syndrome (AIDS), anaemia, asthma, Crohn's disease and multiple sclerosis)
CC and reproductive disorders (e.g. tubal disease, ectopic pregnancy and
CC polycystic ovary syndrome). PKH, its catalytic or immunogenic fragment
CC are used for screening libraries of compounds in any of the drug
CC screening techniques. PKH nucleic acids are used to generate
CC hybridisation probes useful in mapping the naturally occurring genomic
CC sequences. PKH are also used as antigens in the production of antibodies
CC against protein kinases (PK) and in assays to identify modulators of PK
CC expression and activity. PKH is also used in protein therapy
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 41; DB 4; Length 346;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|||||||||
Db 61 LQDNLVIAL 69

RESULT 5
ABB84435
ID ABB84435 standard; protein; 346 AA.
XX
AC ABB84435;
XX
DT 08-NOV-2002 (first entry)
XX
DE Human protein kinase homologue from clone 507669.
XX
KW Protein kinase homologue; PKH; cytostatic; immunosuppressive; antifungal;
KW antiinflammatory; antiallergic; antiasthmatic; antianaemic; antidiabetic;
KW antiarteriosclerotic; antithyroid; dermatological; nephrotropic; human;
KW antigout; thyromimetic; nootropic; osteopathic; antiarthritic; allergy;
KW antirheumatic; ophthalmological; antiulcer; antiviral; antibacterial;
KW antiprotozoal; antiparasitic; antihelmintic; ankylosing spondylitis;
KW acquired immunodeficiency syndrome; AIDS; Addison's disease; amyloidosis;
KW adult respiratory distress syndrome; anaemia; asthma; atherosclerosis;
KW autoimmune haemolytic anaemia; autoimmune thyroiditis; bronchitis;
KW cholecystitis; contact dermatitis; Crohn's disease; atopic dermatitis;
KW dermatomyositis; diabetes mellitus; emphysema; atrophic gastritis; gout;
KW glomerulonephritis; Goodpasture's syndrome; Graves' disease; psoriasis;
KW Hashimoto's thyroiditis; hypereosinophilia; irritable bowel syndrome;
KW multiple sclerosis; myasthenia gravis; myocardial inflammation; uveitis;
KW pericardial inflammation; osteoarthritis; osteoporosis; pancreatitis;
KW polymyositis; Reiter's syndrome; rheumatoid arthritis; scleroderma; SLE;
KW Sjogren's syndrome; systemic lupus erythematosus; systemic sclerosis;
KW thrombocytopenic purpura; ulcerative colitis; Werner syndrome; infection;
KW haemodialysis; extracorporeal circulation; infertility; tubal disease;
KW ovulatory defect; endometriosis; oestrous; menstrual cycle; gene therapy;
KW uterine fibroid; autoimmune disorder; polycystic ovary syndrome; enzyme;

KW ovarian hyperstimulation syndrome; ectopic pregnancy; teratogenesis;
KW cancer.
XX
OS Homo sapiens.
XX
PN US2002081290-A1.
XX
PD 27-JUN-2002.
XX
PF 30-MAY-2001; 2001US-00870962.
XX
PR 15-OCT-1998; 98US-00173581.
PR 20-OCT-1999; 99US-00420915.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Tang YT, Hillman JL, Yue H, Guegler KJ, Corley NC;
PI Gorgone GA, Azimzai Y, Lu DAM;
XX
DR WPI; 2002-655433/70.
DR N-PSDB; ABQ76288.
XX
PT Nucleic acids encoding a human protein kinase homolog useful for
PT preventing, diagnosing and treating cancer, autoimmune/inflammatory
PT disorders and reproductive defects.
XX
PS Claim 47; Page 27; 43pp; English.
XX
CC This invention describes a novel protein kinase homologue (PKH)
CC polypeptides which have cytostatic, immunosuppressive, antiinflammatory,
CC antiallergic, antiasthmatic, antianaemic, antiarteriosclerotic,
CC antithyroid, dermatological, antidiabetic, nephrotropic, antigout,
CC thyromimetic, nootropic, osteopathic, antiarthritic, antirheumatic,
CC ophthalmological, antiulcer, antiviral, antibacterial, antifungal,
CC antiprotozoal, antiparasitic and antihelmintic activity. The polypeptide
CC is used for treating a disease or condition associated with decreased
CC expression of functional PKH. The polypeptide is used to screen for
CC agonists and antagonists of PKH which can also be used in disease
CC treatment. The polypeptide and polynucleotide are used for treating
CC acquired immunodeficiency syndrome (AIDS), Addison's disease, adult
CC respiratory distress syndrome, allergies, ankylosing spondylitis,
CC amyloidosis, anaemia, asthma, atherosclerosis, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, bronchitis, cholecystitis, cancer,
CC contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis,
CC diabetes mellitus, emphysema, atrophic gastritis, glomerulonephritis,
CC Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis,
CC hypereosinophilia, irritable bowel syndrome, multiple sclerosis,
CC myasthenia gravis, myocardial or pericardial inflammation,
CC osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis,
CC Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's syndrome,
CC systemic lupus erythematosus (SLE), systemic sclerosis, thrombocytopenic
CC purpura, ulcerative colitis, uveitis, Werner syndrome, complications of
CC cancer, haemodialysis, and extracorporeal circulation, viral, bacterial,
CC fungal, parasitic, protozoal, and helminthic infections, infertility,
CC including tubal disease, ovulatory defects, and endometriosis,
CC disruptions of the oestrous cycle, disruptions of the menstrual cycle,
CC polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial
CC and ovarian tumours, uterine fibroids, autoimmune disorders, ectopic
CC pregnancies, and teratogenesis. The polypeptides of the invention can be
CC used for gene therapy. This sequence represents a PKH from clone ID
CC 507669 isolated from TMLR3DT02, a library constructed using RNA isolated
CC from non-adherent peripheral blood mononuclear cells collected from a
CC pool of male and female donors
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 41; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|||||||||
Db 61 LQDNLVIAL 69

RESULT 6
ABM82980
ID ABM82980 standard; protein; 355 AA.
XX
AC ABM82980;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3229.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN41632.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 355 AA;

Query Match 100.0%; Score 41; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|||||||||
Db 71 LQDNLVIAL 79

```
RESULT 7
ABR59690
ID   ABR59690 standard; protein; 363 AA.
XX
AC   ABR59690;
XX
DT   25-JUL-2003  (first entry)
XX
DE   Human p56lck.
XX
KW   Human; T lymphocyte activation; T-cell; A-raf-1; TCPTP/PTPN2; asthma;
KW   immunosuppressive; antiasthmatic; antiallergic; antiinflammatory;
KW   lymphocyte activation; lymphocyte migration; cytokine production;
KW   cell surface marker expression; antibody production; apoptosis; allergy;
KW   antibody proliferation; antibody differentiation; hypersensitivity;
KW   graft versus host disease; inflammation; p56lck.
XX
OS   Homo sapiens.
XX
PN   WO2003029277-A2.
XX
PD   10-APR-2003.
XX
PF   02-OCT-2002; 2002WO-US031618.
XX
PR   03-OCT-2001; 2001US-0327212P.
XX
PA   (RIGE-) RIGEL PHARM INC.
XX
PI   Chu P,  Li C,  Liao XC,  Masuda E,  Pardo J,  Zhao H;
XX
DR   WPI; 2003-363276/34.
DR   N-PSDB; ACC81082.
XX
PT   Identifying a compound that modulates T lymphocyte activation, useful for
PT   monitoring changes in cell surface marker expression, comprises
PT   contacting a T cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with
PT   a compound.
XX
PS   Disclosure; Page 64; 126pp; English.
XX
CC   The invention relates to a novel method for identifying a compound that
CC   modulates T lymphocyte activation. The method comprises contacting a T
CC   cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with a compound,
CC   where the A-raf- 1 or TCPTP/PTPN2 polypeptide is encoded by a nucleic
CC   acid that hybridises to a nucleic acid encoding a polypeptide having a
CC   sequence selected from two 606-amino acid sequence and a 415-amino acid
CC   sequence given in the specification. The method of the invention has
CC   immunosuppressive, antiasthmatic, antiallergic, and antiinflammatory
CC   activity. The method is useful for identifying compounds that modulate
CC   lymphocyte activation and migration, and for monitoring changes in cell
CC   surface marker expression, cytokine production, antibody production,
CC   proliferation and differentiation, and apoptosis, using either cell lines
CC   or primary cells. The A-raf- 1 or TCPTP/PTPN2 proteins may be used as
CC   drug targets for compounds that suppress or activate lymphocyte
CC   activation and migration, e.g. for the treatment of diseases in which
CC   modulation of the immune response is desired such as delayed type
CC   hypersensitivity reactions, asthma, allergies, graft versus host disease,
CC   and acute and chronic inflammation. Modulators of lymphocyte activation
CC   are useful for treating disorders related T and B cell activation and
CC   migration. The present sequence is used in the exemplification of the
CC   invention
XX
SQ   Sequence 363 AA;

  Query Match             100.0%;  Score 41;  DB 6;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         61 LQDNLVIAL 69
```

```
RESULT 8
ADP48375
ID   ADP48375 standard; protein; 363 AA.
XX
AC   ADP48375;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human lymphocyte specific tyrosine kinase (Lck) polypeptide #2.
XX
KW   Human; lymphocyte specific tyrosine kinase; Lck;
KW   antisense oligonucleotide; phosphorothioate linkage;
KW   2'-O-methoxyethyl sugar moiety; 5-methylcytosine;
KW   hyperproliferative disorder; cancer; cytostatic; enzyme.
XX
OS   Homo sapiens.
XX
PN   US2004116365-A1.
XX
PD   17-JUN-2004.
XX
PF   10-DEC-2002; 2002US-00316515.
XX
PR   10-DEC-2002; 2002US-00316515.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Borchers AH,  Freier SM;
XX
DR   WPI; 2004-498280/47.
DR   N-PSDB; ADP48372.
XX
PT   New antisense oligonucleotide compounds, useful for diagnosing,
PT   preventing and/or treating diseases or conditions associated with
PT   aberrant expression or activity of Lck, such as hyperproliferative
PT   disorders.
XX
PS   Example 17; SEQ ID NO 75; 40pp; English.
XX
CC   The invention relates to a compound targeted to a nucleic acid molecule
CC   encoding the human lymphocyte specific tyrosine kinase (Lck) polypeptide.
CC   The compound is an antisense oligonucleotide that specifically hybridises
CC   with the nucleic acid and inhibits expression of the polypeptide. The
CC   antisense oligonucleotide comprises at least one modified internucleoside
CC   linkage i.e. a phosphorothioate linkage, at least one modified sugar
CC   moiety, preferably a 2'-O-methoxyethyl sugar moiety, or at least one
CC   modified nucleobase comprising a 5-methylcytosine. The antisense
CC   compounds are useful for modulating the expression of the human Lck
CC   polypeptide and in preparation of a composition for treating
CC   hyperproliferative disorders, e.g. cancer. This sequence represents a
CC   human Lck polypeptide of the invention.
XX
SQ   Sequence 363 AA;

  Query Match             100.0%;  Score 41;  DB 8;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         61 LQDNLVIAL 69
```

```
RESULT 9
ABG79672
ID   ABG79672 standard; protein; 437 AA.
XX
AC   ABG79672;
XX
DT   15-NOV-2002  (first entry)
XX
```

DE Tumour involved gene (TIG) splice variant protein, NV-3.
XX
KW Human; splice variant; tumour-involved gene; TIG;
KW pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;
KW endothelial cell; cell differentiation; cell proliferation; apoptosis;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US2002086384-A1.
XX
PD 04-JUL-2002.
XX
PF 13-MAR-2001; 2001US-00805020.
XX
PR 14-MAR-2000; 2000IL-00135402.
PR 16-MAY-2000; 2000IL-00136154.
XX
PA (LEVI/) LEVINE Z.
PA (DAVI/) DAVID A.
PA (ROMA/) ROMANO C.
PA (BERN/) BERNSTEIN J.
XX
PI Levine Z, David A, Romano C, Bernstein J;
XX
DR WPI; 2002-635679/68.
DR N-PSDB; ABS65202.
XX
PT Novel nucleic acid sequence, which is an alternative splicing variant of
PT tumor involved genes, useful for detecting cancer, predisposition to
PT cancer, for evaluating cancer state and in gene therapy for treating
PT cancer.
XX
PS Claim 4; Page 68-69; 180pp; English.
XX
CC The invention discloses isolated human nucleic acid alternative splicing
CC variants that are all tumour-involved genes (TIGs). The nucleic acids and
CC polypeptides are useful for determining the level of a nucleic acid or
CC polypeptide in a biological sample, for detecting a variant nucleic acid
CC or polypeptide sequence in a biological sample, for determining the level
CC of variant nucleic acid or polypeptide sequences in a biological sample
CC and for determining the ratio between the level of variant sequence in a
CC first biological sample and the level of the original sequence from which
CC the variant has been varied by alternative splicing in a second
CC biological sample and for raising antibodies. A pharmaceutical
CC composition comprising a carrier and the nucleic acid, is useful for
CC treating diseases (e.g. cancer) that can be ameliorated or cured by
CC increasing or decreasing the level of the encoded protein. The nucleic
CC acids are also useful for diagnostic purposes, especially for detecting
CC cancer or a predisposition to cancer, for evaluating the state or
CC aggressiveness of cancer disease, in basic research, for understanding
CC the physiological function of the original TIG, in targeting or
CC developing pharmaceuticals, for distinguishing various stages in the life
CC cycle of the same type of cells which may be helpful for the development
CC of pharmaceuticals for various cancer stages in which cell cycle is non-
CC normal, for determining mutations in tumour-involved genes and in gene
CC therapy. The polypeptides are useful for identifying compounds capable of
CC binding to the variant product and modulating its activity and for
CC modulating endothelial differentiation and proliferation, as well as to
CC modulate apoptosis either ex vivo or in vivo. The sequences presented in
CC ABG796700-ABG79705 are the new variants (NV) 1-36 proteins of the TIGs
CC disclosed
XX
SQ Sequence 437 AA;

Query Match 100.0%; Score 41; DB 5; Length 437;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|||||||||
Db 61 LQDNLVIAL 69

RESULT 10
ADC99048
ID ADC99048 standard; protein; 458 AA.
XX
AC ADC99048;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human KPP protein - SEQ ID 1.
XX
KW anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian;
KW nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
KW antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;
KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;
KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;
KW virucide; protozoacide; fungicide; kinase; phosphatase; KPP;
KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;
KW cancer; developmental; mental retardation; neurological;
KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;
KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
KW helminthic infection; transgenic; gene therapy; human; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003033680-A2.
XX
PD 24-APR-2003.
XX
PF 17-OCT-2002; 2002WO-US033723.
XX
PR 19-OCT-2001; 2001US-0345474P.
PR 02-NOV-2001; 2001US-0343910P.
PR 13-NOV-2001; 2001US-0333098P.
PR 16-NOV-2001; 2001US-0332424P.
PR 30-NOV-2001; 2001US-0334288P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;
PI Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;
PI Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;
PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;
PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;
PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;
PI Zebarjadian Y;
XX
DR WPI; 2003-403214/38.
DR N-PSDB; ADC99100.
XX
PT New human kinases and phosphatases and polynucleotides, useful for
PT diagnosing, treating or preventing autoimmune or inflammatory disorders
PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
PT cancer or hepatitis.
XX
PS Claim 1; SEQ ID NO 1; 424pp; English.
XX
CC The invention relates to a novel isolated polypeptide which is a human
CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,
CC agonists and antagonists are useful for diagnosing, treating or
CC preventing cell proliferative disorders such as atherosclerosis,
CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental
CC retardation, neurological disorders including Alzheimer's disease and
CC Parkinson's disease, autoimmune and inflammatory disorders such as
CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,
CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the
CC polynucleotides encoding KPP may be useful for creating transgenic
CC animals to model human disease, as well as during gene therapy
CC procedures. The current sequence is that of the human KPP protein of the
CC invention.
XX
SQ Sequence 458 AA;

```
  Query Match           100.0%;  Score 41;  DB 7;  Length 458;
  Best Local Similarity  100.0%;  Pred. No. 7.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         61 LQDNLVIAL 69


RESULT 11
AAB37700
ID   AAB37700 standard; protein; 508 AA.
XX
AC   AAB37700;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human lymphocyte kinase.
XX
KW   Human; lymphocyte kinase; protein co-ordinate data; lck; crystal.
XX
OS   Homo sapiens.
XX
PN   WO200070030-A1.
XX
PD   23-NOV-2000.
XX
PF   19-MAY-2000; 2000WO-US013881.
XX
PR   19-MAY-1999;   99US-0134965P.
XX
PA   (KINE-) KINETIX PHARM INC.
XX
PI   Zhu X;
XX
DR   WPI; 2000-687708/67.
XX
PT   Crystal of a protein-ligand complex for identifying kinase inhibitors,
PT   comprises a truncated lymphocyte kinase and a ligand, and diffracts X-
PT   rays to determine atomic coordinates at a resolution greater than 5
PT   angstroms.
XX
PS   Claim 1; Page 434-5; 438pp; English.
XX
CC   The present invention relates to a crystal of a protein-ligand complex
CC   comprising a truncated lymphocyte kinase (lck) and a ligand. The crystal
CC   diffracts X-rays so that the atomic coordinates of the protein-ligand
CC   complex can be determined to a resolution of greater than 5.0 Angstroms.
CC   The truncated lck used in the present invention comprises the globular
CC   core of the corresponding full-length lck. The present sequence is the
CC   full-length human lck protein. The crystal of the present invention may
CC   be used to identify kinase inhibitors in screening assays, in drug
CC   screening and drug design processes, to design, select or test inhibitors
CC   of kinase enzymes, where the inhibitors are used as therapeutics for the
CC   treatment and modulation of diseases, disease symptoms or the effect of
CC   other physiological events mediated by kinases, having one or more kinase
CC   enzymes involved in their pathology
XX
SQ   Sequence 508 AA;

  Query Match           100.0%;  Score 41;  DB 3;  Length 508;
  Best Local Similarity  100.0%;  Pred. No. 8.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         60 LQDNLVIAL 68


RESULT 12
ADE58802
ID   ADE58802 standard; protein; 508 AA.
XX
AC   ADE58802;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein P06239, SEQ ID NO 4689.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P06239.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 508 AA;

  Query Match           100.0%;  Score 41;  DB 7;  Length 508;
  Best Local Similarity  100.0%;  Pred. No. 8.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         60 LQDNLVIAL 68
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RESULT 13
ADE58799
ID   ADE58799 standard; protein; 508 AA.
XX
AC   ADE58799;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein P06239, SEQ ID NO 4686.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P06239.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 508 AA;

  Query Match             100.0%;  Score 41;  DB 7;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 8.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         60 LQDNLVIAL 68


RESULT 14
ADF45072
ID   ADF45072 standard; protein; 508 AA.
XX
AC   ADF45072;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human kinase LCK.
XX
KW   Human; protein kinase; enzyme; inhibitor; LCK.
XX
OS   Homo sapiens.
XX
PN   WO2003081210-A2.
XX
PD   02-OCT-2003.
XX
PF   20-MAR-2003; 2003WO-US008725.
XX
PR   21-MAR-2002; 2002US-0366892P.
XX
PA   (SUNE-) SUNESIS PHARM INC.
XX
PI   Prescott JC,  Braisted A;
XX
DR   WPI; 2003-865136/80.
XX
PT   Identifying ligand binding to inactive conformation of target protein
PT   kinase (T) comprises contacting the conformation modified (T) which
PT   contains reactive group at binding site, with ligands and detecting
PT   kinase-ligand conjugate formation.
XX
PS   Disclosure; SEQ ID NO 41; 260pp; English.
XX
CC   The present invention relates to a method for identifying a ligand (L),
CC   which binds to an inactive conformation of target protein kinase (T). The
CC   method involves contacting inactive conformation of (T), which contains
CC   or is modified to contain a reactive group at or near a binding site of
CC   interest, with one or more ligand candidates capable of covalently
CC   bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC   The method is useful for identifying protein kinase inhibitors that
CC   preferentially bind to inactive conformation of a target protein kinase.
CC   The present sequence is a protein kinase which may be modified via an
CC   amino acid substitution, for use in the method of the invention.
XX
SQ   Sequence 508 AA;

  Query Match             100.0%;  Score 41;  DB 7;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 8.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         60 LQDNLVIAL 68


RESULT 15
ADL34479
ID   ADL34479 standard; peptide; 508 AA.
XX
AC   ADL34479;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human lymphocyte kinase (Lck) globular core.
```

XX
KW cytostatic; immunosuppressive; antiinflammatory; antibacterial; virucide;
KW fungicide; nootropic; neuroprotective; kinase inhibitor; crystal;
KW protein-ligand complex; lymphocyte kinase; Lck; Lck ligand;
KW kinase inhibitor; therapeutic; kinase-mediated physiological event;
KW cancer; autoimmunological; metabolic; inflammatory; infection;
KW central nervous system degenerative disease; transplant rejection; human;
KW globular core; protein co-ordinate data.
XX
OS Homo sapiens.
XX
PN US6589758-B1.
XX
PD 08-JUL-2003.
XX
PF 21-MAY-2001; 2001US-00862154.
XX
PR 19-MAY-2000; 2000US-0205510P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zhu X;
XX
DR WPI; 2003-810380/76.
XX
PT Crystal of protein-ligand complex useful for identifying an inhibitor of
PT lymphocyte kinase (Lck), comprises truncated Lck and a ligand.
XX
PS Claim 1; SEQ ID NO 1; 295pp; English.
XX
CC The invention describes a crystal (I) of a protein-ligand complex (C)
CC comprising a truncated lymphocyte kinase (Lck) and a ligand, where (I)
CC effectively diffracts X-rays for determination of atomic coordinates of
CC (C) to a resolution of greater than 5.0 angstroms, and truncated Lck
CC comprises a sequence (S1) of residues 225-508 of a 508 amino acid
CC sequence, given in specification and retains the globular core of full-
CC length Lck. (I) is useful in an inhibitor screening assay and to
CC identify, design, select, and evaluate potential inhibitors of kinases
CC that would be useful as therapeutics for diseases or symptoms of diseases
CC that are associated with kinase-mediated physiological events. The
CC inhibitors identified by the methods may also be useful for inhibition of
CC kinase activity of one or more enzymes. The inhibitors are also useful
CC for inhibiting the biological activity of any enzyme comprising greater
CC than 90%, alternatively greater than 85%, or alternatively greater than
CC 70% sequence homology with a kinase sequence. The inhibitors are useful
CC for inhibiting the biological activity of any enzyme that binds ATP and
CC thus for treating disease or disease symptoms mediated by any enzyme that
CC binds ATP. The inhibitors are useful in inhibiting kinase activity and
CC are useful in treating kinase-mediated disease or disease symptoms in a
CC mammal, particularly a human e.g., cancer, autoimmunological, metabolic,
CC inflammatory, infection, (bacterial, viral, yeast, fungal, etc.), central
CC nervous system degenerative disease etc. The inhibitors are useful in
CC treating or preventing diseases, including, transplant rejection etc.
CC This is the amino acid sequence of a human lymphocyte kinase (Lck)
CC polypeptide comprising the Lck globular core.
XX
SQ Sequence 508 AA;

```
  Query Match             100.0%;  Score 41;  DB 7;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 8.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         60 LQDNLVIAL 68
```

RESULT 16
ADS88148
ID ADS88148 standard; protein; 508 AA.
XX
AC ADS88148;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human protein of a TNF-alpha signalling pathway protein complex SeqID 3.
XX
KW protein complex; tumour necrosis factor-alpha signalling pathway;
KW TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
KW inflammatory bowel disease; infectious disease; septic shock;
KW bacterial infection; neurological disease; stroke-induced inflammation;
KW neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
KW antirheumatic; cytostatic; antibacterial; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004035783-A2.
XX
PD 29-APR-2004.
XX
PF 24-SEP-2003; 2003WO-EP050655.
XX
PR 26-SEP-2002; 2002EP-00021809.
PR 10-FEB-2003; 2003EP-00100274.
XX
PA (CELL-) CELLZOME AG.
XX
PI Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
PI Superti-Furga G, Kruse U;
XX
DR WPI; 2004-348460/32.
XX
PT New protein complex comprising at least one first and second protein of
PT the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
PT diagnosing or treating inflammation, neurological diseases, infectious
PT diseases or cancer.
XX
PS Example; SEQ ID NO 3; 1980pp; English.
XX
CC This invention relates to novel protein complexes of the tumour necrosis
CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
CC methods for preparing these complexes comprising at least two component
CC proteins, as well as screening methods to identify modulators of the
CC pathway, which include antibodies, agonists and antagonists thereof. The
CC present invention describes a protein complex and kit that are useful for
CC diagnosing, prognosing or treating chronic inflammatory diseases such as
CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases
CC such as septic shock and bacterial infections; neurological diseases such
CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
CC cancer. Accordingly, these complexes can be used for the development of
CC pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
CC antirheumatic, cytostatic and antibacterial activities and can be used
CC for gene therapy purposes. In particular, the invention further provides
CC siRNA-oligonucleotides useful for inhibiting protein expression for in
CC vitro or cell culture assays. This polypeptide is a human protein that
CC can be used in combination with other proteins provided in the
CC specification to form novel complexes of the TNF-alpha signalling pathway
CC of the invention.
XX
SQ Sequence 508 AA;

```
  Query Match             100.0%;  Score 41;  DB 8;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 8.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         60 LQDNLVIAL 68
```

RESULT 17
AAY49420
ID AAY49420 standard; protein; 509 AA.
XX
AC AAY49420;
XX

DT 13-MAR-2000 (first entry)
XX
DE PKA substrate, Src-family protein.
XX
KW Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer;
KW kinase substrate; immunosuppressive disorder; proliferative disease;
KW HIV infection; AIDS; immunodeficiency; autoimmune disease;
KW systemic lupus erythematosus; Src-family.
XX
OS Homo sapiens.
XX
PN WO9962315-A2.
XX
PD 02-DEC-1999.
XX
PF 27-MAY-1999; 99WO-GB001680.
XX
PR 27-MAY-1998; 98NO-00002419.
PR 30-DEC-1998; 98US-0114240P.
XX
PA (LAUR-) LAURAS AS.
PA (JONE/) JONES E L.
XX
PI Hansson V, Levy FO, Mustelin T, Skalhegg BS, Sundvold V;
PI Tasken K, Vang T, Altman A, Munshi A;
XX
DR WPI; 2000-086801/07.
DR N-PSDB; AAZ46491.
XX
PT Altering the activity of protein kinase signaling pathways, used for
PT treating immunosuppressive disorders, e.g. AIDS, proliferative disorders,
PT e.g. cancers or autoimmune diseases.
XX
PS Claim 23; Page 95-96; 111pp; English.
XX
CC The invention provides a novel method of altering the activity of the
CC protein kinase A (PKA) signaling pathway in a cell that comprises
CC altering the extent of phosphorylation of one or more PKA substrates, or
CC kinase substrates downstream in the PKA signaling pathway. Pharmaceutical
CC compositions containing a nucleic acid molecule that encodes a PKA
CC substrate, or fragment, precursor or functionally equivalent variant,
CC where the sequence is modified to alter its susceptibility to
CC phosphorylation by PKA can be used for treating a disorder exhibiting
CC abnormal PKA signaling activity, immunosuppressive disorders or
CC proliferative diseases. They can be used for treating e.g. HIV infection,
CC AIDS, common variable immunodeficiency or cancers. Conditions in which
CC upregulation of the PKA pathway is required, such as autoimmune disease,
CC e.g. systemic lupus erythematosus, may also be treated. The present
CC sequence represents a PKA substrate, wherein the substrate is in the Src-
CC family, preferably Lck, Fyn, Src, Yes, Fgr, Lyn, Hck Blk, Yrk, c-tkl,
CC Fyk, Src-1 or Src-2
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 41; DB 3; Length 509;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|||||||||
Db 61 LQDNLVIAL 69

RESULT 18
ABR58699
ID ABR58699 standard; protein; 509 AA.
XX
AC ABR58699;
XX
DT 09-JUL-2003 (first entry)
XX
DE Human cancer related protein SEQ ID NO:356.
XX
KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.
XX
OS Homo sapiens.
XX
PN WO2003025138-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-US029560.
XX
PR 17-SEP-2001; 2001US-0323469P.
PR 20-SEP-2001; 2001US-0323887P.
PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI Zlotnik A;
XX
DR WPI; 2003-354600/33.
DR N-PSDB; ACC72850.
XX
PT New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX
PS Claim 12; Page 762; 767pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 41; DB 6; Length 509;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|||||||||
Db 61 LQDNLVIAL 69

RESULT 19
ABR56202
ID ABR56202 standard; protein; 509 AA.
XX
AC ABR56202;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human Lymphocyte Cell Kinase, Lck.

XX
KW Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW Src-family protein tyrosine kinase; T-cell; immune response.
XX
OS Homo sapiens.
XX
PN WO2003020880-A2.
XX
PD 13-MAR-2003.
XX
PF 02-AUG-2002; 2002WO-US024546.
XX
PR 03-AUG-2001; 2001US-0310051P.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Borhani DW, Calderwood D, Dixon RW, Hirst GC, Hrnciar P, Loew A;
PI Leung A, Ritter K;
XX
DR WPI; 2003-300872/29.
XX
PT New crystalline polypeptide comprising ligand binding domain or catalytic
PT domain of Lck protein, for determining three-dimensional structure of
PT catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS Claim 5; Fig 1; 994pp; English.
XX
CC The present invention relates to a crystalline polypeptide (I),
CC comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC in T-cells and plays an essential role in immune response. The present
CC sequence is the full-length sequence of human Lck (1-509). (I) is useful
CC for identifying a compound which is an inhibitor of human Lck protein
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 41; DB 7; Length 509;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|||||||||
Db 61 LQDNLVIAL 69

RESULT 20
ADE40449
ID ADE40449 standard; protein; 509 AA.
XX
AC ADE40449;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human proto-oncogene Tyr protein kinase LCK (gene ID 1611) protein.
XX
KW AIDS; acquired immunodeficiency syndrome; human immunodeficiency virus;
KW HIV-related disorder; differential expression; drug screening;
KW viral replication modulation; diagnosis; prognosis; predisposition;
KW anti-HIV; gene therapy; antisense therapy; human;
KW proto-oncogene Tyr protein kinase LCK; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003070883-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004246.
XX
PR 15-FEB-2002; 2002US-0357391P.
PR 13-MAY-2002; 2002US-0380249P.
PR 25-JUN-2002; 2002US-0391306P.
PR 27-AUG-2002; 2002US-0406297P.
PR 19-SEP-2002; 2002US-0412007P.
PR 10-OCT-2002; 2002US-0417508P.
PR 10-DEC-2002; 2002US-0432318P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Powell DM, Weich NS;
XX
DR WPI; 2003-671808/63.
DR N-PSDB; ADE40448.
XX
PT Identifying a compound capable of diagnosing, preventing or treating AIDS
PT or an HIV-related disorder comprises assaying the ability of the compound
PT to modulate e.g. 1414, 1481 or 1553 nucleic acid expression or
PT polypeptide activity.
XX
PS Claim 1; SEQ ID NO 28; 167pp; English.
XX
CC The invention relates to a method of identifying a compound useful in the
CC treatment of AIDS (acquired immunodeficiency syndrome) or an HIV (human
CC immunodeficiency virus)-related disorder. The invention involves assaying
CC the ability of a test compound to modulate the activity or expression of
CC 26 human proteins. These proteins and nucleic acids encoding them
CC (ADE40422-ADE40473) are differentially expressed in tissues relating to
CC AIDS or an HIV-related disorder compared to their expression in normal
CC tissues. The invention also relates to the use of the compounds
CC identified to modulate viral replication in a cell and to treat a patient
CC with AIDS or an HIV-related disorder. The invention further discloses
CC methods for the diagnostic evaluation and prognosis of various HIV-
CC related disorders, and for the identification of individuals exhibiting a
CC predisposition to such conditions. The modulatory compounds identified
CC using the method of the invention may be small organic molecules,
CC peptides, antibodies or antisense nucleic acid molecules. The methods of
CC the invention are useful in diagnosing, preventing or treating AIDS or
CC HIV-related disorders. The present sequence represents a human protein
CC which is differentially expressed in AIDS or HIV-related disorders.
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 41; DB 7; Length 509;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|||||||||
Db 61 LQDNLVIAL 69

RESULT 21
ADL22907
ID ADL22907 standard; protein; 509 AA.
XX
AC ADL22907;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human MP2153 polypeptide sequence SEQ ID NO: 27.
XX
KW human; MP2153; p21; p53; cancer.
XX
OS Homo sapiens.
XX
PN WO2004015069-A2.
XX
PD 19-FEB-2004.
XX
PF 06-AUG-2003; 2003WO-US024505.
XX
PR 07-AUG-2002; 2002US-0401701P.
PR 16-SEP-2002; 2002US-0411017P.
PR 30-DEC-2002; 2002US-0437107P.
XX
PA (EXEL-) EXELIXIS INC.

XX
PI Francis-Lang H, Friedman L, Kidd T, Roche S, Belvin M;
PI Plowman GD, Lickteig K, Zhang H, Amundsen CD;
XX
DR WPI; 2004-180653/17.
DR N-PSDB; ADL22890.
XX
PT Identifying a candidate p21 or p53 pathway modulating agent using an
PT assay system having a modulator of p21 or p53 (MP2153) polypeptide or
PT nucleic acid, useful for diagnosing or treating cancer, such as colon or
PT breast cancer.
XX
PS Example 3; Page 94-96; 110pp; English.
XX
CC The present invention relates to a method of identifying a candidate p21
CC or p53 pathway modulating agent. This comprises providing an assay system
CC comprising a modulator of p21 or p53 (MP2153) polypeptide or nucleic
CC acid, contacting the assay system with a test agent, where in its
CC presence the system provides a reference activity, and detecting a test
CC agent-biased activity of the assay system, wherein a difference between
CC the test agent-biased activity and the reference activity identifies the
CC test agent as a candidate p21 or p53 pathway modulating agent. The
CC methods and compositions of the present invention are useful for the
CC diagnosis and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of the p21 or p53 pathway, such as
CC cancer, preferably colon or head and neck cancer. The present sequence is
CC a human MP2153 protein sequence of the invention.
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 41; DB 8; Length 509;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|||||||||
Db 61 LQDNLVIAL 69

RESULT 22
ADP12458
ID ADP12458 standard; protein; 509 AA.
XX
AC ADP12458;
XX
DT 12-AUG-2004 (first entry)
XX
DE Protein encoded by mRNA of the invention #68.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
OS Homo sapiens.
XX
PN WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX
PR 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
DR WPI; 2004-400724/37.
XX
PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
PS Claim 65; SEQ ID NO 2467; 1762pp; English.
XX
CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein that is encoded by the mRNA cf the invention.
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 41; DB 8; Length 509;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|||||||||
Db 61 LQDNLVIAL 69

RESULT 23
ADP48374
ID ADP48374 standard; protein; 509 AA.
XX
AC ADP48374;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human lymphocyte specific tyrosine kinase (Lck) polypeptide #1.
XX
KW Human; lymphocyte specific tyrosine kinase; Lck;
KW antisense oligonucleotide; phosphorothioate linkage;
KW 2'-O-methoxyethyl sugar moiety; 5-methylcytosine;
KW hyperproliferative disorder; cancer; cytostatic; enzyme.
XX
OS Homo sapiens.
XX
PN US2004116365-A1.
XX
PD 17-JUN-2004.
XX
PF 10-DEC-2002; 2002US-00316515.
XX
PR 10-DEC-2002; 2002US-00316515.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Borchers AH, Freier SM;
XX
DR WPI; 2004-498280/47.
DR N-PSDB; ADP48301.
XX
PT New antisense oligonucleotide compounds, useful for diagnosing,
PT preventing and/or treating diseases or conditions associated with
PT aberrant expression or activity of Lck, such as hyperproliferative
PT disorders.
XX
PS Claim 1; SEQ ID NO 4; 40pp; English.
XX
CC The invention relates to a compound targeted to a nucleic acid molecule
CC encoding the human lymphocyte specific tyrosine kinase (Lck) polypeptide.
CC The compound is an antisense oligonucleotide that specifically hybridises
CC with the nucleic acid and inhibits expression of the polypeptide. The
CC antisense oligonucleotide comprises at least one modified internucleoside

```
CC   linkage i.e. a phosphorothioate linkage, at least one modified sugar
CC   moiety, preferably a 2'-O-methoxyethyl sugar moiety, or at least one
CC   modified nucleobase comprising a 5-methylcytosine. The antisense
CC   compounds are useful for modulating the expression of the human Lck
CC   polypeptide and in preparation of a composition for treating
CC   hyperproliferative disorders, e.g. cancer. This sequence represents a
CC   human Lck polypeptide of the invention.
XX
SQ   Sequence 509 AA;

  Query Match             100.0%;  Score 41;  DB 8;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 8.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         61 LQDNLVIAL 69


RESULT 24
ADZ51107
ID   ADZ51107 standard; protein; 509 AA.
XX
AC   ADZ51107;
XX
DT   30-JUN-2005  (first entry)
XX
DE   Amino acid sequence of human Tyr kinase Lck.
XX
KW   protein kinase inhibitor; inactive conformation; Tethering; Tyr kinase;
KW   Lck.
XX
OS   Homo sapiens.
XX
PN   WO2005034840-A2.
XX
PD   21-APR-2005.
XX
PF   17-SEP-2003; 2003WO-US029870.
XX
PR   17-SEP-2003; 2003WO-US029870.
XX
PA   (SUNE-) SUNESIS PHARM INC.
XX
PI   Prescoot JC;
XX
DR   WPI; 2005-315455/32.
XX
PT   Identifying ligand binding to inactive conformation of target protein
PT   kinase, by contacting inactive conformation of target with ligand
PT   candidates specific to target, detecting formation of kinase-ligand
PT   conjugate and identifying ligand.
XX
PS   Example 1; SEQ ID NO 9; 101pp; English.
XX
CC   The specification describes a method for identifying protein kinase
CC   inhibitors that preferentially bind to the inactive conformation of a
CC   target protein kinase. The inhibitors are identified by locking the
CC   target protein kinase in an inactive conformation, and using Tethering to
CC   identify inhibitors preferentially targeting the inactive conformation.
CC   The method of the invention is useful for identifying a ligand which
CC   binds to an inactive conformation of a target protein kinase. The present
CC   sequence represents the human Tyr kinase Lck. Lck variants were used to
CC   demonstrate the method of the invention.
XX
SQ   Sequence 509 AA;

  Query Match             100.0%;  Score 41;  DB 9;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 8.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         61 LQDNLVIAL 69


RESULT 25
AEA35921
ID   AEA35921 standard; protein; 509 AA.
XX
AC   AEA35921;
XX
DT   25-AUG-2005  (first entry)
XX
DE   Human Lck kinase amino acid sequence SEQ ID NO:8.
XX
KW   Src family kinase; Lck kinase.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 273
FT                   /note= "constant amino acid K in domain SH2"
FT   Misc-difference 316
FT                   /note= "constant amino acid T in domain SH2"
FT   Misc-difference 505
FT                   /note= "constant amino acid Y in domain SH1"
XX
PN   EP1541694-A1.
XX
PD   15-JUN-2005.
XX
PF   12-DEC-2003; 2003EP-00028713.
XX
PR   12-DEC-2003; 2003EP-00028713.
XX
PA   (SIRE-) SIRENADE PHARM AG.
XX
PI   Obermeier A,  Bieger B;
XX
DR   WPI; 2005-428084/44.
XX
PT   Identifying compound which modulates Src family kinase (SFK) activity, by
PT   contacting cells expressed with SFK or mutated SFK with test compound,
PT   where change in phenotype of cells indicates that test compound modulates
PT   SFK activity.
XX
PS   Disclosure; SEQ ID NO 8; 114pp; English.
XX
CC   The invention relates to a method (M1) for identifying, selecting and/or
CC   characterizing a compound which modulates Src family kinase (SFK)
CC   activity, by expressing nucleic acids encoding SFK or mutated SFK in
CC   cells, contacting cells with test compound and determining whether
CC   phenotype of cells is changed as compared with phenotype of cells not
CC   expressed with above nucleic acids, where difference in phenotype
CC   indicates that test compound modulate SFK activity. Also described: (1) a
CC   compound (I) identified, selected and/or characterized by (M1); and (2) a
CC   pharmaceutical composition (PC1) containing (I), and a carrier, adjuvant
CC   or vehicle. (I) is useful as a medicament, particularly for the treatment
CC   of diseases, which are at least in part caused by a Src family kinase.
CC   (I) and PC1 are useful for producing a medicament for the treatment of
CC   diseases, which are at least in part caused by a Src family kinase,
CC   particularly by a dysfunction of a Src family kinase, in particular
CC   cancer, hypercalcemia, restenosis, osteoporosis, osteoarthritis,
CC   symptomatic treatment of bone metastasis, rheumatoid arthritis,
CC   inflammatory bowel disease, multiple sclerosis, psoriasis, lupus, graft
CC   versus host disease, T-cell mediated hypersensitivity disease,
CC   Hashimoto's thyroiditis, Guillain-Barre syndrome, chronic obstructive
CC   pulmonary disorder, contact dermatitis, Paget's disease, asthma, ischemic
CC   or reperfusion injury, allergic disease, atopic dermatitis, transplant
CC   rejection or allergic rhinitis. The present sequence represents human Lck
CC   kinase, which is given in the exemplification of the present invention.
XX
SQ   Sequence 509 AA;

  Query Match             100.0%;  Score 41;  DB 9;  Length 509;
```

Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|||||||||
Db 61 LQDNLVIAL 69

RESULT 26
ABM82981
ID ABM82981 standard; protein; 539 AA.
XX
AC ABM82981;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3230.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN41633.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 539 AA;

Query Match 100.0%; Score 41; DB 8; Length 539;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|||||||||
Db 61 LQDNLVIAL 69

RESULT 27
ABM82982
ID ABM82982 standard; protein; 539 AA.
XX
AC ABM82982;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3231.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN41634.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 539 AA;

Query Match 100.0%; Score 41; DB 8; Length 539;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 LQDNLVIAL 9
              |||||||||
Db         61 LQDNLVIAL 69


RESULT 28
ABG22264
ID   ABG22264 standard; protein; 551 AA.
XX
AC   ABG22264;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #22255.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US008631.
XX
PR   31-MAR-2000; 2000US-00540217.
PR   23-AUG-2000; 2000US-00649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS86451.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity.
XX
PS   Claim 20; SEQ ID NO 52623; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC   sequences. (I) is useful as hybridisation probes, polymerase chain
CC   reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC   and in recombinant production of (II). The polynucleotides are also used
CC   in diagnostics as expressed sequence tags for identifying expressed
CC   genes. (I) is useful in gene therapy techniques to restore normal
CC   activity of (II) or to treat disease states involving (II). (II) is
CC   useful for generating antibodies against it, detecting or quantitating a
CC   polypeptide in tissue, as molecular weight markers and as a food
CC   supplement. (II) and its binding partners are useful in medical imaging
CC   of sites expressing (II). (I) and (II) are useful for treating disorders
CC   involving aberrant protein expression or biological activity. The
CC   polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC   amino acid sequences of the invention. Note: The sequence data for this
CC   patent did not appear in the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 551 AA;

  Query Match             100.0%;  Score 41;  DB 4;  Length 551;
  Best Local Similarity   100.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         78 LQDNLVIAL 86


RESULT 29
AEF30109
ID   AEF30109 standard; protein; 480 AA.
XX
AC   AEF30109;
XX
DT   23-MAR-2006  (first entry)
XX
DE   Lead_CeresClone35742 protein homolog SEQ ID NO:2309.
XX
KW   plant; transgenic plant; crop improvement; abiotic stress tolerance;
KW   plant growth regulation.
XX
OS   Arabidopsis thaliana.
XX
PN   WO2006004955-A2.
XX
PD   12-JAN-2006.
XX
PF   30-JUN-2005; 2005WO-US023326.
XX
PR   30-JUN-2004; 2004US-0583621P.
PR   30-JUN-2004; 2004US-0584800P.
PR   30-JUN-2004; 2004US-0584829P.
XX
PA   (CERE-) CERES INC.
XX
PI   Alexandrov N,  Brover V,  Mascia P,  Feldmann K;
XX
DR   WPI; 2006-090599/09.
XX
PT   New isolated nucleic acid molecule modifying plant phenotypes and
PT   characteristics and the polypeptide it encodes, useful for making
PT   transgenic plants with improved characteristics.
XX
PS   Claim 1; SEQ ID NO 2309; 612pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule modifying
CC   plant phenotypes and characteristics, comprising a nucleotide sequence
CC   that encodes an amino acid sequence exhibiting at least 85% sequence
CC   identity to an amino acid sequence in the sequence listing or in the
CC   ortholog alignments of Figure 1, a nucleic acid, which is a complement of
CC   (a), a nucleic acid, which is the reverse of the nucleotide sequence in
CC   (a)(such that the reverse nucleotide sequence has a sequence order which
CC   is the reverse of the sequence order of (a)) or a nucleic acid capable of
CC   hybridizing (a-c), under conditions that permit formation of a nucleic
CC   acid duplex at a temperature of 40-48 degrees C below the melting
CC   temperature of the nucleic acid duplex. Also included are a vector
CC   construct (comprising a first nucleic acid having a regulatory sequence
CC   capable of causing transcription and/or translation in a plant, operably
CC   linked to a second nucleic acid having the sequence of the isolated
CC   nucleic acid molecule), a host cell comprising the isolated nucleic acid
CC   molecule that is flanked by exogenous sequence, a host cell comprising
CC   the vector construct, an isolated polypeptide comprising an amino acid
CC   sequence exhibiting at least 85% sequence identity to those cited above,
CC   introducing an isolated nucleic acid into a host cell, transforming a
CC   host cell, detecting a nucleic acid in a sample, a host cell or organism
CC   comprising the nucleic acid molecule, a plant generated from the plant
CC   cell or seed, a plant(plant cell, plant material or seed) comprising the
CC   nucleic acid molecule (where the plant has improved characteristics as
CC   compared to a wild type plant), improving plant characteristics in a
CC   plant comprising transforming the plant with the nucleic acid sequence,
CC   and a transgenic plant having a gene construct (comprising the nucleic
CC   encoding a component operably linked to a plant promoter so that the
CC   component is ectopically overexpressed in the transgenic plant). The
CC   transgenic plant exhibits faster rate of growth, greater fresh of dry
CC   weight of maturation, greater fruit or seed yield, higher tolerance to
CC   pH, higher tolerance to low phosphate concentration, or higher tolerance
CC   to low nitrogen concentration than a progenitor plant, which does not
```

CC contain the progenitor construct, when the transgenic plant and
CC progenitor plant are cultivated under identical environmental conditions,
CC where the component is any one of the polypeptides cited above. The
CC nucleic acid molecules are useful for producing transgenic plants with
CC improved characteristics. The present sequence is an ortholog of a
CC protein encoded by a plant nucleic acid (cDNA) of the invention.
XX
SQ Sequence 480 AA;

Query Match 82.9%; Score 34; DB 10; Length 480;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
| |||::||
Db 47 LSDNLIVAL 55

RESULT 30
ABM86174
ID ABM86174 standard; protein; 761 AA.
XX
AC ABM86174;
XX
DT 02-JUN-2005 (first entry)
XX
DE Rice abiotic stress responsive polypeptide SEQ ID NO:4420.
XX
KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
XX
OS Oryza sativa.
XX
PN WO2003008540-A2.
XX
PD 30-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019668.
XX
PR 22-JUN-2001; 2001US-0300112P.
PR 24-AUG-2001; 2001US-0314662P.
PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-0332132P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX
DR WPI; 2003-248011/24.
XX
PT New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
PS Claim 1; SEQ ID NO 4420; 89pp; English.
XX
CC The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
SQ Sequence 761 AA;

Query Match 80.5%; Score 33; DB 7; Length 761;
Best Local Similarity 55.6%; Pred. No. 6.6e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|:||:|:|:
Db 456 LEDNMVVAI 464

Search completed: June 29, 2006, 09:13:18
Job time : 90.8313 secs

OM protein - protein search, using sw model

Run on: June 29, 2006, 09:13:45 ; Search time 13.3373 Seconds
(without alignments)
64.927 Million cell updates/sec

Title: US-10-062-257A-11
Perfect score: 41
Sequence: 1 LQDNLVIAL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	100.0	509	1	I48845	protein-tyrosine k
2	41	100.0	509	1	OKHULK	protein-tyrosine k
3	35	85.4	431	2	G72285	hybrid cluster [4F
4	34	82.9	269	2	G71706	hypothetical prote
5	34	82.9	507	1	A39939	protein-tyrosine k
6	33	80.5	234	2	D97789	hypothetical prote
7	32	78.0	199	2	C90505	conserved hypothet
8	32	78.0	491	2	A59199	hybrid cluster [4F
9	31	75.6	67	2	G97092	endoglucanase (tru
10	31	75.6	473	2	AI0587	deoxyribodipyrimid
11	31	75.6	473	2	S22321	deoxyribodipyrimid
12	31	75.6	496	2	H75122	sarcosine oxidase
13	31	75.6	733	2	E86345	hypothetical prote
14	31	75.6	1488	2	AG2136	polyketide synthas
15	31	75.6	2630	2	T08868	polyprotein P1 - A
16	30	73.2	213	2	S75886	hypothetical prote
17	30	73.2	297	2	E96998	4-hydroxybenzoate
18	30	73.2	319	2	T48504	hypothetical prote
19	30	73.2	361	2	C97009	hypothetical prote
20	30	73.2	420	2	S62541	hypothetical prote
21	30	73.2	498	2	AH2468	hypothetical prote
22	30	73.2	569	2	C69769	hypothetical prote
23	30	73.2	668	2	T36330	cell division prot
24	30	73.2	673	1	B64530	methyl-accepting c
25	30	73.2	673	2	A71978	methyl-accepting c
26	30	73.2	726	2	T16356	hypothetical prote
27	30	73.2	900	2	B70694	probable infB - My
28	30	73.2	2359	2	T03094	A-kinase anchor pr
29	29	70.7	71	2	T42025	hypothetical prote
30	29	70.7	90	2	G84991	hypothetical prote
31	29	70.7	124	2	T10919	3C3.10 protein - S
32	29	70.7	151	2	AG1990	hypothetical prote
33	29	70.7	170	2	S37498	sporozoite antigen
34	29	70.7	179	2	AD1917	hypothetical prote
35	29	70.7	219	2	G86114	hypothetical prote
36	29	70.7	219	2	G91273	hypothetical prote
37	29	70.7	219	2	S56408	hypothetical 25.0K
38	29	70.7	239	2	S39723	spore coat polysac
39	29	70.7	241	2	A75200	hypothetical prote
40	29	70.7	264	2	A59261	tetraspan TSPAN-5
41	29	70.7	307	2	H71944	aspartate carbamoy
42	29	70.7	309	2	AG0368	coproporphyrinogen
43	29	70.7	329	2	F98218	exsG protein (AJ22
44	29	70.7	330	2	AD2130	transcription regu
45	29	70.7	349	2	AE3068	two component sens
46	29	70.7	350	2	AC0813	ethanolamine opero
47	29	70.7	354	2	G71465	hypothetical prote
48	29	70.7	393	2	AI3054	succinoglycan bios
49	29	70.7	393	2	D98231	exoL protein (impo
50	29	70.7	402	2	AH3469	ABC transporter AT
51	29	70.7	435	2	S77156	processing protein
52	29	70.7	475	2	JE0279	peroxisome prolife
53	29	70.7	475	2	JC4264	peroxisome prolife
54	29	70.7	492	2	F96985	probable altronate
55	29	70.7	497	2	D69853	altronate hydrolas
56	29	70.7	497	2	B83711	altronate hydrolas
57	29	70.7	504	2	JE0280	peroxisome prolife
58	29	70.7	505	2	JC5777	peroxisome prolife
59	29	70.7	505	2	JC4859	peroxisome prolife
60	29	70.7	505	2	A54101	peroxisome prolife
61	29	70.7	509	2	C95900	probable sugar ABC
62	29	70.7	519	2	H97724	multidrug resistan
63	29	70.7	561	2	T41301	probable signal re
64	29	70.7	639	2	T15168	hypothetical prote
65	29	70.7	672	2	F71424	hypothetical prote
66	29	70.7	684	2	T37944	hypothetical prote
67	29	70.7	941	2	I40772	hypothetical prote
68	29	70.7	946	2	F81361	probable cell divi
69	29	70.7	969	2	S37886	hypothetical prote
70	29	70.7	1086	2	T40354	hypothetical prote
71	29	70.7	1105	2	A71430	hypothetical prote
72	29	70.7	1314	2	A85176	hypothetical prote
73	29	70.7	1458	1	A49707	phospholipase A2 r
74	29	70.7	3305	2	T18358	apolipophorin prec
75	28	68.3	108	2	D83221	hypothetical prote
76	28	68.3	116	2	T50141	cell division cont
77	28	68.3	136	2	AC0599	probable membrane
78	28	68.3	149	2	T03477	potential phosphat
79	28	68.3	152	2	C69546	hypothetical prote
80	28	68.3	152	2	T00772	protein kinase hom
81	28	68.3	183	2	F69049	conserved hypothet
82	28	68.3	193	2	H83356	probable transcrip
83	28	68.3	193	2	T24208	hypothetical prote
84	28	68.3	197	2	AF2356	hypothetical prote
85	28	68.3	201	2	G87641	transcription regu
86	28	68.3	216	2	C75403	hypothetical prote
87	28	68.3	218	2	T40365	conserved hypothet
88	28	68.3	224	2	E69277	branched-chain ami
89	28	68.3	227	2	S66482	transcription regu
90	28	68.3	236	2	AI0141	probable amino aci
91	28	68.3	250	2	T47611	hypothetical prote
92	28	68.3	256	2	AD3163	hypothetical prote
93	28	68.3	284	2	T06159	probable receptor-
94	28	68.3	285	2	S58359	pepP protein - Sta
95	28	68.3	286	2	T42610	probable immediate
96	28	68.3	296	2	AD2434	hypothetical prote
97	28	68.3	307	2	T20917	hypothetical prote
98	28	68.3	312	2	B69170	UDP-N-acetylmuramy
99	28	68.3	317	2	A64343	hypothetical prote
100	28	68.3	319	2	T36857	conserved hypothet

ALIGNMENTS

RESULT 1
I48845
protein-tyrosine kinase (EC 2.7.1.112) lck, lymphocyte - mouse
N;Alternate names: p56; protein-tyrosine kinase tck
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: I48845; A23639; I57629; I77452
R;Voronova, A.F.; Sefton, B.M.
Nature 319, 682-685, 1986
A;Title: Expression of a new tyrosine protein kinase is stimulated by retrovirus promote
A;Reference number: I48845; MUID:86146842; PMID:3081813
A;Accession: I48845
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-509 <VOR1>
A;Cross-references: UNIPROT:Q91X65; UNIPARC:UPI000000418D; EMBL:X03533; NID:g54813; PIDN
R;Marth, J.D.; Peet, R.; Krebs, E.G.; Perimutter, R.M.
Cell 43, 393-404, 1985
A;Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpres
A;Reference number: A23639; MUID:86079521; PMID:2416464
A;Accession: A23639
A;Molecule type: mRNA
A;Residues: 1-282,'VP',285-509 <MAR>
A;Cross-references: UNIPARC:UPI0000172586; GB:M12056; NID:g198763
A;Note: the sequence is revised in GenBank entry MUSLCK, release 116.0, (PIDN:AAB59674.1
R;Voronova, A.F.; Adler, H.T.; Sefton, B.M.
Mol. Cell. Biol. 7, 4407-4413, 1987
A;Title: Two lck transcripts containing different 5' untranslated regions are present in
A;Reference number: I57629; MUID:88142832; PMID:3501824
A;Accession: I57629
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <VOR>
A;Cross-references: UNIPARC:UPI000016CE9D; GB:M18098; NID:g198766; PIDN:AAA39421.1; PID:
R;Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
Mol. Cell. Biol. 8, 3058-3064, 1988
A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel
A;Reference number: I57636; MUID:89096891; PMID:2850479
A;Accession: I77452
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-35,'VR' <GAR>
A;Cross-references: UNIPARC:UPI000016CE9E; GB:M21511; NID:g198768; PIDN:AAA39422.1; PID:
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro
F;68-116/Domain: SH3 homology <SH3>
F;127-224/Domain: SH2 homology <SH2>
F;243-501/Domain: protein kinase homology <KIN>
F;251-259/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;273/Active site: Lys #status predicted
F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 100.0%; Score 41; DB 1; Length 509;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
|||||||||
Db 61 LQDNLVIAL 69

RESULT 2
OKHULK
protein-tyrosine kinase (EC 2.7.1.112) lck - human
N;Alternate names: kinase-related transforming protein (lck)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 05-Oct-2004
C;Accession: JQ0152; S07822; S07200; S01879; S07143; A32797; I57636
R;Rouer, E.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R.
Gene 84, 105-113, 1989
A;Title: Structure of the human lck gene: differences in genomic organisation within src
A;Reference number: JQ0152; MUID:90108697; PMID:2558056
A;Accession: JQ0152
A;Molecule type: DNA
A;Residues: 1-509 <ROU>
A;Cross-references: UNIPROT:P06239; UNIPARC:UPI0000151F17; EMBL:X14053
R;Perlmutter, R.M.; Marth, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, C.B.
J. Cell. Biochem. 38, 117-126, 1988
A;Title: Structure and expression of lck transcripts in human lymphoid cells.
A;Reference number: S07822; MUID:89123626; PMID:3265417
A;Accession: S07822
A;Molecule type: mRNA
A;Residues: 1-86,'P',88-509 <PER>
A;Cross-references: UNIPARC:UPI0000163BD5; EMBL:X13529; NID:g34294; PIDN:CAA31884.1; PID
R;Koga, Y.; Caccia, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikai, Y.; Mak, T.W.
Eur. J. Immunol. 16, 1643-1646, 1986
A;Title: A human T cell-specific cDNA clone (YT16) encodes a protein with extensive homo
A;Reference number: S07200; MUID:87133831; PMID:3493153
A;Accession: S07200
A;Molecule type: mRNA
A;Residues: 1-205,'ASAITPI',212-257,'RCGW',262,'TTT',266,'T',268-281,'AGRLP',287-503,'ST
A;Cross-references: UNIPARC:UPI000016B09E; EMBL:X05027; NID:g36807; PIDN:CAA28691.1; PID
R;Veillette, A.; Foss, F.M.; Sausville, E.A.; Bolen, J.B.; Rosen, N.
Oncogene Res. 1, 357-374, 1987
A;Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other n
A;Reference number: S01879; MUID:88217332; PMID:2835736
A;Accession: S01879
A;Molecule type: mRNA
A;Residues: 368-471,'H',473-509 <VEI>
A;Cross-references: UNIPARC:UPI000016ABFC; EMBL:X06369; NID:g34288; PIDN:CAA29667.1; PID
R;Trevillyan, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Linna, T.J.
Biochim. Biophys. Acta 888, 286-295, 1986
A;Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56(LSTRA).
A;Reference number: S07143; MUID:87000726; PMID:3489486
A;Accession: S07143
A;Molecule type: mRNA
A;Residues: 'A',376-509 <TRE>
A;Cross-references: UNIPARC:UPI000016AF39; EMBL:X04476; NID:g35779; PIDN:CAA28165.1; PID
R;Takadera, T.; Leung, S.; Gernone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.W
Mol. Cell. Biol. 9, 2173-2180, 1989
A;Title: Structure of the two promoters of the human lck gene: differential accumulation
A;Reference number: A32797; MUID:89313764; PMID:2787474
A;Accession: A32797
A;Molecule type: DNA
A;Residues: 1-35 <TAK>
A;Cross-references: UNIPARC:UPI000016ABFF; GB:M26692; NID:g341523; PIDN:AAA59503.1; PID:
R;Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
Mol. Cell. Biol. 8, 3058-3064, 1988
A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel
A;Reference number: I57636; MUID:89096891; PMID:2850479
A;Accession: I57636
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-35,'VR' <RES>
A;Cross-references: UNIPARC:UPI000016ABFD; GB:M21510; NID:g187031; PIDN:AAA59501.1; PID:
C;Comment: Protein tyrosine kinases play important roles in the control of cell growth a
C;Genetics:
A;Gene: GDB:LCK
A;Cross-references: GDB:119360; OMIM:153390
A;Map position: 1p35-1p34.3
A;Introns: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;2-509/Product: protein-tyrosine kinase lck #status predicted <MAT>
F;68-116/Domain: SH3 homology <SH3>
F;127-224/Domain: SH2 homology <SH2>
F;243-501/Domain: protein kinase homology <KIN>
F;251-259/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3,5/Binding site: palmitate (Cys) (covalent) #status predicted

```
F;273/Active site: Lys #status predicted
F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match            100.0%;  Score 41;  DB 1;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 0.74;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         61 LQDNLVIAL 69


RESULT 3
G72285
hybrid cluster [4Fe-2S-3O] protein TM1172 [similarity] - Thermotoga maritima (strain MSE
N;Alternate names: prismane [6Fe-6S] protein [misnomer]
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: G72285
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: G72285
A;Molecule type: DNA
A;Residues: 1-431 <ARN>
A;Cross-references: UNIPROT:Q9X0Q4; UNIPARC:UPI000012C367; GB:AE001774; GB:AE000512; NID
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1172
C;Superfamily: Thermotoga maritima hybrid cluster [4Fe-2S-3O] protein; hybrid cluster [4
C;Keywords: 4Fe-2S-3O; 4Fe-4S; electron transfer; metalloprotein
F;108-395/Domain: hybrid cluster [4Fe-2S-3O] homology <HCL>
F;5,8,17,23/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
F;131,155,199,286,314,339,373/Binding site: 4Fe-2S-3O cluster (His, Glu, Cys, Cys, Cys,
F;286/Modified site: cysteine persulfide (Cys) #status predicted

  Query Match            85.4%;  Score 35;  DB 2;  Length 431;
  Best Local Similarity  77.8%;  Pred. No. 13;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              ||||||.|:
Db         32 LQDNLVFAI 40


RESULT 4
G71706
hypothetical protein RP474 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: G71706
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U
Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: G71706
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-269 <AND>
A;Cross-references: UNIPROT:Q9ZD70; UNIPARC:UPI0000139866; GB:AJ235271; GB:AJ235269; NID
A;Experimental source: strain Madrid E
C;Genetics:
A;Gene: RP474

  Query Match            82.9%;  Score 34;  DB 2;  Length 269;
  Best Local Similarity  77.8%;  Pred. No. 12;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||:||||:
Db        225 LQDSLVIAI 233


RESULT 5
A39939
protein-tyrosine kinase (EC 2.7.1.112) tkl [similarity] - chicken
N;Alternate names: kinase-related transforming protein (tkl); T-cell surface antigen ass
C;Species: Gallus gallus (chicken)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C;Accession: A42126; A39939
R;Chow, L.M.; Ratcliffe, M.J.; Veillette, A.
Mol. Cell. Biol. 12, 1226-1233, 1992
A;Title: tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene.
A;Reference number: A42126; MUID:92186854; PMID:1545804
A;Accession: A42126
A;Molecule type: mRNA
A;Residues: 1-88 <CHO>
A;Cross-references: UNIPARC:UPI0000172587; GB:M85043
A;Experimental source: thymus, spleen
A;Note: sequence extracted from NCBI backbone (NCBIN:88831, NCBIP:88833)
R;Strebhardt, K.; Mullins, J.I.; Bruck, C.; Ruebsamen-Waigmann, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987
A;Title: Additional member of the protein-tyrosine kinase family: the src-and lck-relate
A;Reference number: A39939; MUID:88097370; PMID:3321053
A;Accession: A39939
A;Molecule type: mRNA
A;Residues: 52-507 <STR>
A;Cross-references: UNIPARC:UPI00001713B3; GB:J03579; NID:g212712; PIDN:AAA49081.1; PID:
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;66-114/Domain: SH3 homology <SH3>
F;125-222/Domain: SH2 homology <SH2>
F;241-499/Domain: protein kinase homology <KIN>
F;249-257/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match            82.9%;  Score 34;  DB 1;  Length 507;
  Best Local Similarity  77.8%;  Pred. No. 25;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              ||| ||:||
Db         59 LQDKLVVAL 67


RESULT 6
D97789
hypothetical protein RC0716 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: D97789
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: D97789
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-234 <KUR>
A;Cross-references: UNIPROT:Q92HQ5; UNIPARC:UPI00000CBE96; GB:AE006914; PIDN:AAL03254.1;
C;Genetics:
A;Gene: RC0716

  Query Match            80.5%;  Score 33;  DB 2;  Length 234;
  Best Local Similarity  66.7%;  Pred. No. 18;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||:||:|:
Db        189 LQDSLVVAI 197
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RESULT 7
C90505
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: C90505
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: C90505
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <KUR>
A;Cross-references: UNIPROT:Q97U24; UNIPARC:UPI00000649BC; GB:AE006641; NID:g13816636; P
C;Genetics:
A;Gene: SSO3201
C;Superfamily: hypothetical protein AF0171

  Query Match             78.0%;  Score 32;  DB 2;  Length 199;
  Best Local Similarity   55.6%;  Pred. No. 24;
  Matches    5;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |:||:::||
Db        115 LKDNVIVAL 123


RESULT 8
A59199
hybrid cluster [4Fe-2S-3O] protein MTH1453 [similarity] - Methanobacterium thermoautotrc
N;Alternate names: prismane [6Fe-6S] protein [misnomer]
C;Species: Methanobacterium thermoautotrophicum
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 28-Jul-2000
C;Accession: A59199; E69060
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: A59199
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-491 <MTH1>
A;Cross-references: UNIPARC:UPI0000174DEA; GB:AE000906; GB:AE000666; NID:g2622557
A;Experimental source: strain Delta H
A;Note: this translation was produced by PIR-International staff from the nucleic acid s
 used in the GenBank entry
A;Accession: E69060
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 'M',17-491 <MTH2>
A;Cross-references: UNIPARC:UPI0000165BBA; GB:AE000906; GB:AE000666; NID:g2622557; PIDN:
A;Experimental source: strain Delta H
A;Note: an incorrect initiation codon was used
C;Genetics:
A;Gene: MTH1453
C;Superfamily: Methanobacterium hybrid cluster [4Fe-2S-3O] protein; hybrid cluster [4Fe-
C;Keywords: 4Fe-2S-3O; 4Fe-4S; electron transfer; iron; iron-sulfur protein; metalloprot
F;2-48/Domain: rubredoxin homology <RUB>
F;170-456/Domain: hybrid cluster [4Fe-2S-3O] homology <HCL>
F;5,8,38,41/Binding site: iron (Cys) #status predicted
F;67,70,79,85/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
F;193,217,261,347,375,400,434/Binding site: 4Fe-2S-3O cluster (His, Glu, Cys, Cys, Cys,
F;347/Modified site: cysteine persulfide (Cys) #status predicted

  Query Match             78.0%;  Score 32;  DB 2;  Length 491;
  Best Local Similarity   66.7%;  Pred. No. 65;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||: |:
Db         94 LQDNLLFAI 102


RESULT 9
G97092
endoglucanase (truncated) [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97092
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G97092
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-67 <KUR>
A;Cross-references: UNIPROT:Q97IS7; UNIPARC:UPI00000D46BD; GB:AE001437; PIDN:AAK79530.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1563

  Query Match             75.6%;  Score 31;  DB 2;  Length 67;
  Best Local Similarity   55.6%;  Pred. No. 12;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |:|||:: |
Db         12 LKDNLIVVL 20


RESULT 10
AI0587
deoxyribodipyrimidine photolyase [imported] - Salmonella enterica subsp. enterica serova
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AI0587
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AI0587
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-473 <PAR>
A;Cross-references: UNIPARC:UPI000005A138; GB:AL513382; PIDN:CAD05171.1; PID:g16501943;
C;Genetics:
A;Gene: STY0749
C;Superfamily: deoxyribodipyrimidine photo-lyase

  Query Match             75.6%;  Score 31;  DB 2;  Length 473;
  Best Local Similarity   75.0%;  Pred. No. 1e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIA 8
              ||||| :|
Db         14 LQDNLALA 21


RESULT 11
S22321
deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - Salmonella typhimurium
N;Alternate names: DNA photolyase; photoreactivating enzyme
C;Species: Salmonella typhimurium
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C;Accession: S22321; S78105
```

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R;Li, Y.F.; Sancar, A.
Nucleic Acids Res. 19, 4885-4890, 1991
A;Title: Cloning, sequencing, expression and characterization of DNA photolyase from Sal
A;Reference number: S22321; MUID:92020120; PMID:1840665
A;Accession: S22321
A;Molecule type: DNA
A;Residues: 1-473 <LIY>
A;Cross-references: UNIPROT:P25078; UNIPARC:UPI000017603D; EMBL:X60662
R;Li, Y.F.
submitted to the EMBL Data Library, July 1991
A;Reference number: S78105
A;Accession: S78105
A;Molecule type: DNA
A;Residues: 1-19,21-39,41-59,61-79,81-99,101-119,121-139,141-159,161-179,181-198,200-219
A;Cross-references: UNIPARC:UPI00001703BB; EMBL:X60662; NID:g48950; PIDN:CAA43069.1; PID
C;Genetics:
A;Gene: phr
C;Function:
A;Description: DNA repair; catalyzes the light-dependent (300-600 nm) monomerization of
A strand, upon exposure to ultraviolet radiation
C;Superfamily: deoxyribodipyrimidine photo-lyase
C;Keywords: carbon-carbon lyase; DNA binding; DNA repair; flavoprotein

  Query Match             75.6%;  Score 31;  DB 2;  Length 473;
  Best Local Similarity   75.0%;  Pred. No. 1e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIA 8
              ||||| :|
Db         14 LQDNLALA 21


RESULT 12
H75122
sarcosine oxidase alpha chain truncated homolog PAB1842 [similarity] - Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: H75122
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: H75122
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-496 <KAW>
A;Cross-references: UNIPROT:Q9V0K6; UNIPARC:UPI000006692E; GB:AJ248285; GB:AL096836; NID
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1842

  Query Match             75.6%;  Score 31;  DB 2;  Length 496;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||:| :||
Db        130 LQDDLTVAL 138


RESULT 13
E86345
hypothetical protein F16F4.9 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
C;Accession: E86345
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E86345
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-733 <STO>
A;Cross-references: UNIPROT:Q9LMN7; UNIPARC:UPI00000A8092; GB:AE005172; NID:g8920637; PI
C;Genetics:
A;Map position: 1
C;Superfamily: wall-associated protein kinase; protein kinase homology

  Query Match             75.6%;  Score 31;  DB 2;  Length 733;
  Best Local Similarity   55.6%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||| ::|:
Db        427 LQDNSIVAI 435


RESULT 14
AG2136
polyketide synthase type I [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AG2136
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2136
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1488 <KUR>
A;Cross-references: UNIPROT:Q8YTR7; UNIPARC:UPI00000CE4EC; GB:BA000019; PIDN:BAB74345.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all2646

  Query Match             75.6%;  Score 31;  DB 2;  Length 1488;
  Best Local Similarity   87.5%;  Pred. No. 3.6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIA 8
              | ||||||
Db        678 LTDNLVIA 685


RESULT 15
T08868
polyprotein P1 - Acyrthosiphon pisum virus
C;Species: Acyrthosiphon pisum virus
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T08868
R;van der Wilk, F.; Dullemans, A.M.; Verbeek, M.; van den Heuvel, J.F.J.M.
Virology 238, 353-362, 1997
A;Title: Nucleotide sequence and genomic organization of Acyrthosiphon pisum virus.
A;Reference number: Z16501; MUID:98063255; PMID:9400608
A;Accession: T08868
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: genomic RNA
A;Residues: 1-2630 <VAN>
A;Cross-references: UNIPROT:O55319; UNIPARC:UPI00000F73C5; EMBL:AF024514; NID:g2668619;

  Query Match             75.6%;  Score 31;  DB 2;  Length 2630;
  Best Local Similarity   66.7%;  Pred. No. 6.7e+02;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
```

```
              ::|||:|||
Db       2017 VRDNLMIAL 2025


RESULT 16
S75886
hypothetical protein sll1089 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75886
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75886
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-213 <KAN>
A;Cross-references: UNIPROT:P74251; UNIPARC:UPI00000C0E3C; EMBL:D90913; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein sll1089

  Query Match             73.2%;  Score 30;  DB 2;  Length 213;
  Best Local Similarity   85.7%;  Pred. No. 72;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QDNLVIA 8
              |||:|||
Db         87 QDNVVIA 93


RESULT 17
E96998
4-hydroxybenzoate octaprenyltransferase related protein CAC0800 [imported] - Clostridium
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: E96998
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: E96998
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-297 <KUR>
A;Cross-references: UNIPROT:Q97KW6; UNIPARC:UPI00000C9FAD; GB:AE001437; PIDN:AAK78776.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0800

  Query Match             73.2%;  Score 30;  DB 2;  Length 297;
  Best Local Similarity   66.7%;  Pred. No. 1e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              :| |||:||
Db        138 IQPNLVLAL 146


RESULT 18
T48504
hypothetical protein F15N18.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48504
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24490
A;Accession: T48504
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <BEV>
A;Cross-references: UNIPROT:P82715; UNIPARC:UPI00000ABB2A; EMBL:AL163815
A;Experimental source: cultivar Columbia; BAC clone F15N18
C;Genetics:
A;Map position: 5
A;Introns: 35/2; 92/1; 135/2; 152/1; 174/3; 206/3; 226/3; 246/3; 265/1; 281/3
A;Note: F15N18.40

  Query Match             73.2%;  Score 30;  DB 2;  Length 319;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              | |||||::
Db        165 LTDNLVISI 173


RESULT 19
C97009
hypothetical protein CAC0886 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97009
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97009
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-361 <KUR>
A;Cross-references: UNIPROT:Q97KN1; UNIPARC:UPI00000C9FFC; GB:AE001437; PIDN:AAK78862.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0886

  Query Match             73.2%;  Score 30;  DB 2;  Length 361;
  Best Local Similarity   55.6%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              :|||:||::
Db        271 VQDNIVISV 279


RESULT 20
S62541
hypothetical protein SPAC12G12.10 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S62541; T37591
R;Devlin, K.; Odell, C.; Churcher, C.M.
submitted to the EMBL Data Library, November 1995
A;Reference number: S62532
A;Accession: S62541
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-420 <DEV>
A;Cross-references: UNIPROT:Q09873; UNIPARC:UPI000013A09E; EMBL:Z66568; NID:g1052518; PI
R;Devlin, K.; Odell, C.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z21727
A;Accession: T37591
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-420 <DE2>
A;Cross-references: UNIPARC:UPI000013A09E; EMBL:Z66568; PIDN:CAA91505.1; GSPDB:GN00066;
A;Experimental source: strain 972h-; cosmid c12G12
C;Genetics:
A;Gene: SPAC12G12.10
```

A;Map position: 1L

Query Match 73.2%; Score 30; DB 2; Length 420;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQDNLVIA 8
| ||||||
Db 262 LGDNLVIA 269

RESULT 21
AH2468
hypothetical protein all5304 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH2468
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2468
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-498 <KUR>
A;Cross-references: UNIPROT:Q8YLJ4; UNIPARC:UPI00000CEE24; GB:BA000019; PIDN:BAB77003.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all5304

Query Match 73.2%; Score 30; DB 2; Length 498;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQDNLVIA 8
|||||| |
Db 192 LQDNLVNA 199

RESULT 22
C69769
hypothetical protein ydaL - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69769
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: C69769
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-569 <KUN>
A;Cross-references: UNIPROT:O31487; UNIPARC:UPI000005FF4F; GB:Z99106; GB:AL009126; NID:g
A;Experimental source: strain 168
C;Genetics:
A;Gene: ydaL
C;Superfamily: Bacillus subtilis hypothetical protein ydaL

Query Match 73.2%; Score 30; DB 2; Length 569;
Best Local Similarity 62.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQDNLVIA 8
| |||::|
Db 186 LNDNLIVA 193

RESULT 23
T36330
cell division protein ftsH2 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36330
R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z21575
A;Accession: T36330
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-668 <OLI>
A;Cross-references: UNIPROT:Q9X8I4; UNIPARC:UPI00000DB081; EMBL:AL049841; PIDN:CAB42757.
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: ftsH2; SCOEDB:SCE9.11c
C;Superfamily: cell division protein ftsH; FtsH/SEC18/CDC48-type ATP-binding domain homo

Query Match 73.2%; Score 30; DB 2; Length 668;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DNLVIAL 9
||||:||
Db 578 DNLVLAL 584

RESULT 24
B64530
methyl-accepting chemotaxis transducer (tlpC) - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: B64530
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: B64530
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-673 <TOM>
A;Cross-references: UNIPROT:O24911; UNIPARC:UPI00000D3119; GB:AE000530; GB:AE000511; NID
C;Superfamily: probable methyl-accepting chemotaxis transducer

Query Match 73.2%; Score 30; DB 1; Length 673;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQDNLVIA 8
:|||| ||
Db 640 VQDNLTIA 647

RESULT 25
A71978
methyl-accepting chemotaxis protein (MCP) - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: A71978

```
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: A71978
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-673 <ARN>
A;Cross-references: UNIPROT:Q9ZMY7; UNIPARC:UPI00000D35CB; GB:AE001446; GB:AE001439; NID
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0075
C;Superfamily: probable methyl-accepting chemotaxis transducer

  Query Match             73.2%;  Score 30;  DB 2;  Length 673;
  Best Local Similarity   75.0%;  Pred. No. 2.5e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIA 8
              :|||| ||
Db        640 VQDNLTIA 647


RESULT 26
T16356
hypothetical protein F43C9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C;Accession: T16356
R;Fulton, B.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F43C9.
A;Reference number: Z18499
A;Accession: T16356
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-726 <FUL>
A;Cross-references: UNIPROT:Q20357; UNIPARC:UPI00000759ED; EMBL:U40427; NID:g1065557; PI
C;Genetics:
A;Gene: CESP:F43C9.3
A;Introns: 34/3; 67/2; 101/1; 178/1; 227/1; 262/3; 307/2; 449/3; 476/1; 502/3; 595/3; 63

  Query Match             73.2%;  Score 30;  DB 2;  Length 726;
  Best Local Similarity   66.7%;  Pred. No. 2.7e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              ::|||| ||
Db        506 IRDNLVTAL 514


RESULT 27
B70694
probable infB - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: B70694
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70694
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-900 <COL>
A;Cross-references: UNIPROT:P71613; UNIPARC:UPI000012D2E2; GB:Z81331; GB:AL123456; NID:g
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: infB
C;Superfamily: translation initiation factor IF-2; translation elongation factor Tu homo
C;Keywords: GTP binding; nucleotide binding; P-loop
F;399-512/Domain: translation elongation factor Tu homology <ETU>
F;405-412/Region: nucleotide-binding motif A (P-loop)
F;509-512/Region: GTP-binding NKXD motif
F;545-547/Region: GTP-binding SAK/L motif
F;411,412,432,509,510,512,545/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #

  Query Match             73.2%;  Score 30;  DB 2;  Length 900;
  Best Local Similarity   62.5%;  Pred. No. 3.5e+02;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIA 8
              |:||:|:|
Db        843 LRDNIVVA 850


RESULT 28
T03094
A-kinase anchor protein DAKAP550 - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03094
R;Han, J.D.; Baker, N.E.; Rubin, C.S.
J. Biol. Chem. 272, 26611-26619, 1997
A;Title: Molecular characterization of a novel A kinase anchor protein from drosophila m
A;Reference number: Z14835; MUID:97476266; PMID:9334242
A;Accession: T03094
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2359 <HAN>
A;Cross-references: UNIPROT:Q9W4E2; UNIPARC:UPI000008370A; EMBL:AF003622; NID:g2393879;
A;Experimental source: strain Canton S
C;Genetics:
A;Cross-references: FlyBase:FBgn0021748
A;Map position: X

  Query Match             73.2%;  Score 30;  DB 2;  Length 2359;
  Best Local Similarity   75.0%;  Pred. No. 9.9e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIA 8
              | |||:||
Db       1733 LADNLIIA 1740


RESULT 29
T42025
hypothetical protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42025
R;Harasym, M.; Bernan, V.; Ally, D.; Piret, J.
submitted to the EMBL Data Library, August 1995
A;Description: Streptomyces coelicolor truncated bldB orfX.
A;Reference number: Z22032
A;Accession: T42025
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-71 <HAR>
A;Cross-references: UNIPROT:Q53864; UNIPARC:UPI00000AFF0B; EMBL:U33195; PIDN:AAA85225.1

  Query Match             70.7%;  Score 29;  DB 2;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLV 6
              ||||||
Db         59 LQDNLV 64


RESULT 30
G84991
```

hypothetical protein [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: G84991
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: G84991
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <STO>
A;Cross-references: UNIPARC:UPI000005E5FA; GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: yheL; BU530

Query Match 70.7%; Score 29; DB 2; Length 90;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 LQDNLVIAL 9
              ||| ::|||
Db         25 LQDGVLIAL 33
```

Search completed: June 29, 2006, 09:31:43
Job time : 15.3373 secs

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:39 ; Search time 105.831 Seconds
(without alignments)
78.664 Million cell updates/sec

Title: US-10-062-257A-11
Perfect score: 41
Sequence: 1 LQDNLVIAL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	100.0	508	1	LCK_AOTNA	Q5pxs1 aotus nancy
2	41	100.0	508	1	LCK_HUMAN	P06239 homo sapien
3	41	100.0	508	1	LCK_MOUSE	P06240 mus musculu
4	41	100.0	508	1	LCK_SAISC	Q95kr7 saimiri sci
5	41	100.0	509	2	Q7RTZ3_HUMAN	Q7rtz3 homo sapien
6	41	100.0	509	2	Q95M32_9PRIM	Q95m32 hylobates s
7	41	100.0	509	2	Q3ZCM0_BOVIN	Q3zcm0 bos taurus
8	37	90.2	663	2	Q4SP61_TETNG	Q4sp61 tetraodon n
9	35	85.4	189	2	Q3YSG0_EHRCJ	Q3ysg0 ehrlichia c
10	35	85.4	431	1	HCP_THEMA	Q9x0q4 thermotoga
11	35	85.4	431	2	Q4FF10_9THEM	Q4ff10 thermotoga
12	35	85.4	463	1	LIP6_CANAL	Q9p4e8 candida alb
13	35	85.4	463	2	Q5APE2_CANAL	Q5ape2 candida alb
14	35	85.4	1045	2	Q82AU6_STRAW	Q82au6 streptomyce
15	34	82.9	189	2	Q40IE4_EHRCH	Q40ie4 ehrlichia c
16	34	82.9	230	2	Q7MS04_WOLSU	Q7ms04 wolinella s
17	34	82.9	269	1	Y474_RICPR	Q9zd70 rickettsia
18	34	82.9	271	2	Q68WQ6_RICTY	Q68wq6 rickettsia
19	34	82.9	301	2	Q4N2A8_THEPA	Q4n2a8 theileria p
20	34	82.9	322	2	Q2SJ95_9GAMM	Q2sj95 hahella che
21	34	82.9	480	2	Q9M5G4_EUPES	Q9m5g4 euphorbia e
22	34	82.9	507	1	LCK_CHICK	P42683 gallus gall
23	34	82.9	731	2	Q3MWW8_9DELT	Q3mww8 syntrophoba
24	33	80.5	94	2	Q371F3_RHOPA	Q371f3 rhodopseudo
25	33	80.5	147	2	Q9BEI2_MACEU	Q9bei2 macropus eu
26	33	80.5	172	2	Q8LKM7_ORYRU	Q8lkm7 oryza rufip
27	33	80.5	224	2	Q7P8Q9_RICSI	Q7p8q9 rickettsia
28	33	80.5	234	2	Q92HQ5_RICCN	Q92hq5 rickettsia
29	33	80.5	248	2	Q4A5I5_MYCS5	Q4a5i5 mycoplasma
30	33	80.5	253	2	Q89UG6_BRAJA	Q89ug6 bradyrhizob
31	33	80.5	284	2	Q4UL91_RICFE	Q4ul91 rickettsia
32	33	80.5	432	2	Q2NF95_9EURY	Q2nf95 methanospha
33	33	80.5	440	2	Q5UZ92_HALMA	Q5uz92 haloarcula
34	33	80.5	769	2	Q6K9B5_ORYSA	Q6k9b5 oryza sativ
35	33	80.5	769	2	Q948H3_ORYSA	Q948h3 oryza sativ
36	33	80.5	872	1	MUTS_COLP3	Q47wn0 colwellia p
37	33	80.5	879	2	Q7S7M7_NEUCR	Q7s7m7 neurospora
38	33	80.5	899	2	Q871R8_NEUCR	Q871r8 neurospora
39	33	80.5	1046	2	Q7PZJ7_ANOGA	Q7pzj7 anopheles g
40	33	80.5	1109	2	Q8H4J0_ORYSA	Q8h4j0 oryza sativ
41	33	80.5	1154	2	Q7QHH4_ANOGA	Q7qhh4 anopheles g
42	32	78.0	122	2	Q373G2_RHOPA	Q373g2 rhodopseudo
43	32	78.0	198	2	Q3IBS5_9BACT	Q3ibs5 uncultured
44	32	78.0	199	2	Q97U24_SULSO	Q97u24 sulfolobus
45	32	78.0	210	2	Q5LPC2_SILPO	Q5lpc2 silicibacte
46	32	78.0	339	2	Q6G0N4_BARQU	Q6g0n4 bartonella
47	32	78.0	345	2	Q3Z6N9_DEHE1	Q3z6n9 dehalococco
48	32	78.0	345	2	Q3ZYU9_DEHSC	Q3zyu9 dehalococco
49	32	78.0	427	1	HCP_METTH	O27502 methanobact
50	32	78.0	466	1	LIP2_CANAL	Q9p8w5 candida alb
51	32	78.0	466	2	Q5APG1_CANAL	Q5apg1 candida alb
52	32	78.0	466	2	Q4RNX3_TETNG	Q4rnx3 tetraodon n
53	32	78.0	483	2	Q485W7_COLP3	Q485w7 colwellia p
54	32	78.0	502	2	Q8QGJ9_FUGRU	Q8qgj9 fugu rubrip
55	32	78.0	510	2	Q2KD09_RHIET	Q2kd09 rhizobium e
56	32	78.0	513	2	Q6CU91_KLULA	Q6cu91 kluyveromyc
57	32	78.0	516	2	Q573B4_HUMAN	Q573b4 homo sapien
58	32	78.0	529	2	Q4MWE4_BACCE	Q4mwe4 bacillus ce
59	32	78.0	570	2	Q8A3R2_BACTN	Q8a3r2 bacteroides
60	32	78.0	593	2	Q5CFB5_CRYHO	Q5cfb5 cryptospori
61	32	78.0	649	2	Q3HBQ7_TRIER	Q3hbq7 trichodesmi
62	32	78.0	690	2	O30436_YEREN	O30436 yersinia en
63	32	78.0	801	2	P91774_PACLE	P91774 pacifastacu
64	32	78.0	833	2	Q82VJ5_NITEU	Q82vj5 nitrosomona
65	32	78.0	842	2	Q35N10_9BRAD	Q35n10 bradyrhizob
66	32	78.0	861	1	MUTS_MANSM	Q65qa9 mannheimia
67	32	78.0	1353	2	Q8G7K1_BIFLO	Q8g7k1 bifidobacte
68	31	75.6	67	2	Q97IS7_CLOAB	Q97is7 clostridium
69	31	75.6	128	2	Q92MW9_RHIME	Q92mw9 rhizobium m
70	31	75.6	144	2	Q3Y9L5_9PERO	Q3y9l5 nibea miich
71	31	75.6	189	2	Q5HBL2_EHRRW	Q5hbl2 ehrlichia r
72	31	75.6	189	2	Q5FHJ7_EHRRG	Q5fhj7 ehrlichia r
73	31	75.6	210	2	Q2Z0R3_9CAUD	Q2z0r3 pseudomonas
74	31	75.6	217	2	Q2LTK1_9DELT	Q2ltk1 syntrophus
75	31	75.6	218	2	Q4IZI0_AZOVI	Q4izi0 azotobacter
76	31	75.6	219	2	Q2W1X8_MAGSA	Q2w1x8 magnetospir
77	31	75.6	231	2	Q6FAS1_ACIAD	Q6fas1 acinetobact
78	31	75.6	248	2	Q98M30_RHILO	Q98m30 rhizobium l
79	31	75.6	252	2	Q349T4_RHOPA	Q349t4 rhodopseudo
80	31	75.6	254	2	Q37N36_RHOPA	Q37n36 rhodopseudo
81	31	75.6	254	2	Q2IZ55_RHOPA	Q2iz55 rhodopseudo
82	31	75.6	254	2	Q6N3M7_RHOPA	Q6n3m7 rhodopseudo
83	31	75.6	256	2	Q426B5_DESHA	Q426b5 desulfitoba
84	31	75.6	263	1	TSN17_HUMAN	Q96fv3 homo sapien
85	31	75.6	270	1	TSN17_MOUSE	Q9d7w4 mus musculu
86	31	75.6	270	2	Q58DN3_BOVIN	Q58dn3 bos taurus
87	31	75.6	270	2	Q3TAQ3_MOUSE	Q3taq3 mus musculu
88	31	75.6	270	2	Q4V8E0_RAT	Q4v8e0 rattus norv
89	31	75.6	270	2	Q6DIL0_XENTR	Q6dil0 xenopus tro
90	31	75.6	270	2	Q6NRM4_XENLA	Q6nrm4 xenopus lae
91	31	75.6	285	2	Q3TLW9_MOUSE	Q3tlw9 mus musculu
92	31	75.6	299	2	Q3GML2_9GAMM	Q3gml2 psychrobact
93	31	75.6	302	2	Q7QTY3_GIALA	Q7qty3 giardia lam
94	31	75.6	302	2	Q7RL87_PLAYO	Q7rl87 plasmodium
95	31	75.6	310	2	Q3P951_PARDE	Q3p951 paracoccus
96	31	75.6	311	2	Q6AQX4_DESPS	Q6aqx4 desulfotale
97	31	75.6	313	2	Q4Z1J9_PLABE	Q4z1j9 plasmodium
98	31	75.6	315	2	Q4XWR8_PLACH	Q4xwr8 plasmodium
99	31	75.6	320	2	Q8I2X0_PLAF7	Q8i2x0 plasmodium
100	31	75.6	322	2	Q4WX83_ASPFU	Q4wx83 aspergillus

ALIGNMENTS

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RESULT 1
LCK_AOTNA
ID   LCK_AOTNA      STANDARD;      PRT;   508 AA.
AC   Q5PXS1;
DT   08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT   08-NOV-2005, sequence version 3.
DT   07-MAR-2006, entry version 13.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Aotus nancymaae (Ma's night monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=37293;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Perez-Quintero L.A., Vernot J.P.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways. Association of the TCR with a peptide
CC       antigen-bound MHC complex facilitates the interaction of CD4 and
CC       CD8 with MHC class II and class I molecules, respectively, and
CC       thereby recruits the associated LCK to the vicinity of the TCR/CD3
CC       complex. LCK then phosphorylates tyrosines residues within the
CC       immunoreceptor tyrosines-based activation motifs (ITAMs) in the
CC       cytoplasmic tails of the TCRgamma chains and CD3 subunits,
CC       initiating the TCR/CD3 signaling pathway. In addition, contributes
CC       to signaling by other receptor molecules. Associates directly with
CC       the cytoplasmic tail of CD2, and upon engagement of the CD2
CC       molecule, LCK undergoes hyperphosphorylation and activation. Also
CC       plays a role in the IL2 receptor-linked signaling pathway that
CC       controls T-cell proliferative response. Binding of IL2 to its
CC       receptor results in increased activity of LCK. Is expressed at all
CC       stages of thymocyte development and is required for the regulation
CC       of maturation events that are governed by both pre-TCR and mature
CC       alpha beta TCR (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also
CC       binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to
CC       other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds
CC       to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes
CC       through its SH3 domain and to the tyrosine phosphorylated form of
CC       KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.
CC       Interacts with phosphorylated LIME1. Interacts with CBLB (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.
CC       Present in lipid rafts in an unactive form (By similarity).
CC   -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.
CC       Interaction is regulated by Ser-58 phosphorylation (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY821852; AAV70114.2; -; mRNA.
DR   SMR; Q5PXS1; 64-508.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    508       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088123.
FT   DOMAIN       60    120       SH3.
FT   DOMAIN      126    223       SH2.
FT   DOMAIN      244    497       Protein kinase.
FT   NP_BIND     250    258       ATP (By similarity).
FT   REGION        1     71       Interactions with CD4 and CD8 (By
FT                                similarity).
FT   ACT_SITE    363    363       Proton acceptor (By similarity).
FT   BINDING     272    272       ATP (By similarity).
FT   MOD_RES     393    393       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     504    504       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   508 AA;  58041 MW;  8B61951BC192A3A4 CRC64;

  Query Match             100.0%;  Score 41;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 8.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         60 LQDNLVIAL 68


RESULT 2
LCK_HUMAN
ID   LCK_HUMAN      STANDARD;      PRT;   508 AA.
AC   P06239; P07100; Q12850; Q13152; Q5TDH8; Q5TDH9; Q96DW4; Q9NYT8;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1994, sequence version 5.
DT   07-MAR-2006, entry version 87.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase) (LSK) (T cell-
DE   specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=87133831; PubMed=3493153;
RA   Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
RA   Mak T.W.;
RT   "A human T cell-specific cDNA clone (YT16) encodes a protein with
```

RT extensive homology to a family of protein-tyrosine kinases.";
RL Eur. J. Immunol. 16:1643-1646(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=89123626; PubMed=3265417;
RA Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F.,
RA Wilson C.B.;
RT "Structure and expression of lck transcripts in human lymphoid
RT cells.";
RL J. Cell. Biochem. 38:117-126(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=90108697; PubMed=2558056; DOI=10.1016/0378-1119(89)90144-3;
RA Rouer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
RA Benarous R.;
RT "Structure of the human lck gene: differences in genomic organisation
RT within src-related genes affect only N-terminal exons.";
RL Gene 84:105-113(1989).
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA], VARIANTS LEU-27; GLN-LYS-PRO-231 INS;
RP VAL-352 AND LEU-446, AND PHOSPHORYLATION SITES TYR-393 AND TYR-504.
RC TISSUE=Leukemia;
RX MEDLINE=94187714; PubMed=8139546;
RA Wright D.D., Sefton B.M., Kamps M.P.;
RT "Oncogenic activation of the Lck protein accompanies translocation of
RT the LCK gene in the human HSB2 T-cell leukemia.";
RL Mol. Cell. Biol. 14:2429-2437(1994).
RN [5]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM SHORT), AND ALTERNATIVE SPLICING.
RC TISSUE=Leukemic T-cell;
RX MEDLINE=96085119; PubMed=7495859; DOI=10.1016/0167-4781(95)00162-A;
RA Vogel L.B., Arthur R., Fujita D.J.;
RT "An aberrant lck mRNA in two human T-cell lines.";
RL Biochim. Biophys. Acta 1264:168-172(1995).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG Human chromosome 1 international sequencing consortium;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX MEDLINE=89096891; PubMed=2850479;
RA Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT "Structure of the murine lck gene and its rearrangement in a murine
RT lymphoma cell line.";
RL Mol. Cell. Biol. 8:3058-3064(1988).
RN [9]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX MEDLINE=89313764; PubMed=2787474;
RA Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
RA Miyamoto N.G., Mak T.W.;
RT "Structure of the two promoters of the human lck gene: differential
RT accumulation of two classes of lck transcripts in T cells.";
RL Mol. Cell. Biol. 9:2173-2180(1989).
RN [10]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 13-508.
RC TISSUE=Peripheral blood lymphocyte;
RX MEDLINE=20462621; PubMed=11009097;
RX DOI=10.1002/1521-4141(200009)30:9<2632::AID-IMMU2632>3.0.CO;2-C;
RA Boncristiano M., Majolini M.B., D'Elios M.M., Pacini S., Valensin S.,
RA Ulivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,
RA Baldari C.T.;
RT "Defective recruitment and activation of ZAP-70 in common variable
RT immunodeficiency patients with T cell defects.";
RL Eur. J. Immunol. 30:2632-2638(2000).
RN [11]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 367-508.
RX MEDLINE=88217332; PubMed=2835736;
RA Veillette A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.;
RT "Expression of the lck tyrosine kinase gene in human colon carcinoma
RT and other non-lymphoid human tumor cell lines.";
RL Oncogene Res. 1:357-374(1987).
RN [12]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 374-508.
RX MEDLINE=87000726; PubMed=3489486; DOI=10.1016/0167-4889(86)90228-4;
RA Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
RA Linna T.J.;
RT "Human T lymphocytes express a protein-tyrosine kinase homologous to
RT p56LSTRA.";
RL Biochim. Biophys. Acta 888:286-295(1986).
RN [13]
RP PHOSPHORYLATION SITE TYR-504.
RX MEDLINE=92347326; PubMed=1639064;
RA Bergman M., Mustelin T., Oetken C., Partanen J., Flint N.A.,
RA Amrein K.E., Autero M., Burn P., Alitalo K.;
RT "The human p50csk tyrosine kinase phosphorylates p56lck at Tyr-505 and
RT down regulates its catalytic activity.";
RL EMBO J. 11:2919-2924(1992).
RN [14]
RP INTERACTION WITH PI3K.
RX MEDLINE=94067101; PubMed=7504174;
RA Vogel L.B., Fujita D.J.;
RT "The SH3 domain of p56lck is involved in binding to
RT phosphatidylinositol 3'-kinase from T lymphocytes.";
RL Mol. Cell. Biol. 13:7408-7417(1993).
RN [15]
RP INTERACTION WITH KHDRBS1.
RX MEDLINE=95155308; PubMed=7852312; DOI=10.1074/jbc.270.6.2506;
RA Vogel L.B., Fujita D.J.;
RT "p70 phosphorylation and binding to p56lck is an early event in
RT interleukin-2-induced onset of cell cycle progression in T-
RT lymphocytes.";
RL J. Biol. Chem. 270:2506-2511(1995).
RN [16]
RP INTERACTION WITH SQSTM1, AND MUTAGENESIS OF SER-58 AND ARG-153.
RX PubMed=8618896;
RA Park I., Chung J., Walsh C.T., Yun Y., Strominger J.L., Shin J.;
RT "Phosphotyrosine-independent binding of a 62-kDa protein to the src
RT homology 2 (SH2) domain of p56lck and its regulation by
RT phosphorylation of Ser-59 in the lck unique N-terminal region.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:12338-12342(1995).
RN [17]
RP INTERACTION WITH HIV-1 NEF.
RX MEDLINE=96386556; PubMed=8794306;
RA Greenway A.L., Azad A., Mills J., McPhee D.A.;
RT "Human immunodeficiency virus type 1 Nef binds directly to LCK and
RT mitogen-activated protein kinase, inhibiting kinase activity.";
RL J. Virol. 70:6701-6708(1996).
RN [18]
RP REVIEW.
RX PubMed=10848956;
RA Isakov N., Biesinger B.;
RT "Lck protein tyrosine kinase is a key regulator of T-cell activation

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RT   and a target for signal intervention by Herpesvirus saimiri and other
RT   viral gene products.";
RL   Eur. J. Biochem. 267:3413-3421(2000).
RN   [19]
RP   SUBCELLULAR LOCATION.
RX   PubMed=12218089;
RA   Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA   Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT   "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT   protein/phosphoprotein associated with glycolipid-enriched
RT   microdomains in lipid rafts in resting T cells.";
RL   J. Immunol. 169:2813-2817(2002).
RN   [20]
RP   MASS SPECTROMETRY.
RC   TISSUE=Mammary cancer;
RX   MEDLINE=21829512; PubMed=11840567;
RX   DOI=10.1002/1615-9861(200202)2:2<212::AID-PROT212>3.0.CO;2-H;
RA   Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
RA   Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
RA   Zvelebil M.J.;
RT   "Cluster analysis of an extensive human breast cancer cell line
RT   protein expression map database.";
RL   Proteomics 2:212-223(2002).
RN   [21]
RP   INTERACTION WITH LIME1.
RX   PubMed=14610046; DOI=10.1084/jem.20031484;
RA   Brdickova N., Brdicka T., Angelisova P., Horvath O., Spicka J.,
RA   Hilgert I., Paces J., Simeoni L., Kliche S., Merten C., Schraven B.,
RA   Horejsi V.;
RT   "LIME: a new membrane raft-associated adaptor protein involved in CD4
RT   and CD8 coreceptor signaling.";
RL   J. Exp. Med. 198:1453-1462(2003).
RN   [22]
RP   INTERACTION WITH LIME1.
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  Query Match             100.0%;  Score 41;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 8.1;
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Qy          1 LQDNLVIAL 9
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Db         60 LQDNLVIAL 68
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RESULT 3
LCK_MOUSE
ID   LCK_MOUSE      STANDARD;      PRT;   508 AA.
AC   P06240; Q61794; Q61795; Q62320; Q91X65;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   25-OCT-2005, sequence version 3.
DT   07-MAR-2006, entry version 74.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase) (LSK).
GN   Name=Lck; Synonyms=Lsk-t;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86079521; PubMed=2416464; DOI=10.1016/0092-8674(85)90169-2;
RA   Marth J.D., Peet R., Krebs E.G., Perlmutter R.M.;
RT   "A lymphocyte-specific protein-tyrosine kinase gene is rearranged and
RT   overexpressed in the murine T cell lymphoma LSTRA.";
RL   Cell 43:393-404(1985).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86146842; PubMed=3081813;
RA   Voronova A.F., Sefton B.M.;
RT   "Expression of a new tyrosine protein kinase is stimulated by
RT   retrovirus promoter insertion.";
RL   Nature 319:682-685(1986).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=NOD; TISSUE=Thymus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX   MEDLINE=89096891; PubMed=2850479;
RA   Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT   "Structure of the murine lck gene and its rearrangement in a murine
RT   lymphoma cell line.";
```

RL Mol. Cell. Biol. 8:3058-3064(1988).
RN [6]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-10.
RX MEDLINE=88142832; PubMed=3501824;
RA Voronova A.F., Adler H.T., Sefton B.M.;
RT "Two lck transcripts containing different 5' untranslated regions are
RT present in T cells.";
RL Mol. Cell. Biol. 7:4407-4413(1987).
RN [7]
RP MUTAGENESIS OF TYR-504.
RX MEDLINE=88248001; PubMed=3380790;
RA Amrein K.E., Sefton B.M.;
RT "Avian reovirus mRNAs are nonfunctional in infected mouse cells:
RT translational basis for virus host-range restriction.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:4257-4261(1988).
RN [8]
RP INTERACTIONS WITH CD4 AND CD8, AND MUTAGENESIS OF 2-CYS--CYS-4; CYS-19
RP AND CYS-22.
RX MEDLINE=90182665; PubMed=2107025; DOI=10.1016/0092-8674(90)90090-2;
RA Turner J.M., Brodsky M.H., Irving B.A., Levin S.D., Perlmutter R.M.,
RA Littman D.R.;
RT "Interaction of the unique N-terminal region of tyrosine kinase p56lck
RT with cytoplasmic domains of CD4 and CD8 is mediated by cysteine
RT motifs.";
RL Cell 60:755-765(1990).
RN [9]
RP MUTAGENESIS.
RX MEDLINE=93059694; PubMed=1279202;
RA Hurley T.R., Amrein K.E., Sefton B.M.;
RT "Creation and characterization of temperature-sensitive mutants of the
RT lck tyrosine protein kinase.";
RL J. Virol. 66:7406-7413(1992).
RN [10]
RP MUTAGENESIS OF LYS-272.
RX MEDLINE=91163633; PubMed=1706070; DOI=10.1038/350062a0;
RA Abraham N., Miceli M.C., Parnes J.C., Veillette A.;
RT "Enhancement of T-cell responsiveness by the lymphocyte-specific
RT tyrosine protein kinase p56lck.";
RL Nature 350:62-66(1991).
RN [11]
RP MUTAGENESIS OF TYR-504.
RX MEDLINE=91219495; PubMed=1708890;
RA Abraham K.M., Levin S.D., Marth J.D., Forbush K.A., Perlmutter R.M.;
RT "Thymic tumorigenesis induced by overexpression of p56lck.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981(1991).
RN [12]
RP PHOSPHORYLATION BY CSK.
RX PubMed=8371758; DOI=10.1038/365156a0;
RA Chow L.M., Fournel M., Davidson D., Veillette A.;
RT "Negative regulation of T-cell receptor signalling by tyrosine protein
RT kinase p50csk.";
RL Nature 365:156-160(1993).
RN [13]
RP MUTAGENESIS.
RX MEDLINE=93133805; PubMed=8421674;
RA Carrera A.C., Alexandrov K., Roberts T.M.;
RT "The conserved lysine of the catalytic domain of protein kinases is
RT actively involved in the phosphotransfer reaction and not required for
RT anchoring ATP.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:442-446(1993).
RN [14]
RP PALMITOYLATION.
RX MEDLINE=94019312; PubMed=8413237;
RA Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;
RT "Palmitylation of an amino-terminal cysteine motif of protein tyrosine
RT kinases p56lck and p59fyn mediates interaction with glycosyl-
RT phosphatidylinositol-anchored proteins.";
RL Mol. Cell. Biol. 13:6385-6392(1993).
RN [15]
RP PALMITOYLATION.
RX MEDLINE=95071286; PubMed=7980442;
RA Koegl M., Zlatkine P., Ley S.C., Courtneidge S.A., Magee A.I.;
RT "Palmitoylation of multiple Src-family kinases at a homologous N-
RT terminal motif.";
RL Biochem. J. 303:749-753(1994).
RN [16]
RP INTERACTION WITH CBLB.
RX PubMed=10646608; DOI=10.1038/35003228;
RA Bachmaier K., Krawczyk C., Kozieradzki I., Kong Y.-Y., Sasaki T.,
RA Oliveira-dos-Santos A., Mariathasan S., Bouchard D., Wakeham A.,
RA Itie A., Le J., Ohashi P.S., Sarosi I., Nishina H., Lipkowitz S.,
RA Penninger J.M.;
RT "Negative regulation of lymphocyte activation and autoimmunity by the
RT molecular adaptor Cbl-b.";
RL Nature 403:211-216(2000).
RN [17]
RP SUBCELLULAR LOCATION.
RX PubMed=12218089;
RA Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT protein/phosphoprotein associated with glycolipid-enriched
RT microdomains in lipid rafts in resting T cells.";
RL J. Immunol. 169:2813-2817(2002).
RN [18]
RP PHOSPHORYLATION SITE TYR-393, AND MASS SPECTROMETRY.
RX PubMed=15592455; DOI=10.1038/nbt1046;
RA Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
RA Zha X.-M., Polakiewicz R.D., Comb M.J.;
RT "Immunoaffinity profiling of tyrosine phosphorylation in cancer

Query Match 100.0%; Score 41; DB 1; Length 508;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQDNLVIAL 9
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Db 60 LQDNLVIAL 68

RESULT 4
LCK_SAISC
ID LCK_SAISC STANDARD; PRT; 508 AA.
AC Q95KR7;
DT 08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT 08-NOV-2005, sequence version 2.
DT 07-MAR-2006, entry version 26.
DE Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE (Lymphocyte cell-specific protein-tyrosine kinase).
GN Name=LCK;
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], ENZYME REGULATION, AND INTERACTION WITH
RP SAIMIRINE HERPESVIRUS 2 TIP.
RC TISSUE=T-cell;
RX MEDLINE=21424508; PubMed=11533187;
RX DOI=10.1128/JVI.75.19.9252-9261.2001;
RA Greve T., Tamgueney G., Fleischer B., Fickenscher H., Broeker B.M.;
RT "Downregulation of p56Lck tyrosine kinase activity in T cells of
RT squirrel monkeys (Saimiri sciureus) correlates with the non-
RT transforming and apathogenic properties of herpesvirus saimiri in its
RT natural host.";
RL J. Virol. 75:9252-9261(2001).
CC -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC selection and maturation of developing T-cell in the thymus and in
CC mature T-cell function. Is constitutively associated with the
CC cytoplasmic portions of the CD4 and CD8 surface receptors and
CC plays a key role in T-cell antigen receptor(TCR)-linked signal
CC transduction pathways. Association of the TCR with a peptide
CC antigen-bound MHC complex facilitates the interaction of CD4 and
CC CD8 with MHC class II and class I molecules, respectively, and
CC thereby recruits the associated LCK to the vicinity of the TCR/CD3

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CC       complex. LCK then phosphorylates tyrosines residues within the
CC       immunoreceptor tyrosines-based activation motifs (ITAMs) in the
CC       cytoplasmic tails of the TCRgamma chains and CD3 subunits,
CC       initiating the TCR/CD3 signaling pathway. In addition, contributes
CC       to signaling by other receptor molecules. Associates directly with
CC       the cytoplasmic tail of CD2, and upon engagement of the CD2
CC       molecule, LCK undergoes hyperphosphorylation and activation. Also
CC       plays a role in the IL2 receptor-linked signaling pathway that
CC       controls T-cell proliferative response. Binding of IL2 to its
CC       receptor results in increased activity of LCK. Is expressed at all
CC       stages of thymocyte development and is required for the regulation
CC       of maturation events that are governed by both pre-TCR and mature
CC       alpha beta TCR (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- ENZYME REGULATION: Regulated by phosphatases.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also
CC       binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to
CC       other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds
CC       to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes
CC       through its SH3 domain and to the tyrosine phosphorylated form of
CC       KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.
CC       Interacts with phosphorylated LIME1. Interacts with CBLB (By
CC       similarity). Interacts with saimirine herpesvirus 2 TIP.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.
CC       Present in lipid rafts in an unactive form (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed specificaly in lymphoid cells.
CC   -!- DEVELOPMENTAL STAGE: Levels remain relatively constant throughout
CC       T-cell ontogeny.
CC   -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.
CC       Interaction is regulated by Ser-58 phosphorylation (By
CC       similarity).
CC   -!- PTM: Phosphorylated on Tyr-504 presumably by CSK. This
CC       phosphorylation downregulates catalytic activity. Phosphorylated
CC       on Tyr-393 either by itself or another kinase, leading to
CC       increased enzymatic activity.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   -!- CAUTION: LCK seems to be active in all vertebrates, except in
CC       squirrel monkey T-cells, in which it is inactivated. The reason
CC       seems to be that squirrel monkey are the natural host for
CC       Saimiriine herpesvirus 2, which is able to efficiently transform
CC       T-cells through a mecanism involving viral Tip/ host LCK
CC       interaction. Its inactivation may a mecanism that specificaly
CC       counteracts the transformation effects of viral Tip.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ277921; CAC38871.1; -; mRNA.
DR   HSSP; P06239; 1LKK.
DR   SMR; Q95KR7; 64-508.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    508       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088127.
FT   DOMAIN       60    120       SH3.
FT   DOMAIN      126    223       SH2.
FT   DOMAIN      244    497       Protein kinase.
FT   NP_BIND     250    258       ATP (By similarity).
FT   REGION        1     71       Interactions with CD4 and CD8 (By
FT                                similarity).
FT   ACT_SITE    363    363       Proton acceptor (By similarity).
FT   BINDING     272    272       ATP (By similarity).
FT   MOD_RES     393    393       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     504    504       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   508 AA;  58122 MW;  5088C64061853819 CRC64;

  Query Match             100.0%;  Score 41;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 8.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
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Db         60 LQDNLVIAL 68


RESULT 5
Q7RTZ3_HUMAN
ID   Q7RTZ3_HUMAN   PRELIMINARY;   PRT;   509 AA.
AC   Q7RTZ3;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Protein tyrosine kinase.
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22289034; PubMed=12401726;
RA   Nervi S., Nicodeme S., Gartioux C., Atlan C., Lathrop M., Reviron D.,
RA   Naquet P., Matsuda F., Imbert J., Vialettes B.;
RT   "No association between lck gene polymorphisms and protein level in
RT   type 1 diabetes.";
RL   Diabetes 51:3326-3330(2002).
CC   -!- MISCELLANEOUS: The sequence shcwn here is derived from an
CC       EMBL/GenBank/DDBJ third party annotation (TPA) entry.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BN000073; CAD55807.1; -; Genomic_DNA.
DR   HSSP; P06239; 1BHF.
DR   SMR; Q7RTZ3; 65-509.
DR   Ensembl; ENSG00000182866; Homo sapiens.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
```

```
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   509 AA;  58001 MW;  44BFF0D43FFB420D CRC64;

  Query Match            100.0%;  Score 41;  DB 2;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 8.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         61 LQDNLVIAL 69


RESULT 6
Q95M32_9PRIM
ID   Q95M32_9PRIM   PRELIMINARY;   PRT;   509 AA.
AC   Q95M32;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Lck protein.
GN   Name=lck;
OS   Hylobates sp. (gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Hylobatidae; Hylobates.
OX   NCBI_TaxID=9581;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22031236; PubMed=12033791; DOI=10.1006/viro.2002.1381;
RA   Picard C., Greenway A., Holloway G., Olive D., Collette Y.;
RT   "Interaction with simian Hck tyrosine kinase reveals convergent
RT   evolution of the Nef protein from simian and human immunodeficiency
RT   viruses despite differential molecular surface usage.";
RL   Virology 295:320-327(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Picard C.;
RL   Thesis (2001), Department of Experimental Oncology laboratory, U.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ320182; CAC44027.1; -; mRNA.
DR   HSSP; P06239; 1LCK.
DR   SMR; Q95M32; 65-509.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   509 AA;  57947 MW;  F1BFE5C237C8DB7E CRC64;

  Query Match            100.0%;  Score 41;  DB 2;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 8.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         61 LQDNLVIAL 69


RESULT 7
Q3ZCM0_BOVIN
ID   Q3ZCM0_BOVIN   PRELIMINARY;   PRT;   509 AA.
AC   Q3ZCM0;
DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
DT   07-MAR-2006, entry version 6.
DE   Hypothetical protein MGC126900.
GN   Name=MGC126900;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
```

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OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Crossbred x Angus; TISSUE=Ileum;
RA   Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA   Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA   Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA   Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA   Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA   Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC102046; AAI02047.1; -; mRNA.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   509 AA;  58116 MW;  CE0E80DCD6D0F2F8 CRC64;

  Query Match           100.0%;  Score 41;  DB 2;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 8.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||||||
Db         61 LQDNLVIAL 69


RESULT 8
Q4SP61_TETNG
ID   Q4SP61_TETNG   PRELIMINARY;   PRT;   663 AA.
AC   Q4SP61;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 4.
DE   Chromosome 15 SCAF14542, whole genome shotgun sequence. (Fragment).
GN   ORFNames=GSTENG00014985001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CAAE01014542; CAF97571.1; -; Genomic_DNA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   InterPro; IPR000210; BTB.
DR   InterPro; IPR007087; Znf_C2H2.
DR   Pfam; PF00651; BTB; 1.
DR   Pfam; PF00096; zf-C2H2; 4.
DR   SMART; SM00225; BTB; 1.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS50097; BTB; 1.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
FT   NON_TER     663    663
SQ   SEQUENCE   663 AA;  73294 MW;  4C0D615FE38FCB37 CRC64;

  Query Match           90.2%;  Score 37;  DB 2;  Length 663;
  Best Local Similarity  77.8%;  Pred. No. 79;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              ||||||:|:
Db         97 LQDNLVLAI 105


RESULT 9
Q3YSG0_EHRCJ
ID   Q3YSG0_EHRCJ   PRELIMINARY;   PRT;   189 AA.
AC   Q3YSG0;
DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
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```
DT   21-FEB-2006, entry version 7.
DE   Elongation factor P (EF-P).
GN   OrderedLocusNames=Ecaj_0301;
OS   Ehrlichia canis (strain Jake).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC   Anaplasmataceae; Ehrlichia.
OX   NCBI_TaxID=269484;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG   US DOE Joint Genome Institute;
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M.,
RA   Vergez L., Schmutz J., Larimer F., Land M., Mavrommatis K.,
RA   Richardson P.;
RT   "Complete sequence of Ehrlichia canis str. Jake.";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CP000107; AAZ68345.1; -; Genomic_DNA.
DR   GO; GO:0005737; C:cytoplasm; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0003746; F:translation elongation factor activity; IEA.
DR   GO; GO:0006412; P:protein biosynthesis; IEA.
DR   GO; GO:0006414; P:translational elongation; IEA.
DR   InterPro; IPR011768; EF-P.
DR   InterPro; IPR001059; EF-P/YeiP.
DR   InterPro; IPR013185; EFP_KOW_N.
DR   Pfam; PF01132; EFP; 2.
DR   PIRSF; PIRSF005901; EF-P; 1.
DR   TIGRFAMs; TIGR00038; efp; 1.
KW   Complete proteome; Elongation factor.
SQ   SEQUENCE   189 AA;  21323 MW;  19455CCD8CE40D50 CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 189;
  Best Local Similarity   77.8%;  Pred. No. 59;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              ||||:|| |
Db        106 LQDNIVITL 114


RESULT 10
HCP_THEMA
ID   HCP_THEMA      STANDARD;      PRT;   431 AA.
AC   Q9X0Q4;
DT   30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1999, sequence version 1.
DT   07-MAR-2006, entry version 38.
DE   Hydroxylamine reductase (EC 1.7.-.-) (Hybrid-cluster protein) (HCP).
GN   Name=hcp; OrderedLocusNames=TM1172;
OS   Thermotoga maritima.
OC   Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX   NCBI_TaxID=2336;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=MSB8 / DSM 3109 / ATCC 43589;
RX   MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
RA   Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA   Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA   McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA   Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
RA   Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA   Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT   "Evidence for lateral gene transfer between Archaea and Bacteria from
RT   genome sequence of Thermotoga maritima.";
RL   Nature 399:323-329(1999).
CC   -!- FUNCTION: Catalyzes the reduction of hydroxylamine to form NH(3)
CC       and H(2)O (By similarity).
CC   -!- COFACTOR: Binds 1 4Fe-4S cluster (By similarity).
CC   -!- COFACTOR: Binds 1 hybrid 4Fe-2O-2S cluster (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC   -!- SIMILARITY: Belongs to the HCP family.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AE000512; AAD36247.1; -; Genomic_DNA.
DR   PIR; G72285; G72285.
DR   HSSP; Q01770; 1GNL.
DR   GenomeReviews; AE000512_GR; TM1172.
DR   TIGR; TM1172; -.
DR   BioCyc; TMAR2336:TM1172-MONOMER; -.
DR   HAMAP; MF_00069; -; 1.
DR   InterPro; IPR010048; Hybrid_clust.
DR   InterPro; IPR004137; Prismane.
DR   Pfam; PF03063; Prismane; 1.
DR   TIGRFAMs; TIGR01703; hybrid_clust; 1.
KW   4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding;
KW   Oxidoreductase.
FT   CHAIN         1    431       Hydroxylamine reductase.
FT                                /FTId=PRO_0000151684.
FT   METAL         5      5       Iron-sulfur (4Fe-4S) (By similarity).
FT   METAL         8      8       Iron-sulfur (4Fe-4S) (By similarity).
FT   METAL        17     17       Iron-sulfur (4Fe-4S) (By similarity).
FT   METAL        23     23       Iron-sulfur (4Fe-4S) (By similarity).
FT   METAL       131    131       Iron-oxo-sulfur (4Fe-2O-2S) (By
FT                                similarity).
FT   METAL       155    155       Iron-oxo-sulfur (4Fe-2O-2S) (By
FT                                similarity).
FT   METAL       199    199       Iron-oxo-sulfur (4Fe-2O-2S) (By
FT                                similarity).
FT   METAL       286    286       Iron-oxo-sulfur (4Fe-2O-2S) (By
FT                                similarity).
FT   METAL       314    314       Iron-oxo-sulfur (4Fe-2O-2S) (By
FT                                similarity).
FT   METAL       339    339       Iron-oxo-sulfur (4Fe-2O-2S) (By
FT                                similarity).
FT   METAL       373    373       Iron-oxo-sulfur (4Fe-2O-2S) (By
FT                                similarity).
SQ   SEQUENCE   431 AA;  47958 MW;  6D9E224F0F7706A4 CRC64;

  Query Match             85.4%;  Score 35;  DB 1;  Length 431;
  Best Local Similarity   77.8%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||| |:
Db         32 LQDNLVFAI 40


RESULT 11
Q4FF10_9THEM
ID   Q4FF10_9THEM   PRELIMINARY;   PRT;   431 AA.
AC   Q4FF10;
DT   30-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   30-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Prismane protein.
OS   Thermotoga sp. RQ2.
OC   Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX   NCBI_TaxID=126740;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=RQ2;
RX   PubMed=15995209; DOI=10.1128/JB.187.14.4935-4944.2005;
RA   Mongodin E.F., Hance I.R., Deboy R.T., Gill S.R., Daugherty S.,
RA   Huber R., Fraser C.M., Stetter K., Nelson K.E.;
RT   "Gene transfer and genome plasticity in Thermotoga maritima, a model
RT   hyperthermophilic species.";
RL   J. Bacteriol. 187:4935-4944(2005).
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ----------------------------------------------------------------------
DR   EMBL; DQ073436; AAZ04353.1; -; Genomic_DNA.
DR   GO; GO:0005737; C:cytoplasm; IEA.
DR   GO; GO:0005506; F:iron ion binding; IEA.
DR   GO; GO:0016661; F:oxidoreductase activity, acting on other ni. . .; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR010048; Hybrid_clust.
DR   Pfam; PF03063; Prismane; 1.
DR   TIGRFAMs; TIGR01703; hybrid_clust; 1.
SQ   SEQUENCE   431 AA;  47929 MW;  D7C7B2C4E309E7FC CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 431;
  Best Local Similarity   77.8%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||||| |:
Db         32 LQDNLVFAI 40


RESULT 12
LIP6_CANAL
ID   LIP6_CANAL     STANDARD;      PRT;   463 AA.
AC   Q9P4E8;
DT   21-NOV-2003, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-2000, sequence version 1.
DT   07-FEB-2006, entry version 24.
DE   Lipase 6 precursor (EC 3.1.1.3).
GN   Name=LIP6;
OS   Candida albicans (Yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX   NCBI_TaxID=5476;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND SUBCELLULAR LOCATION.
RC   STRAIN=SC5314;
RX   MEDLINE=21014758; PubMed=11131027; DOI=10.1007/s002030000218;
RA   Hube B., Stehr F., Bossenz M., Mazur A., Kretschmar M., Schaefer W.;
RT   "Secreted lipases of Candida albicans: cloning, characterisation and
RT   expression analysis of a new gene family with at least ten members.";
RL   Arch. Microbiol. 174:362-374(2000).
CC   -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC       carboxylate.
CC   -!- SUBCELLULAR LOCATION: Secreted protein.
CC   -!- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
CC       family.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AF191319; AAF79927.1; -; Genomic_DNA.
DR   InterPro; IPR005152; LIP.
DR   Pfam; PF03583; LIP; 1.
KW   Glycoprotein; Hydrolase; Lipid degradation; Signal.
FT   SIGNAL        1     16       Potential.
FT   CHAIN        17    463       Lipase 6.
FT                                /FTId=PRO_0000017825.
FT   ACT_SITE    196    196       Charge relay system (By similarity).
FT   ACT_SITE    344    344       Charge relay system (By similarity).
FT   CARBOHYD    231    231       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    422    422       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   463 AA;  50480 MW;  21F5E66B04F73DAF CRC64;

  Query Match             85.4%;  Score 35;  DB 1;  Length 463;
  Best Local Similarity   77.8%;  Pred. No. 1.5e+02;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |:|||:|||
Db        322 LEDNLLIAL 330


RESULT 13
Q5APE2_CANAL
ID   Q5APE2_CANAL   PRELIMINARY;   PRT;   463 AA.
AC   Q5APE2;
DT   26-APR-2005, integrated into UniProtKB/TrEMBL.
DT   26-APR-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   C. albicans secretory lipase 6.
GN   Name=LIP6; ORFNames=CaO19.12286, CaO19.4823;
OS   Candida albicans SC5314.
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX   NCBI_TaxID=237561;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=SC5314;
RX   PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA   Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA   Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA   Davis R.W., Scherer S.;
RT   "The diploid genome sequence of Candida albicans.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AACQ01000002; EAL04615.1; -; Genomic_DNA.
DR   EMBL; AACQ01000001; EAL04811.1; -; Genomic_DNA.
DR   InterPro; IPR002453; Beta_tubulin.
DR   InterPro; IPR005152; LIP.
DR   Pfam; PF03583; LIP; 1.
DR   PROSITE; PS00228; TUBULIN_B_AUTOREG; UNKNOWN_1.
SQ   SEQUENCE   463 AA;  50480 MW;  21F5E66B04F73DAF CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 463;
  Best Local Similarity   77.8%;  Pred. No. 1.5e+02;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |:|||:|||
Db        322 LEDNLLIAL 330


RESULT 14
Q82AU6_STRAW
ID   Q82AU6_STRAW   PRELIMINARY;   PRT;  1045 AA.
AC   Q82AU6;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   21-FEB-2006, entry version 23.
DE   Putative LuxR-family transcriptional regulator.
GN   OrderedLocusNames=SAV5959;
OS   Streptomyces avermitilis.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=33903;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX   MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
RA   Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA   Sakaki Y., Hattori M., Omura S.;
RT   "Complete genome sequence and comparative analysis of the industrial
RT   microorganism Streptomyces avermitilis.";
RL   Nat. Biotechnol. 21:526-531(2003).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX   MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA   Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
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RA   Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA   Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT   "Genome sequence of an industrial microorganism Streptomyces
RT   avermitilis: deducing the ability of producing secondary
RT   metabolites.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BA000030; BAC73671.1; -; Genomic_DNA.
DR   BioCyc; SAVE227882:SAV5959-MONOMER; -.
DR   GO; GO:0004176; F:ATP-dependent peptidase activity; IEA.
DR   GO; GO:0005488; F:binding; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR   GO; GO:0000156; F:two-component response regulator activity; IEA.
DR   GO; GO:0042829; P:defense response to pathogen; IEA.
DR   GO; GO:0006508; P:proteolysis; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0006350; P:transcription; IEA.
DR   GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR   InterPro; IPR003439; ABC_transp_like.
DR   InterPro; IPR005158; BTAD.
DR   InterPro; IPR000767; Disease_resist.
DR   InterPro; IPR001984; Peptidase_S16.
DR   InterPro; IPR011990; TPR-like_helical.
DR   InterPro; IPR001867; Trans_reg_C.
DR   InterPro; IPR011991; Wing_hlx_DNA_bd.
DR   Pfam; PF03704; BTAD; 1.
DR   Pfam; PF00486; Trans_reg_C; 1.
DR   PRINTS; PR00364; DISEASERSIST.
DR   PRINTS; PR00830; ENDOLAPTASE.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
KW   Complete proteome.
SQ   SEQUENCE   1045 AA;  111412 MW;  D4FA33F74544EB98 CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 1045;
  Best Local Similarity   87.5%;  Pred. No. 3.5e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QDNLVIAL 9
              |||||:||
Db        607 QDNLVLAL 614


RESULT 15
Q40IE4_EHRCH
ID   Q40IE4_EHRCH   PRELIMINARY;   PRT;   189 AA.
AC   Q40IE4;
DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
DT   21-FEB-2006, entry version 5.
DE   Elongation factor P (EF-P).
GN   ORFNames=EchaDRAFT_0084;
OS   Ehrlichia chaffeensis str. Sapulpa.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC   Anaplasmataceae; Ehrlichia.
OX   NCBI_TaxID=332415;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sapulpa;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome and assembly of Ehrlichia chaffeensis
RT   str. Sapulpa.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sapulpa;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Ehrlichia chaffeensis str.
RT   Sapulpa.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AAIF01000095; EAM85378.1; -; Genomic_DNA.
DR   GO; GO:0005737; C:cytoplasm; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0003746; F:translation elongation factor activity; IEA.
DR   GO; GO:0006412; P:protein biosynthesis; IEA.
DR   GO; GO:0006414; P:translational elongation; IEA.
DR   InterPro; IPR011768; EF-P.
DR   InterPro; IPR001059; EF-P/YeiP.
DR   InterPro; IPR013185; EFP_KOW_N.
DR   Pfam; PF01132; EFP; 2.
DR   PIRSF; PIRSF005901; EF-P; 1.
DR   TIGRFAMs; TIGR00038; efp; 1.
KW   Elongation factor.
SQ   SEQUENCE   189 AA;  21277 MW;  078E0F807C6C0C08 CRC64;

  Query Match             82.9%;  Score 34;  DB 2;  Length 189;
  Best Local Similarity   66.7%;  Pred. No. 97;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              ||||::| |
Db        106 LQDNIIITL 114


RESULT 16
Q7MS04_WOLSU
ID   Q7MS04_WOLSU   PRELIMINARY;   PRT;   230 AA.
AC   Q7MS04;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 17.
DE   Hypothetical protein.
GN   OrderedLocusNames=WS0898;
OS   Wolinella succinogenes.
OC   Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC   Helicobacteraceae; Wolinella.
OX   NCBI_TaxID=844;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=DSMZ 1740;
RX   MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
RA   Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
RA   Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
RA   Meyer F., Lederer H., Schuster S.C.;
RT   "Complete genome sequence and analysis of Wolinella succinogenes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BX571659; CAE10003.1; -; Genomic_DNA.
DR   BioCyc; WSUC844:WS0898-MONOMER; -.
DR   GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR   GO; GO:0009116; P:nucleoside metabolism; IEA.
DR   InterPro; IPR000836; PRtransferase.
DR   Pfam; PF00156; Pribosyltran; 1.
KW   Complete proteome; Glycosyltransferase; Hypothetical protein;
KW   Transferase.
SQ   SEQUENCE   230 AA;  25924 MW;  E91635CA8E3A967F CRC64;

  Query Match             82.9%;  Score 34;  DB 2;  Length 230;
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  Best Local Similarity   75.0%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QDNLVIAL 9
              |||||:|:
Db         30 QDNLVVAI 37


RESULT 17
Y474_RICPR
ID   Y474_RICPR     STANDARD;      PRT;   269 AA.
AC   Q9ZD70;
DT   30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT   01-MAY-1999, sequence version 1.
DT   07-MAR-2006, entry version 25.
DE   Hypothetical protein RP474.
GN   OrderedLocusNames=RP474;
OS   Rickettsia prowazekii.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC   Rickettsiaceae; Rickettsieae; Rickettsia; typhus group.
OX   NCBI_TaxID=782;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Madrid E;
RX   MEDLINE=99039499; PubMed=9823893; DOI=10.1038/24094;
RA   Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA   Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA   Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT   "The genome sequence of Rickettsia prowazekii and the origin of
RT   mitochondria.";
RL   Nature 396:133-140(1998).
RN   [2]
RP   DOMAIN RPE1.
RX   MEDLINE=20485642; PubMed=11030655; DOI=10.1126/science.290.5490.347;
RA   Ogata H., Audic S., Barbe V., Artiguenave F., Fournier P.-E.,
RA   Raoult D., Claverie J.-M.;
RT   "Selfish DNA in protein-coding genes of Rickettsia.";
RL   Science 290:347-350(2000).
CC   -!- SIMILARITY: Contains 1 RPE1 insert domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ235271; CAA14929.1; -; Genomic_DNA.
DR   PIR; G71706; G71706.
DR   GenomeReviews; AJ235269_GR; RP474.
DR   BioCyc; RPRO782:RP474-MONOMER; -.
DR   InterPro; IPR003788; DUF185.
DR   InterPro; IPR003754; HEM4_synth.
DR   InterPro; IPR005728; Rickett_RPE.
DR   PANTHER; PTHR12049; DUF185; 1.
DR   TIGRFAMs; TIGR01045; RPE; 1.
KW   Complete proteome; Hypothetical protein.
FT   CHAIN         1    269       Hypothetical protein RP474.
FT                                /FTId=PRO_0000101380.
FT   DOMAIN      152    197       RPE1 insert.
SQ   SEQUENCE   269 AA;  31209 MW;  7FF311961FB11716 CRC64;

  Query Match             82.9%;  Score 34;  DB 1;  Length 269;
  Best Local Similarity   77.8%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||:||||:
Db        225 LQDSLVIAI 233


RESULT 18
Q68WQ6_RICTY
ID   Q68WQ6_RICTY   PRELIMINARY;   PRT;   271 AA.
AC   Q68WQ6;
DT   11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2004, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   Hypothetical protein.
GN   OrderedLocusNames=RT0461;
OS   Rickettsia typhi.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC   Rickettsiaceae; Rickettsieae; Rickettsia; typhus group.
OX   NCBI_TaxID=785;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Wilmington;
RX   PubMed=15317790; DOI=10.1128/JB.186.17.5842-5855.2004;
RA   McLeod M.P., Qin X., Karpathy S.E., Gioia J., Highlander S.K.,
RA   Fox G.E., McNeill T.Z., Jiang H., Muzny D., Jacob L.S., Hawes A.C.,
RA   Sodergren E., Gill R., Hume J., Morgan M., Fan G., Amin A.G.,
RA   Gibbs R.A., Hong C., Yu X.-J., Walker D.H., Weinstock G.M.;
RT   "Complete genome sequence of Rickettsia typhi and comparison with
RT   sequences of other Rickettsiae.";
RL   J. Bacteriol. 186:5842-5855(2004).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE017197; AAU03936.1; -; Genomic_DNA.
DR   GO; GO:0004852; F:uroporphyrinogen-III synthase activity; IEA.
DR   GO; GO:0006783; P:heme biosynthesis; IEA.
DR   InterPro; IPR003788; DUF185.
DR   InterPro; IPR003754; HEM4_synth.
DR   InterPro; IPR005728; Rickett_RPE.
DR   PANTHER; PTHR12049; DUF185; 1.
DR   TIGRFAMs; TIGR01045; RPE; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   271 AA;  31679 MW;  5502F890BFFF8CA0 CRC64;

  Query Match             82.9%;  Score 34;  DB 2;  Length 271;
  Best Local Similarity   77.8%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||:||||:
Db        226 LQDSLVIAI 234


RESULT 19
Q4N2A8_THEPA
ID   Q4N2A8_THEPA   PRELIMINARY;   PRT;   301 AA.
AC   Q4N2A8;
DT   02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   02-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Hypothetical protein.
GN   ORFNames=TP04_0444;
OS   Theileria parva.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC   Theileria.
OX   NCBI_TaxID=5875;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Muguga;
RX   PubMed=15994558; DOI=10.1126/science.1110439;
RA   Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA   Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.,
RA   Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA   Jiang L., Lynn J., Weaver B., Shoaibi A., Domingo A.R., Wasawo D.,
RA   Crabtree J., Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C.,
RA   Suh B., Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M.,
RA   Allen J., Nierman W.C., Taracha E.L., Salzberg S.L., White O.R.,
RA   Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;
RT   "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
RT   Lymphocytes.";
RL   Science 309:134-137(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Muguga;
```

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RA   Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA   Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA   Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA   Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA   Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA   Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
RA   Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA   Fraser C.M., Nene V.;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AAGK01000004; EAN31796.1; -; Genomic_DNA.
DR   InterPro; IPR003639; Mov34-1.
DR   InterPro; IPR000555; Mov34_MPN_PAD1.
DR   Pfam; PF01398; Mov34; 1.
DR   ProDom; PD363422; Mov34-1; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   301 AA;  34174 MW;  B2EC5E9D0BD7592C CRC64;

  Query Match             82.9%;  Score 34;  DB 2;  Length 301;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIA 8
              |||||:||
Db        274 LQDNLMIA 281


RESULT 20
Q2SJ95_9GAMM
ID   Q2SJ95_9GAMM   PRELIMINARY;   PRT;   322 AA.
AC   Q2SJ95;
DT   24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT   24-JAN-2006, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Transaldolase (EC 2.2.1.2).
GN   Name=tal2; ORFNames=HCH_02473;
OS   Hahella chejuensis KCTC 2396.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
OC   Hahellaceae; Hahella.
OX   NCBI_TaxID=349521;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=KCTC 2396;
RX   PubMed=16352867; DOI=10.1093/nar/gki1016;
RA   Jeong H., Yim J.H., Lee C., Choi S.-H., Park Y.K., Yoon S.H.,
RA   Hur C.-G., Kang H.-Y., Kim D., Lee H.H., Park K.H., Park S.-H.,
RA   Park H.-S., Lee H.K., Oh T.K., Kim J.F.;
RT   "Genomic blueprint of Hahella chejuensis, a marine microbe producing
RT   an algicidal agent.";
RL   Nucleic Acids Res. 33:7066-7073(2005).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; CP000155; ABC29279.1; -; Genomic_DNA.
DR   GO; GO:0016740; F:transferase activity; IEA.
KW   Transferase.
SQ   SEQUENCE   322 AA;  35693 MW;  9B9FF4C6AD3635E2 CRC64;

  Query Match             82.9%;  Score 34;  DB 2;  Length 322;
  Best Local Similarity   75.0%;  Pred. No. 1.7e+02;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QDNLVIAL 9
              |||||:|:
Db         75 QDNLVVAM 82


RESULT 21
Q9M5G4_EUPES
ID   Q9M5G4_EUPES   PRELIMINARY;   PRT;   480 AA.
AC   Q9M5G4;
DT   01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2000, sequence version 1.
DT   07-FEB-2006, entry version 27.
DE   CDK-activating kinase.
OS   Euphorbia esula (Leafy spurge).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   rosids; eurosids I; Malpighiales; Euphorbiaceae; Euphorbioideae;
OC   Euphorbieae; Euphorbia.
OX   NCBI_TaxID=3993;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Underground adventitious buds;
RA   Anderson J.V., Horvath D.P.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF230740; AAF34804.1; -; mRNA.
DR   HSSP; P24941; 1OIQ.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   480 AA;  54187 MW;  6E3924F21BD9AF45 CRC64;

  Query Match             82.9%;  Score 34;  DB 2;  Length 480;
  Best Local Similarity   66.7%;  Pred. No. 2.6e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              | |||::||
Db         47 LSDNLIVAL 55


RESULT 22
LCK_CHICK
ID   LCK_CHICK      STANDARD;      PRT;   507 AA.
AC   P42683; Q53WS8;
DT   01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1995, sequence version 1.
DT   07-MAR-2006, entry version 47.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (Protein-
DE   tyrosine kinase C-TKL) (p56tk1).
GN   Name=LCK;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Spleen;
```

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RA   Gaertner T., Khnel H., Strebhardt K., Ruebsamen-Waigmann H.;
RL   Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 1-88.
RX   MEDLINE=92186854; PubMed=1545804;
RA   Chow L., Ratcliffe M., Veillette A.;
RT   "tkl is the avian homolog of the mammalian lck tyrosine protein kinase
RT   gene.";
RL   Mol. Cell. Biol. 12:1226-1233(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 46-507.
RX   MEDLINE=88097370; PubMed=3321053;
RA   Strebhardt K., Mullins J.I., Bruck C., Ruebsamen-Waigmann H.;
RT   "Additional member of the protein-tyrosine kinase family: the src- and
RT   lck-related protooncogene c-tkl.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:8778-8782(1987).
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD4, CD8 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Bound to the cytoplasmic domain of either
CC       CD4 or CD8 (By similarity).
CC   -!- PTM: Phosphorylated on Tyr-503. This phosphorylation downregulates
CC       catalytic activity. Phosphorylated on Tyr-392 either by itself or
CC       another kinase, leading to increased enzymatic activity.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X60380; CAA42930.1; -; mRNA.
DR   EMBL; M85043; AAA49003.1; -; mRNA.
DR   EMBL; J03579; AAA49081.1; ALT_INIT; mRNA.
DR   HSSP; P06239; 3LCK.
DR   SMR; P42683; 63-507.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    507       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088128.
FT   DOMAIN       59    119       SH3.
FT   DOMAIN      125    222       SH2.
FT   DOMAIN      243    496       Protein kinase.
FT   NP_BIND     249    257       ATP (By similarity).
FT   ACT_SITE    362    362       Proton acceptor (By similarity).
FT   BINDING     271    271       ATP (By similarity).
FT   MOD_RES     392    392       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     503    503       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   507 AA;  58009 MW;  BC83C4FA891B6170 CRC64;

  Query Match             82.9%;  Score 34;  DB 1;  Length 507;
  Best Local Similarity   77.8%;  Pred. No. 2.7e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              ||| ||:||
Db         59 LQDKLVVAL 67


RESULT 23
Q3MWW8_9DELT
ID   Q3MWW8_9DELT   PRELIMINARY;   PRT;   731 AA.
AC   Q3MWW8;
DT   25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   25-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Hypothetical protein.
GN   ORFNames=SfumDRAFT_0052;
OS   Syntrophobacter fumaroxidans MPOB.
OC   Bacteria; Proteobacteria; Deltaproteobacteria; Syntrophobacterales;
OC   Syntrophobacteraceae; Syntrophobacter.
OX   NCBI_TaxID=335543;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=MPOB;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome and assembly of Syntrophobacter
RT   fumaroxidans MPOB.";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=MPOB;
RG   US DOE Joint Genome Institute (JGI_ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Syntrophobacter
RT   fumaroxidans MPOB.";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AAJF01000065; EAO19434.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   731 AA;  81207 MW;  DCF63286081FAB29 CRC64;

  Query Match             82.9%;  Score 34;  DB 2;  Length 731;
  Best Local Similarity   77.8%;  Pred. No. 3.9e+02;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |:|||:|||
Db        587 LRDNLLIAL 595
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RESULT 24
Q371F3_RHOPA
ID   Q371F3_RHOPA   PRELIMINARY;   PRT;    94 AA.
AC   Q371F3;
DT   06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT   06-DEC-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Hypothetical protein.
GN   ORFNames=RPEDRAFT_1953;
OS   Rhodopseudomonas palustris BisA53.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Bradyrhizobiaceae; Rhodopseudomonas.
OX   NCBI_TaxID=316055;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BisA53;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome and assembly of Rhodopseudomonas
RT   palustris BisA53.";
RL   Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BisA53;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome of Rhodopseudomonas palustris
RT   BisA53.";
RL   Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AALA01000011; EAO89920.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   94 AA;  10700 MW;  1853E2990023DE2F CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 94;
  Best Local Similarity   77.8%;  Pred. No. 78;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              | ||||||:
Db         64 LSDNLVIAV 72


RESULT 25
Q9BEI2_MACEU
ID   Q9BEI2_MACEU   PRELIMINARY;   PRT;   147 AA.
AC   Q9BEI2;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 20.
DE   Omega globin.
OS   Macropus eugenii (Tammar wallaby).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX   NCBI_TaxID=9315;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21107677; PubMed=11158601; DOI=10.1073/pnas.98.3.1101;
RA   Wheeler D., Hope R., Cooper S.J., Dolman G., Webb G.C., Bottema C.D.,
RA   Gooley A.A., Goodman M., Holland R.A.;
RT   "An orphaned mammalian beta-globin gene of ancient evolutionary
RT   origin.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:1101-1106(2001).
CC   -!- FUNCTION: Involved in oxygen transport from the lung to the
CC       various peripheral tissues (By similarity).
CC   -!- SUBUNIT: Heterotetramer of two alpha chains and two beta chains
CC       (By similarity).
CC   -!- SIMILARITY: Belongs to the globin family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY014769; AAK11484.1; -; Genomic_DNA.
DR   HSSP; P02112; 1HBR.
DR   SMR; Q9BEI2; 2-147.
DR   GO; GO:0005833; C:hemoglobin complex; IEA.
DR   GO; GO:0020037; F:heme binding; IEA.
DR   GO; GO:0005506; F:iron ion binding; IEA.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0019825; F:oxygen binding; IEA.
DR   GO; GO:0005344; F:oxygen transporter activity; IEA.
DR   GO; GO:0015671; P:oxygen transport; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR002337; Beta_haem.
DR   InterPro; IPR000971; Globin.
DR   InterPro; IPR012292; Globin_related.
DR   Pfam; PF00042; Globin; 1.
DR   PRINTS; PR00814; BETAHAEM.
DR   PROSITE; PS01033; GLOBIN; 1.
KW   Heme; Iron; Metal-binding; Oxygen transport; Transport.
SQ   SEQUENCE   147 AA;  16109 MW;  54AD783F0B5BF488 CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 147;
  Best Local Similarity   77.8%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              | |||:|||
Db        107 LGDNLIIAL 115


RESULT 26
Q8LKM7_ORYRU
ID   Q8LKM7_ORYRU   PRELIMINARY;   PRT;   172 AA.
AC   Q8LKM7;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 17.
DE   Serine/threonine protein kinase (Fragment).
GN   Name=ys207;
OS   Oryza rufipogon (Wild rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4529;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Yang M.Z., Wu C.J., Liu J.M., Sun Y.D., Cheng Z.Q., Zhao Y.C.,
RA   Huang X.Q.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF510990; AAM44844.1; -; Genomic_DNA.
DR   Gramene; Q8LKM7; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
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DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW   Kinase; Serine/threonine-protein kinase.
FT   NON_TER       1      1
FT   NON_TER     172    172
SQ   SEQUENCE   172 AA;  19047 MW;  D51E19848444428A CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 172;
  Best Local Similarity   55.6%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |:||:|:|:
Db          9 LEDNMVVAI 17


RESULT 27
Q7P8Q9_RICSI
ID   Q7P8Q9_RICSI   PRELIMINARY;   PRT;   224 AA.
AC   Q7P8Q9;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Hypothetical protein.
GN   Name=rsib_orf.1346;
OS   Rickettsia sibirica.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC   Rickettsiaceae; Rickettsieae; Rickettsia; spotted fever group;
OC   Rickettsia sibirica subgroup.
OX   NCBI_TaxID=35793;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Malek J.A., Eremeeva M.E., Dasch G.A.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AABW01000001; EAA26484.1; -; Genomic_DNA.
DR   GO; GO:0004852; F:uroporphyrinogen-III synthase activity; IEA.
DR   GO; GO:0006783; P:heme biosynthesis; IEA.
DR   InterPro; IPR003754; HEM4_synth.
KW   Hypothetical protein.
SQ   SEQUENCE   224 AA;  25910 MW;  87DC770DDEF0CE5A CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 224;
  Best Local Similarity   66.7%;  Pred. No. 1.9e+02;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||:||:|:
Db        179 LQDSLVVAI 187


RESULT 28
Q92HQ5_RICCN
ID   Q92HQ5_RICCN   PRELIMINARY;   PRT;   234 AA.
AC   Q92HQ5;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   Hypothetical protein.
GN   OrderedLocusNames=RC0716;
OS   Rickettsia conorii.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC   Rickettsiaceae; Rickettsieae; Rickettsia; spotted fever group.
OX   NCBI_TaxID=781;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Malish 7;
RX   MEDLINE=21442074; PubMed=11557893; DOI=10.1126/science.1061471;
RA   Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA   Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA   Raoult D.;
RT   "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL   Science 293:2093-2098(2001).
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AE008629; AAL03254.1; -; Genomic_DNA.
DR   PIR; D97789; D97789.
DR   BioCyc; RCON781:RC0716-MONOMER; -.
DR   GO; GO:0004852; F:uroporphyrinogen-III synthase activity; IEA.
DR   GO; GO:0006783; P:heme biosynthesis; IEA.
DR   InterPro; IPR003754; HEM4_synth.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   234 AA;  27272 MW;  59822E33674E014F CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 234;
  Best Local Similarity   66.7%;  Pred. No. 2e+02;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              |||:||:|:
Db        189 LQDSLVVAI 197


RESULT 29
Q4A5I5_MYCS5
ID   Q4A5I5_MYCS5   PRELIMINARY;   PRT;   248 AA.
AC   Q4A5I5;
DT   13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   13-SEP-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Methionyl aminopeptidase (EC 3.4.11.18).
GN   Name=map; OrderedLocusNames=MS53_0579;
OS   Mycoplasma synoviae (strain 53).
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=262723;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=16077101; DOI=10.1128/JB.187.16.5568-5577.2005;
RA   Vasconcelos A.T.R., Ferreira H.B., Bizarro C.V., Bonatto S.L.,
RA   Carvalho M.O., Pinto P.M., Almeida D.F., Almeida L.G.P., Almeida R.,
RA   Alves-Junior L., Assuncao E.N., Azevedo V.A.C., Bogo M.R.,
RA   Brigido M.M., Brocchi M., Burity H.A., Camargo A.A., Camargo S.S.,
RA   Carepo M.S., Carraro D.M., de Mattos Cascardo J.C., Castro L.A.,
RA   Cavalcanti G., Chemale G., Collevatti R.G., Cunha C.W.,
RA   Dallagiovanna B., Dambros B.P., Dellagostin O.A., Falcao C.,
RA   Fantinatti-Garboggini F., Felipe M.S.S., Fiorentin L., Franco G.R.,
RA   Freitas N.S.A., Frias D., Grangeiro T.B., Grisard E.C.,
RA   Guimaraes C.T., Hungria M., Jardim S.N., Krieger M.A., Laurino J.P.,
RA   Lima L.F.A., Lopes M.I., Loreto E.L.S., Madeira H.M.F., Manfio G.P.,
RA   Maranhao A.Q., Martinkovics C.T., Medeiros S.R.B., Moreira M.A.M.,
RA   Neiva M., Ramalho-Neto C.E., Nicolas M.F., Oliveira S.C.,
RA   Paixao R.F.C., Pedrosa F.O., Pena S.D.J., Pereira M.,
RA   Pereira-Ferrari L., Piffer I., Pinto L.S., Potrich D.P., Salim A.C.M.,
RA   Santos F.R., Schmitt R., Schneider M.P.C., Schrank A., Schrank I.S.,
RA   Schuck A.F., Seuanez H.N., Silva D.W., Silva R., Silva S.C.,
RA   Soares C.M.A., Souza K.R.L., Souza R.C., Staats C.C., Steffens M.B.R.,
RA   Teixeira S.M.R., Urmenyi T.P., Vainstein M.H., Zuccherato L.W.,
RA   Simpson A.J.G., Zaha A.;
RT   "Swine and poultry pathogens: the complete genome sequences of two
RT   strains of Mycoplasma hyopneumoniae and a strain of Mycoplasma
RT   synoviae.";
RL   J. Bacteriol. 187:5568-5577(2005).
CC   ---------------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------------
DR   EMBL; AE017245; AAZ43986.1; -; Genomic_DNA.
DR   GO; GO:0050897; F:cobalt ion binding; IEA.
```

```
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0004239; F:methionyl aminopeptidase activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis; IEA.
DR   InterPro; IPR001714; Pept_M24_MAP.
DR   InterPro; IPR002467; Pept_M24A_MAP1.
DR   Pfam; PF00557; Peptidase_M24; 1.
DR   PRINTS; PR00599; MAPEPTIDASE.
DR   TIGRFAMs; TIGR00500; met_pdase_I; 1.
KW   Aminopeptidase; Cobalt; Complete proteome; Hydrolase; Metal-binding;
KW   Protease.
SQ   SEQUENCE   248 AA;  27397 MW;  189E63EF9DE86F5B CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 248;
  Best Local Similarity   66.7%;  Pred. No. 2.1e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              ||||:|| :
Db        192 LQDNMVICI 200


RESULT 30
Q89UG6_BRAJA
ID   Q89UG6_BRAJA   PRELIMINARY;   PRT;   253 AA.
AC   Q89UG6;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 22.
DE   ABC transporter ATP-binding protein.
GN   OrderedLocusNames=blr1451;
OS   Bradyrhizobium japonicum.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Bradyrhizobiaceae; Bradyrhizobium.
OX   NCBI_TaxID=375;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=USDA 110;
RX   MEDLINE=22484998; PubMed=12597275; DOI=10.1093/dnares/9.6.189;
RA   Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA   Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA   Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA   Tabata S.;
RT   "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT   Bradyrhizobium japonicum USDA110.";
RL   DNA Res. 9:189-197(2002).
CC   -!- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
CC   -!- SIMILARITY: Belongs to the ABC transporter family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BA000040; BAC46716.1; -; Genomic_DNA.
DR   HSSP; Q58663; 1G9X.
DR   BioCyc; BJAP224911:BLR1451-MONOMER; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0019866; C:organelle inner membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0016887; F:ATPase activity; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transp_like.
DR   Pfam; PF00005; ABC_tran; 1.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   ATP-binding; Complete proteome; Inner membrane; Membrane;
KW   Nucleotide-binding; Transport.
SQ   SEQUENCE   253 AA;  27939 MW;  5C953BC4B0E8CDE8 CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 253;
  Best Local Similarity   66.7%;  Pred. No. 2.2e+02;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LQDNLVIAL 9
              :||||::||
Db        105 VQDNLLLAL 113


Search completed: June 29, 2006, 09:29:51
Job time : 110.942 secs
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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:14 ; Search time 87.8313 Seconds
(without alignments)
46.851 Million cell updates/sec

Title: US-10-062-257A-12
Perfect score: 41
Sequence: 1 KLVERLGAA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	100.0	9	4	AAB73128	Aab73128 Tumour an
2	41	100.0	9	6	ABR84354	Abr84354 Human lck
3	41	100.0	9	8	ADS87126	Ads87126 Human gen
4	41	100.0	9	10	AEE99217	Aee99217 Cancer an
5	41	100.0	509	3	AAY49420	Aay49420 PKA subst
6	41	100.0	509	8	ADL22907	Adl22907 Human MP2
7	41	100.0	509	8	ADP48374	Adp48374 Human lym
8	37	90.2	259	2	AAY43956	Aay43956 Mouse pro
9	37	90.2	259	2	AAY43955	Aay43955 Human pro
10	37	90.2	263	8	ADR88385	Adr88385 LCK tyros
11	37	90.2	265	7	ABR56203	Abr56203 Mutant Ly
12	37	90.2	271	7	ABR56204	Abr56204 Mutant Ly
13	37	90.2	279	9	ADY85449	Ady85449 Catalytic
14	37	90.2	363	6	ABR59690	Abr59690 Human p56
15	37	90.2	363	8	ADP48375	Adp48375 Human lym
16	37	90.2	417	2	AAR14201	Aar14201 (Beta-gal
17	37	90.2	437	5	ABG79672	Abg79672 Tumour in
18	37	90.2	508	3	AAB37700	Aab37700 Human lym
19	37	90.2	508	7	ADE58802	Ade58802 Human Pro
20	37	90.2	508	7	ADE58799	Ade58799 Human Pro
21	37	90.2	508	7	ADF45072	Adf45072 Human kin
22	37	90.2	508	7	ADL34479	Adl34479 Human lym
23	37	90.2	508	8	ADS88148	Ads88148 Human pro
24	37	90.2	509	6	ABR58699	Abr58699 Human can
25	37	90.2	509	7	ABR56202	Abr56202 Human Lym
26	37	90.2	509	7	ADE40449	Ade40449 Human pro
27	37	90.2	509	8	ADP12458	Adp12458 Protein e
28	37	90.2	509	9	ADZ51107	Adz51107 Amino aci
29	37	90.2	509	9	AEA35921	Aea35921 Human Lck
30	37	90.2	539	8	ABM82981	Abm82981 Human dia
31	37	90.2	539	8	ABM82982	Abm82982 Human dia
32	37	90.2	551	4	ABG22264	Abg22264 Novel hum
33	37	90.2	567	5	ABG79673	Abg79673 Tumour in
34	36	87.8	419	6	ABU27416	Abu27416 Protein e
35	35	85.4	336	9	ADZ10527	Adz10527 P. gingiv
36	35	85.4	369	9	ABM93756	Abm93756 M. xanthu
37	35	85.4	462	5	AAU74623	Aau74623 Oestrogen
38	35	85.4	462	8	ADJ76183	Adj76183 Marker ge
39	34	82.9	24	7	ADJ62344	Adj62344 Epitopic
40	34	82.9	24	9	AEC11002	Aec11002 Haemophil
41	34	82.9	168	8	ADR95678	Adr95678 Novel S.
42	34	82.9	168	9	AEA59548	Aea59548 Streptoco
43	34	82.9	170	8	ADN26016	Adn26016 Bacterial
44	34	82.9	180	7	ADJ62337	Adj62337 H_influen
45	34	82.9	180	7	ADJ62339	Adj62339 H_influen
46	34	82.9	180	9	AEC10997	Aec10997 Haemophil
47	34	82.9	180	9	AEC10995	Aec10995 Haemophil
48	34	82.9	227	6	ABU01216	Abu01216 S. pneumo
49	34	82.9	246	8	ADK46190	Adk46190 Streptoco
50	34	82.9	321	8	ADS28757	Ads28757 Bacterial
51	34	82.9	474	8	ADS24718	Ads24718 Bacterial
52	34	82.9	500	7	ABO63226	Abo63226 Klebsiell
53	33	80.5	161	8	ADS17865	Ads17865 Human IKB
54	33	80.5	168	8	ADS43375	Ads43375 Bacterial
55	33	80.5	231	8	ADY11628	Ady11628 Plant ful
56	33	80.5	251	9	ADY52569	Ady52569 Human onc
57	33	80.5	260	2	AAY43954	Aay43954 Human pro
58	33	80.5	359	8	ADS44521	Ads44521 Bacterial
59	33	80.5	368	8	ADS17863	Ads17863 Human IKB
60	33	80.5	385	7	ADF05452	Adf05452 Bacterial
61	33	80.5	400	8	ADS24642	Ads24642 Bacterial
62	33	80.5	416	2	AAY27430	Aay27430 Human RIP
63	33	80.5	419	6	ABB82782	Abb82782 Human NEM
64	33	80.5	419	6	ABO17485	Abo17485 Human NEM
65	33	80.5	419	8	ADK71963	Adk71963 Human I K
66	33	80.5	419	8	ADS88168	Ads88168 Human pro
67	33	80.5	419	9	ADZ00656	Adz00656 Human NEM
68	33	80.5	439	9	ADY52636	Ady52636 Human tra
69	33	80.5	440	9	ADY52635	Ady52635 Human tra
70	33	80.5	444	9	ADY52634	Ady52634 Human tra
71	33	80.5	447	9	ADY52633	Ady52633 Human tra
72	33	80.5	452	9	ADY52632	Ady52632 Human tra
73	33	80.5	459	9	ADY52631	Ady52631 Human tra
74	33	80.5	467	9	ADY52630	Ady52630 Human tra
75	33	80.5	472	9	ADY52629	Ady52629 Human tra
76	33	80.5	473	9	ADY52628	Ady52628 Human tra
77	33	80.5	474	8	ADN18172	Adn18172 Bacterial
78	33	80.5	474	9	AED82019	Aed82019 Hyperimmu
79	33	80.5	474	9	AED82466	Aed82466 Hyperimmu
80	33	80.5	481	9	ADY52627	Ady52627 Human tra
81	33	80.5	483	9	ADY52626	Ady52626 Human tra
82	33	80.5	493	9	ADY52625	Ady52625 Human tra
83	33	80.5	511	7	ADF45073	Adf45073 Human kin
84	33	80.5	512	7	ADD19014	Add19014 Human dis
85	33	80.5	512	7	ADN95430	Adn95430 Human BEC
86	33	80.5	512	8	ADL22908	Adl22908 Human MP2
87	33	80.5	512	8	ADN04498	Adn04498 Antipsori
88	33	80.5	512	8	ADP12483	Adp12483 Protein e
89	33	80.5	512	8	ADR14269	Adr14269 Human NF-
90	33	80.5	512	8	ADS88430	Ads88430 Human pro
91	33	80.5	512	8	ADP23372	Adp23372 PRO polyp
92	33	80.5	512	9	ADY16487	Ady16487 PRO polyp
93	33	80.5	512	9	ADY19685	Ady19685 PRO polyp
94	33	80.5	512	9	ADY14848	Ady14848 PRO polyp
95	33	80.5	512	9	ADY52574	Ady52574 Human onc
96	33	80.5	512	9	AEA35920	Aea35920 Human Lyn

97	33	80.5	609	9	ADY14846	Ady14846 PRO polyp
98	33	80.5	864	9	ABM92571	Abm92571 M. xanthu
99	32	78.0	297	8	ADY10869	Ady10869 Plant ful
100	32	78.0	339	6	ABU20456	Abu20456 Protein e

ALIGNMENTS

RESULT 1
AAB73128
ID AAB73128 standard; peptide; 9 AA.
XX
AC AAB73128;
XX
DT 09-MAY-2001 (first entry)
XX
DE Tumour antigen peptide #12.
XX
KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS Homo sapiens.
XX
PN WO200111044-A1.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-JP005220.
XX
PR 05-AUG-1999; 99JP-00222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT polynucleotides encoding them for treatment of cancer.
XX
PS Claim 1; Page 69; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVERLGAA 9
|||||||||
Db 1 KLVERLGAA 9

RESULT 2
ABR84354
ID ABR84354 standard; peptide; 9 AA.
XX
AC ABR84354;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human lck HLA-A2 epitope, SEQ ID NO:5.
XX
KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW human; human leukocyte antigen; HLA-A2 epitope.
XX
OS Homo sapiens.
XX
PN JP2002365286-A.
XX
PD 18-DEC-2002.
XX
PF 18-SEP-2001; 2001JP-00283413.
XX
PR 13-NOV-2000; 2000JP-00345094.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2003-508315/48.
XX
PT A detection method of antigen specific T-cells, comprises the use of
PT plural antigenic peptides, useful in semi-quantitative determination of
PT cancer specific T-cell frequencies and for monitoring cellular immunity.
XX
PS Example 7; Page 8; 18pp; Japanese.
XX
CC The invention relates to a method for the detection of antigen specific T
CC -cells in a blood sample involving the use of a plurality of antigenic
CC peptides. The method comprises sampling of peripheral blood monocytes;
CC stimulation of the collected peripheral blood monocytes with antigens
CC without direct use of antigen presenting cells; and detection of T-cells
CC specific to the antigen in the stimulated monocytes. The method is
CC particularly used for the detection of cancer as it can be used in semi-
CC quantitative determination of cancer specific T-cells. It can also be
CC used for cancer vaccine therapy for patients with cervical or prostate
CC cancer. The method can additionally be used to monitor of cellular
CC immunity and cancer immune therapy by detection of specific T-cell
CC frequencies. Sequences ABR84350-ABR84365 represent HLA-A2 (human
CC leukocyte antigen) peptides of human origin used in an example from the
CC invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVERLGAA 9
|||||||||
Db 1 KLVERLGAA 9

RESULT 3
ADS87126
ID ADS87126 standard; peptide; 9 AA.
XX
AC ADS87126;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human genetic vaccine/ubiquitin (Ub)/Lck-related epitope peptide 4.
XX
KW vaccine; ubiquitin; Ub; T-cell target; melanoma; sarcoma;
KW Hodgkins lymphoma; non-Hodgkins; leukaemia; neuroblastoma; myeloma;
KW lung cancer; stomach; skin; thyroid; ovary; prostate; womb; pancreas;
KW colon; bladder; breast; oesophagus; kidney; brain; human; epitope; Lck.
XX
OS Homo sapiens.
XX
PN WO2004035085-A1.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-JP013279.
XX
PR 17-OCT-2002; 2002JP-00302816.
XX
PA (KYUS-) KYUSHU TLO CO LTD.
XX

PI Himeno K, Furue M, Maehara Y;
XX
DR WPI; 2004-357144/33.
XX
PT Gene vaccine containing cancer antigen genes ligated to ubiquitin genes
PT or cytokine genes for prevention and treatment of cancer.
XX
PS Disclosure; SEQ ID NO 142; 266pp; Japanese.
XX
CC The invention relates to a novel genetic vaccine containing the ubiquitin
CC gene together with a gene encoding an antigenic protein containing a T-
CC cell target sequence. The vaccine of the invention may be useful for
CC prevention and treatment of cancers including melanoma, sarcoma, lymphoma
CC (Hodgkins or non-Hodgkins), leukaemia, neuroblastoma, myeloma and cancer
CC of the lung, stomach, skin, thyroid, ovary, prostate, womb, pancreas,
CC colon, bladder, breast, oesophagus, kidney or brain. The current sequence
CC is that of a human genetic vaccine/ubiquitin (Ub)-related epitope peptide
CC of the invention.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVERLGAA 9
|||||||||
Db 1 KLVERLGAA 9

RESULT 4
AEE99217
ID AEE99217 standard; peptide; 9 AA.
XX
AC AEE99217;
XX
DT 23-FEB-2006 (first entry)
XX
DE Cancer antigen lck peptide SEQ ID NO 7.
XX
KW Cytostatic; Vaccine; cancer; neoplasm; antigen; lck.
XX
OS Unidentified.
XX
PN WO2005123122-A1.
XX
PD 29-DEC-2005.
XX
PF 21-JUN-2005; 2005WO-JP011357.
XX
PR 21-JUN-2004; 2004JP-00182811.
XX
PA (UYKU-) UNIV KURUME.
XX
PI Itoh K;
XX
DR WPI; 2006-057212/06.
XX
PT Treating cancer by evaluating specific cytotoxic T-lymphocyte precursors
PT for each peptide of cancer antigen peptide set, in patient, administering
PT peptide set obtained after removing peptide being non-specific to
PT precursors, to patient.
XX
PS Example 1; SEQ ID NO 7; 36pp; Japanese.
XX
CC The invention relates to a method of treating a cancer patient by
CC administering cancer antigens to patient, involves evaluating presence or
CC absence of specific cytotoxic T-lymphocyte precursors for individual
CC peptides contained in set of cancer antigen peptides, in patient,
CC removing peptide being non-specific to precursors, from cancer antigen
CC peptide set, to prepare set for administration, and administering cancer
CC antigen peptide set to patient. The method is useful for treating cancer
CC patient by administering cancer antigens to patient. The present sequence
CC represents the amino acid sequence of a lck peptide cancer antigen.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVERLGAA 9
|||||||||
Db 1 KLVERLGAA 9

RESULT 5
AAY49420
ID AAY49420 standard; protein; 509 AA.
XX
AC AAY49420;
XX
DT 13-MAR-2000 (first entry)
XX
DE PKA substrate, Src-family protein.
XX
KW Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer;
KW kinase substrate; immunosuppressive disorder; proliferative disease;
KW HIV infection; AIDS; immunodeficiency; autoimmune disease;
KW systemic lupus erythematosus; Src-family.
XX
OS Homo sapiens.
XX
PN WO9962315-A2.
XX
PD 02-DEC-1999.
XX
PF 27-MAY-1999; 99WO-GB001680.
XX
PR 27-MAY-1998; 98NO-00002419.
PR 30-DEC-1998; 98US-0114240P.
XX
PA (LAUR-) LAURAS AS.
PA (JONE/) JONES E L.
XX
PI Hansson V, Levy FO, Mustelin T, Skalhegg BS, Sundvold V;
PI Tasken K, Vang T, Altman A, Munshi A;
XX
DR WPI; 2000-086801/07.
DR N-PSDB; AAZ46491.
XX
PT Altering the activity of protein kinase signaling pathways, used for
PT treating immunosuppressive disorders, e.g. AIDS, proliferative disorders,
PT e.g. cancers or autoimmune diseases.
XX
PS Claim 23; Page 95-96; 111pp; English.
XX
CC The invention provides a novel method of altering the activity of the
CC protein kinase A (PKA) signaling pathway in a cell that comprises
CC altering the extent of phosphorylation of one or more PKA substrates, or
CC kinase substrates downstream in the PKA signaling pathway. Pharmaceutical
CC compositions containing a nucleic acid molecule that encodes a PKA
CC substrate, or fragment, precursor or functionally equivalent variant,
CC where the sequence is modified to alter its susceptibility to
CC phosphorylation by PKA can be used for treating a disorder exhibiting
CC abnormal PKA signaling activity, immunosuppressive disorders or
CC proliferative diseases. They can be used for treating e.g. HIV infection,
CC AIDS, common variable immunodeficiency or cancers. Conditions in which
CC upregulation of the PKA pathway is required, such as autoimmune disease,
CC e.g. systemic lupus erythematosus, may also be treated. The present
CC sequence represents a PKA substrate, wherein the substrate is in the Src-
CC family, preferably Lck, Fyn, Src, Yes, Fgr, Lyn, Hck Blk, Yrk, c-tkl,
CC Fyk, Src-1 or Src-2
XX
SQ Sequence 509 AA;

```
  Query Match           100.0%;  Score 41;  DB 3;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              |||||||||
Db        246 KLVERLGAA 254
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RESULT 6
ADL22907
ID   ADL22907 standard; protein; 509 AA.
XX
AC   ADL22907;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human MP2153 polypeptide sequence SEQ ID NO: 27.
XX
KW   human; MP2153; p21; p53; cancer.
XX
OS   Homo sapiens.
XX
PN   WO2004015069-A2.
XX
PD   19-FEB-2004.
XX
PF   06-AUG-2003; 2003WO-US024505.
XX
PR   07-AUG-2002; 2002US-0401701P.
PR   16-SEP-2002; 2002US-0411017P.
PR   30-DEC-2002; 2002US-0437107P.
XX
PA   (EXEL-) EXELIXIS INC.
XX
PI   Francis-Lang H,  Friedman L,  Kidd T,  Roche S,  Belvin M;
PI   Plowman GD,  Lickteig K,  Zhang H,  Amundsen CD;
XX
DR   WPI; 2004-180653/17.
DR   N-PSDB; ADL22890.
XX
PT   Identifying a candidate p21 or p53 pathway modulating agent using an
PT   assay system having a modulator of p21 or p53 (MP2153) polypeptide or
PT   nucleic acid, useful for diagnosing or treating cancer, such as colon or
PT   breast cancer.
XX
PS   Example 3; Page 94-96; 110pp; English.
XX
CC   The present invention relates to a method of identifying a candidate p21
CC   or p53 pathway modulating agent. This comprises providing an assay system
CC   comprising a modulator of p21 or p53 (MP2153) polypeptide or nucleic
CC   acid, contacting the assay system with a test agent, where in its
CC   presence the system provides a reference activity, and detecting a test
CC   agent-biased activity of the assay system, wherein a difference between
CC   the test agent-biased activity and the reference activity identifies the
CC   test agent as a candidate p21 or p53 pathway modulating agent. The
CC   methods and compositions of the present invention are useful for the
CC   diagnosis and/or treatment of diseases or conditions associated with
CC   aberrant expression or activity of the p21 or p53 pathway, such as
CC   cancer, preferably colon or head and neck cancer. The present sequence is
CC   a human MP2153 protein sequence of the invention.
XX
SQ   Sequence 509 AA;
```

```
  Query Match           100.0%;  Score 41;  DB 8;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              |||||||||
Db        246 KLVERLGAA 254
```

```
RESULT 7
ADP48374
ID   ADP48374 standard; protein; 509 AA.
XX
AC   ADP48374;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human lymphocyte specific tyrosine kinase (Lck) polypeptide #1.
XX
KW   Human; lymphocyte specific tyrosine kinase; Lck;
KW   antisense oligonucleotide; phosphorothioate linkage;
KW   2'-O-methoxyethyl sugar moiety; 5-methylcytosine;
KW   hyperproliferative disorder; cancer; cytostatic; enzyme.
XX
OS   Homo sapiens.
XX
PN   US2004116365-A1.
XX
PD   17-JUN-2004.
XX
PF   10-DEC-2002; 2002US-00316515.
XX
PR   10-DEC-2002; 2002US-00316515.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Borchers AH,  Freier SM;
XX
DR   WPI; 2004-498280/47.
DR   N-PSDB; ADP48301.
XX
PT   New antisense oligonucleotide compounds, useful for diagnosing,
PT   preventing and/or treating diseases or conditions associated with
PT   aberrant expression or activity of Lck, such as hyperproliferative
PT   disorders.
XX
PS   Claim 1; SEQ ID NO 4; 40pp; English.
XX
CC   The invention relates to a compound targeted to a nucleic acid molecule
CC   encoding the human lymphocyte specific tyrosine kinase (Lck) polypeptide.
CC   The compound is an antisense oligonucleotide that specifically hybridises
CC   with the nucleic acid and inhibits expression of the polypeptide. The
CC   antisense oligonucleotide comprises at least one modified internucleoside
CC   linkage i.e. a phosphorothioate linkage, at least one modified sugar
CC   moiety, preferably a 2'-O-methoxyethyl sugar moiety, or at least one
CC   modified nucleobase comprising a 5-methylcytosine. The antisense
CC   compounds are useful for modulating the expression of the human Lck
CC   polypeptide and in preparation of a composition for treating
CC   hyperproliferative disorders, e.g. cancer. This sequence represents a
CC   human Lck polypeptide of the invention.
XX
SQ   Sequence 509 AA;
```

```
  Query Match           100.0%;  Score 41;  DB 8;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              |||||||||
Db        246 KLVERLGAA 254
```

```
RESULT 8
AAY43956
ID   AAY43956 standard; protein; 259 AA.
XX
AC   AAY43956;
XX
DT   21-DEC-1999  (first entry)
XX
DE   Mouse protein kinase #6.
XX
```

KW Prediction; secondary structure; alignment; evolutionary conservation;
KW homology; periodicity; co-variation analysis; antigenic site;
KW site directed mutagenesis; interaction.
XX
OS Mus sp.
XX
PN US5958784-A.
XX
PD 28-SEP-1999.
XX
PF 25-MAR-1992; 92US-00857224.
XX
PR 25-MAR-1992; 92US-00857224.
XX
PA (BENN/) BENNER S A.
XX
PI Benner SA;
XX
DR WPI; 1999-570766/48.
XX
PT Predicting the folded structure of proteins.
XX
PS Disclosure; Col 255-258; 113pp; English.
XX
CC Sequences AAY43902-Y44015 represent proteins used in a novel method of
CC predicting the folded structure of proteins, by aligning sequences of
CC homologous proteins and using patterns of evolutionarily conserved and
CC varied sequences to assign positions. Positions in the alignment are
CC assigned to the surface or inside of the folded structure, active sites,
CC and parsing segments. Secondary structural units are assigned by
CC identifying periodicity in the assignments, and assembled into globular
CC form using distance constraints imposed by disulfide bridges, active site
CC assignments and co-variation analysis. The predicted secondary structures
CC are useful for identifying antigenic sites on a protein molecule, as
CC guides for site directed mutagenesis studies, and for understanding the
CC interaction of a protein with other molecules
XX
SQ Sequence 259 AA;

Query Match 90.2%; Score 37; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVERLGA 8
||||||||
Db 4 KLVERLGA 11

RESULT 9
AAY43955
ID AAY43955 standard; protein; 259 AA.
XX
AC AAY43955;
XX
DT 21-DEC-1999 (first entry)
XX
DE Human protein kinase #15.
XX
KW Prediction; secondary structure; alignment; evolutionary conservation;
KW homology; periodicity; co-variation analysis; antigenic site;
KW site directed mutagenesis; interaction.
XX
OS Homo sapiens.
XX
PN US5958784-A.
XX
PD 28-SEP-1999.
XX
PF 25-MAR-1992; 92US-00857224.
XX
PR 25-MAR-1992; 92US-00857224.
XX
PA (BENN/) BENNER S A.
XX
PI Benner SA;
XX
DR WPI; 1999-570766/48.
XX
PT Predicting the folded structure of proteins.
XX
PS Disclosure; Col 253-256; 113pp; English.
XX
CC Sequences AAY43902-Y44015 represent proteins used in a novel method of
CC predicting the folded structure of proteins, by aligning sequences of
CC homologous proteins and using patterns of evolutionarily conserved and
CC varied sequences to assign positions. Positions in the alignment are
CC assigned to the surface or inside of the folded structure, active sites,
CC and parsing segments. Secondary structural units are assigned by
CC identifying periodicity in the assignments, and assembled into globular
CC form using distance constraints imposed by disulfide bridges, active site
CC assignments and co-variation analysis. The predicted secondary structures
CC are useful for identifying antigenic sites on a protein molecule, as
CC guides for site directed mutagenesis studies, and for understanding the
CC interaction of a protein with other molecules
XX
SQ Sequence 259 AA;

Query Match 90.2%; Score 37; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVERLGA 8
||||||||
Db 4 KLVERLGA 11

RESULT 10
ADR88385
ID ADR88385 standard; protein; 263 AA.
XX
AC ADR88385;
XX
DT 18-NOV-2004 (first entry)
XX
DE LCK tyrosine kinase protein.
XX
KW Molecular scaffold; nuclear hormone receptor; TNF receptor;
KW G-protein coupled receptor; methyl transferase; ligase;
KW LCK tyrosine kinase; enzyme.
XX
OS Unidentified.
XX
PN US2004171062-A1.
XX
PD 02-SEP-2004.
XX
PF 28-FEB-2003; 2003US-00377268.
XX
PR 28-FEB-2002; 2002US-0360651P.
PR 16-SEP-2002; 2002US-0411398P.
PR 20-SEP-2002; 2002US-0412341P.
PR 02-JAN-2003; 2003US-0437929P.
XX
PA (PLEX-) PLEXXIKON INC.
XX
PI Hirth K, Milburn MV;
XX
DR WPI; 2004-642017/62.
XX
PT Designing a ligand binding to a target molecule, comprises identifying as
PT molecular scaffolds compounds binding to members of a molecular family,
PT detecting orientation of scaffolds at a binding site of target, and
PT synthesizing ligand.
XX
PS Disclosure; SEQ ID NO 24; 186pp; English.
XX

```
CC   The present invention relates to a method of designing a ligand binding
CC   to a target molecule. The method involves identifying as molecular
CC   scaffolds compounds binding to members of a molecular family, detecting
CC   orientation of scaffolds at a binding site of target, and synthesising
CC   ligand. The invention is useful for designing drug products and for
CC   designing ligand binding to target molecules such as nuclear hormone
CC   receptors, TNF receptors, G-protein coupled receptors, methyl
CC   transferases, ligases, etc. The present sequence is the LCK tyrosine
CC   kinase protein. This sequence is used to illustrate the method of
CC   invention.
XX
SQ   Sequence 263 AA;

  Query Match             90.2%;  Score 37;  DB 8;  Length 263;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db          8 KLVERLGA 15


RESULT 11
ABR56203
ID   ABR56203 standard; protein; 265 AA.
XX
AC   ABR56203;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Mutant Lymphocyte Cell Kinase, Lck, fragment (237-501, D364N).
XX
KW   Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW   Src-family protein tyrosine kinase; T-cell; immune response; mutein;
KW   mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 128
FT                   /note= "Wild-type D substituted with N. This position is
FT                   364 in the full-length sequence (see ABR56202 for the
FT                   wild-type full length sequence"
FT   Modified-site   158
FT                   /note= "Phosphorylation site"
XX
PN   WO2003020880-A2.
XX
PD   13-MAR-2003.
XX
PF   02-AUG-2002; 2002WO-US024546.
XX
PR   03-AUG-2001; 2001US-0310051P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Borhani DW,  Calderwood D,  Dixon RW,  Hirst GC,  Hrnciar P,  Loew A;
PI   Leung A,  Ritter K;
XX
DR   WPI; 2003-300872/29.
XX
PT   New crystalline polypeptide comprising ligand binding domain or catalytic
PT   domain of Lck protein, for determining three-dimensional structure of
PT   catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS   Claim 12; Fig 2; 994pp; English.
XX
CC   The present invention relates to a crystalline polypeptide (I),
CC   comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC   protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC   in T-cells and plays an essential role in immune response. (I) is useful
CC   for identifying a compound which is an inhibitor of human Lck protein.
CC   The present sequence is a mutated fragment of the human Lck sequence,
CC   which approximately comprises the catalytic domain
XX
SQ   Sequence 265 AA;

  Query Match             90.2%;  Score 37;  DB 7;  Length 265;
  Best Local Similarity   100.0%;  Pred. No. 60;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db         10 KLVERLGA 17


RESULT 12
ABR56204
ID   ABR56204 standard; protein; 271 AA.
XX
AC   ABR56204;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Mutant Lymphocyte Cell Kinase, Lck, fragment (231-501, D364N).
XX
KW   Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW   Src-family protein tyrosine kinase; T-cell; immune response; mutein;
KW   mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 134
FT                   /note= "Wild-type D substituted with N. This position is
FT                   364 in the full-length sequence (see ABR56202 for the
FT                   wild-type full length sequence"
FT   Modified-site   164
FT                   /note= "Phosphorylation site"
XX
PN   WO2003020880-A2.
XX
PD   13-MAR-2003.
XX
PF   02-AUG-2002; 2002WO-US024546.
XX
PR   03-AUG-2001; 2001US-0310051P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Borhani DW,  Calderwood D,  Dixon RW,  Hirst GC,  Hrnciar P,  Loew A;
PI   Leung A,  Ritter K;
XX
DR   WPI; 2003-300872/29.
XX
PT   New crystalline polypeptide comprising ligand binding domain or catalytic
PT   domain of Lck protein, for determining three-dimensional structure of
PT   catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS   Example 1; Fig 3; 994pp; English.
XX
CC   The present invention relates to a crystalline polypeptide (I),
CC   comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC   protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC   in T-cells and plays an essential role in immune response. (I) is useful
CC   for identifying a compound which is an inhibitor of human Lck protein.
CC   The present sequence is a mutated fragment of the human Lck sequence,
CC   which approximately comprises the catalytic domain
XX
SQ   Sequence 271 AA;

  Query Match             90.2%;  Score 37;  DB 7;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy          1 KLVERLGA 8
              ||||||||
Db         16 KLVERLGA 23
```

RESULT 13
ADY85449
ID ADY85449 standard; protein; 279 AA.
XX
AC ADY85449;
XX
DT 16-JUN-2005 (first entry)
XX
DE Catalytic domain of PIM kinase-like protein LCK.
XX
KW Kinase; protein co-ordinate data; protein structure; cancer; cytostatic;
KW neoplasm; inflammation; antiinflammatory.
XX
OS Unidentified.
XX
PN WO2005028624-A2.
XX
PD 31-MAR-2005.
XX
PF 15-SEP-2004; 2004WO-US030360.
XX
PR 15-SEP-2003; 2003US-0503277P.
XX
PA (PLEX-) PLEXXIKON INC.
XX
PI Artis DR, Bremer RE, Gillette SJ, Hurt CR, Ibrahim PL;
PI Zuckerman RL;
XX
DR WPI; 2005-273155/28.
XX
PT New scaffold library used for identifying and developing ligands for
PT protein kinases and treating kinase associated disorders e.g. cancer,
PT comprises set of compounds comprising N-heterocyclic compounds.
XX
PS Disclosure; Page 170-174; 236pp; English.
XX
CC The invention relates to a new kinase scaffold library comprises at least
CC 1 set of compounds, each set comprising at least 1 N-heterocyclic
CC compound of formulae (I)-(VII) given in the specification. Also included
CC are a system for fitting compounds in binding sites of protein kinases
CC (comprising an electronic kinase scaffold, and a scaffold library
CC comprising at least 1 collection of electronic representations of (I)-
CC (VII), where the scaffold library is embedded in a computer device and
CC the electronic representations of the compounds can be selectively
CC retrieved and functionally connected with computer software adapted to
CC fit electronic representations of compounds in an electronic
CC representation of a binding site of a kinase), obtaining improved ligands
CC binding to a protein kinase (which comprises determining if a derivative
CC of (I)-(VII) binds to the kinase with greater affinity and/or specificity
CC than (I)-(VII)), developing ligands specific for a particular kinase
CC (which comprises determining if a derivative of (I)-(VII) that binds to
CC kinases has greater for specificity for the particular kinase than (I)-
CC (VII), developing ligands binding to a kinase (which comprises
CC determining the orientation of at least 1 molecular scaffold of (I)-(VII)
CC in co-crystals with the kinase, identifying chemical structures of the
CC scaffolds, that, when modified, change the binding affinity and/or
CC specificity between the scaffold and kinase and synthesizing a ligand in
CC which at least 1 chemical structure of the scaffold is modified),
CC developing ligands with increased specificity on a kinase (which
CC comprises testing a derivative of a kinase binding compound (I)-(VII) for
CC increased specificity on the kinase), identifying a ligand binding to a
CC kinase (which comprises determining if a derivative compound including a
CC core structure (I)-(VII) binds to the kinase with changed binding
CC affinity and/or specificity), a co-crystal of a kinase and a binding
CC compound (I)-(VII), preparation of co-crystals of Pim-1 with (I)-(VII),
CC identifying potential kinase binding compounds (which comprises fitting
CC electronic representations of (I)-(VII) in an electronic representation
CC of a kinase binding site), attaching a kinase binding compound to an
CC attachment component (which comprises identifying energetically allowed
CC sites for attachment of the component on a kinase binding compound (I)-
CC (VII) and attaching the compound or derivative to the attachment
CC component at the allowed site), modified compounds (comprising (I)-(VIII)
CC with an attached linker group, and developing a ligand for a kinase
CC comprising conserved residues matching at least on of Pim-1 residues 49,
CC 52, 67, 121, 128 and 186 which comprises determining if (I)-(VII) binds
CC to the kinase. The kinases comprise Pim-1, Pyk2, c-Ab1, Her2, cMet,
CC vascular endothelial growth factor receptor, endothelial growth factor
CC receptor, cKit, Pkcbeta, p38, Cdk2, Akt or Gsk3beta. The kinase scaffold
CC library is used for identifying and developing ligands binding to
CC kinases, for modulating kinase activity and for treating disease
CC condition associated with abnormal kinase activity e.g. cancer,
CC inflammatory disease. The method identifies improved ligands binding to a
CC kinase resulting in ligands having high affinity and specificity towards
CC kinase. The co-crystals of kinase and the binding compound are of
CC sufficient size and quality to allow structural determination of at least
CC 2 Angstroms. The present sequence is a catalytic domain from a PIM-like
CC kinase. NOTE: It is not clear whether the sequence as presented
CC represents a continuous amino acid sequence.
XX
SQ Sequence 279 AA;

```
  Query Match             90.2%;  Score 37;  DB 9;  Length 279;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db         16 KLVERLGA 23
```

RESULT 14
ABR59690
ID ABR59690 standard; protein; 363 AA.
XX
AC ABR59690;
XX
DT 25-JUL-2003 (first entry)
XX
DE Human p56lck.
XX
KW Human; T lymphocyte activation; T-cell; A-raf-1; TCPTP/PTPN2; asthma;
KW immunosuppressive; antiasthmatic; antiallergic; antiinflammatory;
KW lymphocyte activation; lymphocyte migration; cytokine production;
KW cell surface marker expression; antibody production; apoptosis; allergy;
KW antibody proliferation; antibody differentiation; hypersensitivity;
KW graft versus host disease; inflammation; p56lck.
XX
OS Homo sapiens.
XX
PN WO2003029277-A2.
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031618.
XX
PR 03-OCT-2001; 2001US-0327212P.
XX
PA (RIGE-) RIGEL PHARM INC.
XX
PI Chu P, Li C, Liao XC, Masuda E, Pardo J, Zhao H;
XX
DR WPI; 2003-363276/34.
DR N-PSDB; ACC81082.
XX
PT Identifying a compound that modulates T lymphocyte activation, useful for
PT monitoring changes in cell surface marker expression, comprises
PT contacting a T cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with
PT a compound.
XX
PS Disclosure; Page 64; 126pp; English.

```
XX
CC   The invention relates to a novel method for identifying a compound that
CC   modulates T lymphocyte activation. The method comprises contacting a T
CC   cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with a compound,
CC   where the A-raf- 1 or TCPTP/PTPN2 polypeptide is encoded by a nucleic
CC   acid that hybridises to a nucleic acid encoding a polypeptide having a
CC   sequence selected from two 606-amino acid sequence and a 415-amino acid
CC   sequence given in the specification. The method of the invention has
CC   immunosuppressive, antiasthmatic, antiallergic, and antiinflammatory
CC   activity. The method is useful for identifying compounds that modulate
CC   lymphocyte activation and migration, and for monitoring changes in cell
CC   surface marker expression, cytokine production, antibody production,
CC   proliferation and differentiation, and apoptosis, using either cell lines
CC   or primary cells. The A-raf- 1 or TCPTP/PTPN2 proteins may be used as
CC   drug targets for compounds that suppress or activate lymphocyte
CC   activation and migration, e.g. for the treatment of diseases in which
CC   modulation of the immune response is desired such as delayed type
CC   hypersensitivity reactions, asthma, allergies, graft versus host disease,
CC   and acute and chronic inflammation. Modulators of lymphocyte activation
CC   are useful for treating disorders related T and B cell activation and
CC   migration. The present sequence is used in the exemplification of the
CC   invention
XX
SQ   Sequence 363 AA;

  Query Match             90.2%;  Score 37;  DB 6;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 80;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db        246 KLVERLGA 253


RESULT 15
ADP48375
ID   ADP48375 standard; protein; 363 AA.
XX
AC   ADP48375;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human lymphocyte specific tyrosine kinase (Lck) polypeptide #2.
XX
KW   Human; lymphocyte specific tyrosine kinase; Lck;
KW   antisense oligonucleotide; phosphorothioate linkage;
KW   2'-O-methoxyethyl sugar moiety; 5-methylcytosine;
KW   hyperproliferative disorder; cancer; cytostatic; enzyme.
XX
OS   Homo sapiens.
XX
PN   US2004116365-A1.
XX
PD   17-JUN-2004.
XX
PF   10-DEC-2002; 2002US-00316515.
XX
PR   10-DEC-2002; 2002US-00316515.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Borchers AH,  Freier SM;
XX
DR   WPI; 2004-498280/47.
DR   N-PSDB; ADP48372.
XX
PT   New antisense oligonucleotide compounds, useful for diagnosing,
PT   preventing and/or treating diseases or conditions associated with
PT   aberrant expression or activity of Lck, such as hyperproliferative
PT   disorders.
XX
PS   Example 17; SEQ ID NO 75; 40pp; English.
XX
CC   The invention relates to a compound targeted to a nucleic acid molecule
CC   encoding the human lymphocyte specific tyrosine kinase (Lck) polypeptide.
CC   The compound is an antisense oligonucleotide that specifically hybridises
CC   with the nucleic acid and inhibits expression of the polypeptide. The
CC   antisense oligonucleotide comprises at least one modified internucleoside
CC   linkage i.e. a phosphorothioate linkage, at least one modified sugar
CC   moiety, preferably a 2'-O-methoxyethyl sugar moiety, or at least one
CC   modified nucleobase comprising a 5-methylcytosine. The antisense
CC   compounds are useful for modulating the expression of the human Lck
CC   polypeptide and in preparation of a composition for treating
CC   hyperproliferative disorders, e.g. cancer. This sequence represents a
CC   human Lck polypeptide of the invention.
XX
SQ   Sequence 363 AA;

  Query Match             90.2%;  Score 37;  DB 8;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 80;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db        246 KLVERLGA 253


RESULT 16
AAR14201
ID   AAR14201 standard; protein; 417 AA.
XX
AC   AAR14201;
XX
DT   13-DEC-1991  (first entry)
XX
DE   (Beta-galactosidase N-terminal)-(lck gene prod.) fusion protein.
XX
KW   Multi-cloning site.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .26
FT                   /note= "beta-galactosidase fragment"
FT   Region          27. .417
FT                   /note= "lck gene polypeptide"
XX
PN   JP03201994-A.
XX
PD   03-SEP-1991.
XX
PF   28-DEC-1989;   89JP-00338268.
XX
PR   28-DEC-1989;   89JP-00338268.
XX
PA   (TOKU ) TOKUYAMA SODA KK.
XX
DR   WPI; 1991-300980/41.
DR   N-PSDB; AAQ14201.
XX
PT   Fused polypeptide - has amino acid sequence of beta-galactosidase with a
PT   LCK gene conjugated to the N-terminal via DNA having multi-cloning site.
XX
PS   Claim 1; Fig 4,2; 15pp; Japanese.
XX
CC   The sequence consists of the N-terminal amino acids of the beta-
CC   galactosidase gene fused with the lck gene. It is produced by E.coli
CC   transformed with a recombinant vector (see AAQ13983). It is useful for
CC   producing an antibody specifically immunoreactive with only a lck gene-
CC   derived polypeptide in T cells. The antibody may recognise lck gene-
CC   derived polypeptides in human cells
XX
SQ   Sequence 417 AA;

  Query Match             90.2%;  Score 37;  DB 2;  Length 417;
  Best Local Similarity   100.0%;  Pred. No. 91;
```

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 KLVERLGA 8
              ||||||||
Db        154 KLVERLGA 161
```

RESULT 17
ABG79672
ID ABG79672 standard; protein; 437 AA.
XX
AC ABG79672;
XX
DT 15-NOV-2002 (first entry)
XX
DE Tumour involved gene (TIG) splice variant protein, NV-3.
XX
KW Human; splice variant; tumour-involved gene; TIG;
KW pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;
KW endothelial cell; cell differentiation; cell proliferation; apoptosis;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US2002086384-A1.
XX
PD 04-JUL-2002.
XX
PF 13-MAR-2001; 2001US-00805020.
XX
PR 14-MAR-2000; 2000IL-00135402.
PR 16-MAY-2000; 2000IL-00136154.
XX
PA (LEVI/) LEVINE Z.
PA (DAVI/) DAVID A.
PA (ROMA/) ROMANO C.
PA (BERN/) BERNSTEIN J.
XX
PI Levine Z, David A, Romano C, Bernstein J;
XX
DR WPI; 2002-635679/68.
DR N-PSDB; ABS65202.
XX
PT Novel nucleic acid sequence, which is an alternative splicing variant of
PT tumor involved genes, useful for detecting cancer, predisposition to
PT cancer, for evaluating cancer state and in gene therapy for treating
PT cancer.
XX
PS Claim 4; Page 68-69; 180pp; English.
XX
CC The invention discloses isolated human nucleic acid alternative splicing
CC variants that are all tumour-involved genes (TIGs). The nucleic acids and
CC polypeptides are useful for determining the level of a nucleic acid or
CC polypeptide in a biological sample, for detecting a variant nucleic acid
CC or polypeptide sequence in a biological sample, for determining the level
CC of variant nucleic acid or polypeptide sequences in a biological sample
CC and for determining the ratio between the level of variant sequence in a
CC first biological sample and the level of the original sequence from which
CC the variant has been varied by alternative splicing in a second
CC biological sample and for raising antibodies. A pharmaceutical
CC composition comprising a carrier and the nucleic acid, is useful for
CC treating diseases (e.g. cancer) that can be ameliorated or cured by
CC increasing or decreasing the level of the encoded protein. The nucleic
CC acids are also useful for diagnostic purposes, especially for detecting
CC cancer or a predisposition to cancer, for evaluating the state or
CC aggressiveness of cancer disease, in basic research, for understanding
CC the physiological function of the original TIG, in targeting or
CC developing pharmaceuticals, for distinguishing various stages in the life
CC cycle of the same type of cells which may be helpful for the development
CC of pharmaceuticals for various cancer stages in which cell cycle is non-
CC normal, for determining mutations in tumour-involved genes and in gene
CC therapy. The polypeptides are useful for identifying compounds capable of
CC binding to the variant product and modulating its activity and for
CC modulating endothelial differentiation and proliferation, as well as to
CC modulate apoptosis either ex vivo or in vivo. The sequences presented in
CC ABG796700-ABG79705 are the new variants (NV) 1-36 proteins of the TIGs
CC disclosed
XX
SQ Sequence 437 AA;

Query Match 90.2%; Score 37; DB 5; Length 437;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KLVERLGA 8
              ||||||||
Db        246 KLVERLGA 253
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RESULT 18
AAB37700
ID AAB37700 standard; protein; 508 AA.
XX
AC AAB37700;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human lymphocyte kinase.
XX
KW Human; lymphocyte kinase; protein co-ordinate data; lck; crystal.
XX
OS Homo sapiens.
XX
PN WO200070030-A1.
XX
PD 23-NOV-2000.
XX
PF 19-MAY-2000; 2000WO-US013881.
XX
PR 19-MAY-1999; 99US-0134965P.
XX
PA (KINE-) KINETIX PHARM INC.
XX
PI Zhu X;
XX
DR WPI; 2000-687708/67.
XX
PT Crystal of a protein-ligand complex for identifying kinase inhibitors,
PT comprises a truncated lymphocyte kinase and a ligand, and diffracts X-
PT rays to determine atomic coordinates at a resolution greater than 5
PT angstroms.
XX
PS Claim 1; Page 434-5; 438pp; English.
XX
CC The present invention relates to a crystal of a protein-ligand complex
CC comprising a truncated lymphocyte kinase (lck) and a ligand. The crystal
CC diffracts X-rays so that the atomic coordinates of the protein-ligand
CC complex can be determined to a resolution of greater than 5.0 Angstroms.
CC The truncated lck used in the present invention comprises the globular
CC core of the corresponding full-length lck. The present sequence is the
CC full-length human lck protein. The crystal of the present invention may
CC be used to identify kinase inhibitors in screening assays, in drug
CC screening and drug design processes, to design, select or test inhibitors
CC of kinase enzymes, where the inhibitors are used as therapeutics for the
CC treatment and modulation of diseases, disease symptoms or the effect of
CC other physiological events mediated by kinases; having one or more kinase
CC enzymes involved in their pathology
XX
SQ Sequence 508 AA;

Query Match 90.2%; Score 37; DB 3; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KLVERLGA 8
              ||||||||
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Db        245 KLVERLGA 252

RESULT 19
ADE58802
ID   ADE58802 standard; protein; 508 AA.
XX
AC   ADE58802;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein P06239, SEQ ID NO 4689.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P06239.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 508 AA;

  Query Match             90.2%;  Score 37;  DB 7;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db        245 KLVERLGA 252


RESULT 20
ADE58799
ID   ADE58799 standard; protein; 508 AA.
XX
AC   ADE58799;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein P06239, SEQ ID NO 4686.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P06239.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
```

```
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 508 AA;

  Query Match             90.2%;  Score 37;  DB 7;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db        245 KLVERLGA 252


RESULT 21
ADF45072
ID   ADF45072 standard; protein; 508 AA.
XX
AC   ADF45072;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human kinase LCK.
XX
KW   Human; protein kinase; enzyme; inhibitor; LCK.
XX
OS   Homo sapiens.
XX
PN   WO2003081210-A2.
XX
PD   02-OCT-2003.
XX
PF   20-MAR-2003; 2003WO-US008725.
XX
PR   21-MAR-2002; 2002US-0366892P.
XX
PA   (SUNE-) SUNESIS PHARM INC.
XX
PI   Prescott JC,  Braisted A;
XX
DR   WPI; 2003-865136/80.
XX
PT   Identifying ligand binding to inactive conformation of target protein
PT   kinase (T) comprises contacting the conformation modified (T) which
PT   contains reactive group at binding site, with ligands and detecting
PT   kinase-ligand conjugate formation.
XX
PS   Disclosure; SEQ ID NO 41; 260pp; English.
XX
CC   The present invention relates to a method for identifying a ligand (L),
CC   which binds to an inactive conformation of target protein kinase (T). The
CC   method involves contacting inactive conformation of (T), which contains
CC   or is modified to contain a reactive group at or near a binding site of
CC   interest, with one or more ligand candidates capable of covalently
CC   bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC   The method is useful for identifying protein kinase inhibitors that
CC   preferentially bind to inactive conformation of a target protein kinase.
CC   The present sequence is a protein kinase which may be modified via an
CC   amino acid substitution, for use in the method of the invention.
XX
SQ   Sequence 508 AA;

  Query Match             90.2%;  Score 37;  DB 7;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db        245 KLVERLGA 252


RESULT 22
ADL34479
ID   ADL34479 standard; peptide; 508 AA.
XX
AC   ADL34479;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human lymphocyte kinase (Lck) globular core.
XX
KW   cytostatic; immunosuppressive; antiinflammatory; antibacterial; virucide;
KW   fungicide; nootropic; neuroprotective; kinase inhibitor; crystal;
KW   protein-ligand complex; lymphocyte kinase; Lck; Lck ligand;
KW   kinase inhibitor; therapeutic; kinase-mediated physiological event;
KW   cancer; autoimmunological; metabolic; inflammatory; infection;
KW   central nervous system degenerative disease; transplant rejection; human;
KW   globular core; protein co-ordinate data.
XX
OS   Homo sapiens.
XX
PN   US6589758-B1.
XX
PD   08-JUL-2003.
XX
PF   21-MAY-2001; 2001US-00862154.
XX
PR   19-MAY-2000; 2000US-0205510P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Zhu X;
XX
DR   WPI; 2003-810380/76.
XX
PT   Crystal of protein-ligand complex useful for identifying an inhibitor of
PT   lymphocyte kinase (Lck), comprises truncated Lck and a ligand.
XX
PS   Claim 1; SEQ ID NO 1; 295pp; English.
XX
CC   The invention describes a crystal (I) of a protein-ligand complex (C)
CC   comprising a truncated lymphocyte kinase (Lck) and a ligand, where (I)
CC   effectively diffracts X-rays for determination of atomic coordinates of
CC   (C) to a resolution of greater than 5.0 angstroms, and truncated Lck
CC   comprises a sequence (S1) of residues 225-508 of a 508 amino acid
CC   sequence, given in specification and retains the globular core of full-
CC   length Lck. (I) is useful in an inhibitor screening assay and to
CC   identify, design, select, and evaluate potential inhibitors of kinases
CC   that would be useful as therapeutics for diseases or symptoms of diseases
CC   that are associated with kinase-mediated physiological events. The
CC   inhibitors identified by the methods may also be useful for inhibition of
CC   kinase activity of one or more enzymes. The inhibitors are also useful
CC   for inhibiting the biological activity of any enzyme comprising greater
CC   than 90%, alternatively greater than 85%, or alternatively greater than
CC   70% sequence homology with a kinase sequence. The inhibitors are useful
CC   for inhibiting the biological activity of any enzyme that binds ATP and
CC   thus for treating disease or disease symptoms mediated by any enzyme that
CC   binds ATP. The inhibitors are useful in inhibiting kinase activity and
CC   are useful in treating kinase-mediated disease or disease symptoms in a
CC   mammal, particularly a human e.g., cancer, autoimmunological, metabolic,
CC   inflammatory, infection, (bacterial, viral, yeast, fungal, etc.), central
CC   nervous system degenerative disease etc. The inhibitors are useful in
CC   treating or preventing diseases, including, transplant rejection etc.
CC   This is the amino acid sequence of a human lymphocyte kinase (Lck)
CC   polypeptide comprising the Lck globular core.
XX
SQ   Sequence 508 AA;

  Query Match             90.2%;  Score 37;  DB 7;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db        245 KLVERLGA 252
```

RESULT 23
ADS88148
ID ADS88148 standard; protein; 508 AA.
XX
AC ADS88148;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human protein of a TNF-alpha signalling pathway protein complex SeqID 3.
XX
KW protein complex; tumour necrosis factor-alpha signalling pathway;
KW TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
KW inflammatory bowel disease; infectious disease; septic shock;
KW bacterial infection; neurological disease; stroke-induced inflammation;
KW neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
KW antirheumatic; cytostatic; antibacterial; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004035783-A2.
XX
PD 29-APR-2004.
XX
PF 24-SEP-2003; 2003WO-EP050655.
XX
PR 26-SEP-2002; 2002EP-00021809.
PR 10-FEB-2003; 2003EP-00100274.
XX
PA (CELL-) CELLZOME AG.
XX
PI Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
PI Superti-Furga G, Kruse U;
XX
DR WPI; 2004-348460/32.
XX
PT New protein complex comprising at least one first and second protein of
PT the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
PT diagnosing or treating inflammation, neurological diseases, infectious
PT diseases or cancer.
XX
PS Example; SEQ ID NO 3; 1980pp; English.
XX
CC This invention relates to novel protein complexes of the tumour necrosis
CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
CC methods for preparing these complexes comprising at least two component
CC proteins, as well as screening methods to identify modulators of the
CC pathway, which include antibodies, agonists and antagonists thereof. The
CC present invention describes a protein complex and kit that are useful for
CC diagnosing, prognosing or treating chronic inflammatory diseases such as
CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases
CC such as septic shock and bacterial infections; neurological diseases such
CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
CC cancer. Accordingly, these complexes can be used for the development of
CC pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
CC antirheumatic, cytostatic and antibacterial activities and can be used
CC for gene therapy purposes. In particular, the invention further provides
CC siRNA-oligonucleotides useful for inhibiting protein expression for in
CC vitro or cell culture assays. This polypeptide is a human protein that
CC can be used in combination with other proteins provided in the
CC specification to form novel complexes of the TNF-alpha signalling pathway
CC of the invention.
XX
SQ Sequence 508 AA;

Query Match 90.2%; Score 37; DB 8; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVERLGA 8
||||||||
Db 245 KLVERLGA 252

RESULT 24
ABR58699
ID ABR58699 standard; protein; 509 AA.
XX
AC ABR58699;
XX
DT 09-JUL-2003 (first entry)
XX
DE Human cancer related protein SEQ ID NO:356.
XX
KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.
XX
OS Homo sapiens.
XX
PN WO2003025138-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-US029560.
XX
PR 17-SEP-2001; 2001US-0323469P.
PR 20-SEP-2001; 2001US-0323887P.
PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI Zlotnik A;
XX
DR WPI; 2003-354600/33.
DR N-PSDB; ACC72850.
XX
PT New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX
PS Claim 12; Page 762; 767pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies
XX
SQ Sequence 509 AA;

Query Match 90.2%; Score 37; DB 6; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVERLGA 8
||||||||
Db 246 KLVERLGA 253

RESULT 25
ABR56202
ID ABR56202 standard; protein; 509 AA.
XX
AC ABR56202;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human Lymphocyte Cell Kinase, Lck.
XX
KW Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW Src-family protein tyrosine kinase; T-cell; immune response.
XX
OS Homo sapiens.
XX
PN WO2003020880-A2.
XX
PD 13-MAR-2003.
XX
PF 02-AUG-2002; 2002WO-US024546.
XX
PR 03-AUG-2001; 2001US-0310051P.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Borhani DW, Calderwood D, Dixon RW, Hirst GC, Hrnciar P, Loew A;
PI Leung A, Ritter K;
XX
DR WPI; 2003-300872/29.
XX
PT New crystalline polypeptide comprising ligand binding domain or catalytic
PT domain of Lck protein, for determining three-dimensional structure of
PT catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS Claim 5; Fig 1; 994pp; English.
XX
CC The present invention relates to a crystalline polypeptide (I),
CC comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC in T-cells and plays an essential role in immune response. The present
CC sequence is the full-length sequence of human Lck (1-509). (I) is useful
CC for identifying a compound which is an inhibitor of human Lck protein
XX
SQ Sequence 509 AA;

Query Match 90.2%; Score 37; DB 7; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVERLGA 8
||||||||
Db 246 KLVERLGA 253

RESULT 26
ADE40449
ID ADE40449 standard; protein; 509 AA.
XX
AC ADE40449;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human proto-oncogene Tyr protein kinase LCK (gene ID 1611) protein.
XX
KW AIDS; acquired immunodeficiency syndrome; human immunodeficiency virus;
KW HIV-related disorder; differential expression; drug screening;
KW viral replication modulation; diagnosis; prognosis; predisposition;
KW anti-HIV; gene therapy; antisense therapy; human;
KW proto-oncogene Tyr protein kinase LCK; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003070883-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004246.
XX
PR 15-FEB-2002; 2002US-0357391P.
PR 13-MAY-2002; 2002US-0380249P.
PR 25-JUN-2002; 2002US-0391306P.
PR 27-AUG-2002; 2002US-0406297P.
PR 19-SEP-2002; 2002US-0412007P.
PR 10-OCT-2002; 2002US-0417508P.
PR 10-DEC-2002; 2002US-0432318P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Powell DM, Weich NS;
XX
DR WPI; 2003-671808/63.
DR N-PSDB; ADE40448.
XX
PT Identifying a compound capable of diagnosing, preventing or treating AIDS
PT or an HIV-related disorder comprises assaying the ability of the compound
PT to modulate e.g. 1414, 1481 or 1553 nucleic acid expression or
PT polypeptide activity.
XX
PS Claim 1; SEQ ID NO 28; 167pp; English.
XX
CC The invention relates to a method of identifying a compound useful in the
CC treatment of AIDS (acquired immunodeficiency syndrome) or an HIV (human
CC immunodeficiency virus)-related disorder. The invention involves assaying
CC the ability of a test compound to modulate the activity or expression of
CC 26 human proteins. These proteins and nucleic acids encoding them
CC (ADE40422-ADE40473) are differentially expressed in tissues relating to
CC AIDS or an HIV-related disorder compared to their expression in normal
CC tissues. The invention also relates to the use of the compounds
CC identified to modulate viral replication in a cell and to treat a patient
CC with AIDS or an HIV-related disorder. The invention further discloses
CC methods for the diagnostic evaluation and prognosis of various HIV-
CC related disorders, and for the identification of individuals exhibiting a
CC predisposition to such conditions. The modulatory compounds identified
CC using the method of the invention may be small organic molecules,
CC peptides, antibodies or antisense nucleic acid molecules. The methods of
CC the invention are useful in diagnosing, preventing or treating AIDS or
CC HIV-related disorders. The present sequence represents a human protein
CC which is differentially expressed in AIDS or HIV-related disorders.
XX
SQ Sequence 509 AA;

Query Match 90.2%; Score 37; DB 7; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVERLGA 8
||||||||
Db 246 KLVERLGA 253

RESULT 27
ADP12458
ID ADP12458 standard; protein; 509 AA.
XX
AC ADP12458;
XX
DT 12-AUG-2004 (first entry)
XX
DE Protein encoded by mRNA of the invention #68.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
OS Homo sapiens.
XX

PN WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX
PR 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
DR WPI; 2004-400724/37.
XX
PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
PS Claim 65; SEQ ID NO 2467; 1762pp; English.
XX
CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein that is encoded by the mRNA of the invention.
XX
SQ Sequence 509 AA;

Query Match 90.2%; Score 37; DB 8; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVERLGA 8
||||||||
Db 246 KLVERLGA 253

RESULT 28
ADZ51107
ID ADZ51107 standard; protein; 509 AA.
XX
AC ADZ51107;
XX
DT 30-JUN-2005 (first entry)
XX
DE Amino acid sequence of human Tyr kinase Lck.
XX
KW protein kinase inhibitor; inactive conformation; Tethering; Tyr kinase;
KW Lck.
XX
OS Homo sapiens.
XX
PN WO2005034840-A2.
XX
PD 21-APR-2005.
XX
PF 17-SEP-2003; 2003WO-US029870.
XX
PR 17-SEP-2003; 2003WO-US029870.
XX
PA (SUNE-) SUNESIS PHARM INC.
XX
PI Prescoot JC;
XX
DR WPI; 2005-315455/32.
XX
PT Identifying ligand binding to inactive conformation of target protein
PT kinase, by contacting inactive conformation of target with ligand
PT candidates specific to target, detecting formation of kinase-ligand
PT conjugate and identifying ligand.
XX
PS Example 1; SEQ ID NO 9; 101pp; English.
XX
CC The specification describes a method for identifying protein kinase
CC inhibitors that preferentially bind to the inactive conformation of a
CC target protein kinase. The inhibitors are identified by locking the
CC target protein kinase in an inactive conformation, and using Tethering to
CC identify inhibitors preferentially targeting the inactive conformation.
CC The method of the invention is useful for identifying a ligand which
CC binds to an inactive conformation of a target protein kinase. The present
CC sequence represents the human Tyr kinase Lck. Lck variants were used to
CC demonstrate the method of the invention.
XX
SQ Sequence 509 AA;

Query Match 90.2%; Score 37; DB 9; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVERLGA 8
||||||||
Db 246 KLVERLGA 253

RESULT 29
AEA35921
ID AEA35921 standard; protein; 509 AA.
XX
AC AEA35921;
XX
DT 25-AUG-2005 (first entry)
XX
DE Human Lck kinase amino acid sequence SEQ ID NO:8.
XX
KW Src family kinase; Lck kinase.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 273
FT /note= "constant amino acid K in domain SH2"
FT Misc-difference 316
FT /note= "constant amino acid T in domain SH2"
FT Misc-difference 505
FT /note= "constant amino acid Y in domain SH1"
XX
PN EP1541694-A1.
XX
PD 15-JUN-2005.
XX
PF 12-DEC-2003; 2003EP-00028713.
XX
PR 12-DEC-2003; 2003EP-00028713.
XX
PA (SIRE-) SIRENADE PHARM AG.
XX
PI Obermeier A, Bieger B;
XX
DR WPI; 2005-428084/44.
XX
PT Identifying compound which modulates Src family kinase (SFK) activity, by
PT contacting cells expressed with SFK or mutated SFK with test compound,
PT where change in phenotype of cells indicates that test compound modulates
PT SFK activity.
XX

PS Disclosure; SEQ ID NO 8; 114pp; English.
XX
CC The invention relates to a method (M1) for identifying, selecting and/or
CC characterizing a compound which modulates Src family kinase (SFK)
CC activity, by expressing nucleic acids encoding SFK or mutated SFK in
CC cells, contacting cells with test compound and determining whether
CC phenotype of cells is changed as compared with phenotype of cells not
CC expressed with above nucleic acids, where difference in phenotype
CC indicates that test compound modulate SFK activity. Also described: (1) a
CC compound (I) identified, selected and/or characterized by (M1); and (2) a
CC pharmaceutical composition (PC1) containing (I), and a carrier, adjuvant
CC or vehicle. (I) is useful as a medicament, particularly for the treatment
CC of diseases, which are at least in part caused by a Src family kinase.
CC (I) and PC1 are useful for producing a medicament for the treatment of
CC diseases, which are at least in part caused by a Src family kinase,
CC particularly by a dysfunction of a Src family kinase, in particular
CC cancer, hypercalcemia, restenosis, osteoporosis, osteoarthritis,
CC symptomatic treatment of bone metastasis, rheumatoid arthritis,
CC inflammatory bowel disease, multiple sclerosis, psoriasis, lupus, graft
CC versus host disease, T-cell mediated hypersensitivity disease,
CC Hashimoto's thyroiditis, Guillain-Barre syndrome, chronic obstructive
CC pulmonary disorder, contact dermatitis, Paget's disease, asthma, ischemic
CC or reperfusion injury, allergic disease, atopic dermatitis, transplant
CC rejection or allergic rhinitis. The present sequence represents human Lck
CC kinase, which is given in the exemplification of the present invention.
XX
SQ Sequence 509 AA;

Query Match 90.2%; Score 37; DB 9; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVERLGA 8
||||||||
Db 246 KLVERLGA 253

RESULT 30
ABM82981
ID ABM82981 standard; protein; 539 AA.
XX
AC ABM82981;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3230.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN41633.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 539 AA;

Query Match 90.2%; Score 37; DB 8; Length 539;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVERLGA 8
||||||||
Db 276 KLVERLGA 283

Search completed: June 29, 2006, 09:13:06
Job time : 90.8313 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:39 ; Search time 105.831 Seconds
(without alignments)
78.664 Million cell updates/sec

Title: US-10-062-257A-12
Perfect score: 41
Sequence: 1 KLVERLGAA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	38	92.7	559	2	Q2S8X6_9GAMM	Q2s8x6 hahella che
2	37	90.2	173	2	Q4K6W6_PSEF5	Q4k6w6 pseudomonas
3	37	90.2	226	1	RPIA_METTH	P72012 methanobact
4	37	90.2	331	2	Q43YL3_SOLUS	Q43yl3 solibacter
5	37	90.2	368	2	Q3TLX4_MOUSE	Q3tlx4 mus musculu
6	37	90.2	379	2	Q4FZR6_RAT	Q4fzr6 rattus norv
7	37	90.2	508	1	LCK_AOTNA	Q5pxs1 aotus nancy
8	37	90.2	508	1	LCK_HUMAN	P06239 homo sapien
9	37	90.2	508	1	LCK_MOUSE	P06240 mus musculu
10	37	90.2	508	1	LCK_SAISC	Q95kr7 saimiri sci
11	37	90.2	509	2	Q7RTZ3_HUMAN	Q7rtz3 homo sapien
12	37	90.2	509	2	Q95M32_9PRIM	Q95m32 hylobates s
13	37	90.2	509	2	Q3ZCM0_BOVIN	Q3zcm0 bos taurus
14	36	87.8	179	2	Q40AH8_9RHOB	Q40ah8 jannaschia
15	36	87.8	399	2	Q48EP0_PSE14	Q48ep0 pseudomonas
16	36	87.8	399	2	Q4ZP81_PSEU2	Q4zp81 pseudomonas
17	36	87.8	399	2	Q87X81_PSESM	Q87x81 pseudomonas
18	36	87.8	400	2	Q4KH35_PSEF5	Q4kh35 pseudomonas
19	36	87.8	419	1	Y906_CHLMU	Q9pjc5 chlamydia m
20	36	87.8	467	2	Q44GN0_CHRSL	Q44gn0 chromohalob
21	36	87.8	508	2	Q4CPA3_TRYCR	Q4cpa3 trypanosoma
22	36	87.8	597	2	Q4D4X4_TRYCR	Q4d4x4 trypanosoma
23	36	87.8	791	2	Q4CY55_TRYCR	Q4cy55 trypanosoma
24	35	85.4	160	2	Q3S4S6_9MICC	Q3s4s6 arthrobacte
25	35	85.4	252	2	Q2LC71_9MICC	Q2lc71 arthrobacte
26	35	85.4	322	2	Q84H43_ALCDF	Q84h43 alcaligenes
27	35	85.4	336	2	Q7MVH9_PORGI	Q7mvh9 porphyromon
28	35	85.4	341	2	Q8BUD6_MOUSE	Q8bud6 mus musculu
29	35	85.4	393	2	Q4ZZL7_PSEU2	Q4zzl7 pseudomonas
30	35	85.4	462	2	Q5FVQ0_RAT	Q5fvq0 rattus norv
31	35	85.4	462	2	Q8BTQ3_MOUSE	Q8btq3 mus musculu
32	35	85.4	462	2	Q91W10_MOUSE	Q91w10 mus musculu
33	35	85.4	462	2	Q9D426_MOUSE	Q9d426 mus musculu
34	35	85.4	462	2	Q9D5V4_MOUSE	Q9d5v4 mus musculu
35	35	85.4	711	2	Q47S17_THEFY	Q47s17 thermobifid
36	34	82.9	91	2	Q9F3P4_STRCO	Q9f3p4 streptomyce
37	34	82.9	108	2	Q8VJR1_MYCTU	Q8vjr1 mycobacteri
38	34	82.9	126	2	Q5YP25_NOCFA	Q5yp25 nocardia fa
39	34	82.9	179	2	Q3PYZ1_NITHA	Q3pyz1 nitrobacter
40	34	82.9	180	1	APT_HAEI8	Q4qjv7 haemophilus
41	34	82.9	180	1	APT_HAEIN	P43856 haemophilus
42	34	82.9	190	2	Q3RY59_RALME	Q3ry59 ralstonia m
43	34	82.9	205	2	Q476D8_RALEJ	Q476d8 ralstonia e
44	34	82.9	224	2	Q2KYQ1_BORAV	Q2kyq1 bordetella
45	34	82.9	227	1	RPIA_STRPN	Q97ri7 streptococc
46	34	82.9	227	1	RPIA_STRR6	Q8dqd1 streptococc
47	34	82.9	297	2	Q64DR0_9ARCH	Q64dr0 uncultured
48	34	82.9	338	2	Q3GY67_9ACTO	Q3gy67 nocardioide
49	34	82.9	339	2	Q35DS9_9BRAD	Q35ds9 bradyrhizob
50	34	82.9	349	2	Q2W7N5_MAGSA	Q2w7n5 magnetospir
51	34	82.9	418	2	Q9K9F3_BACHD	Q9k9f3 bacillus ha
52	34	82.9	474	2	Q3KHG9_PSEPF	Q3khg9 pseudomonas
53	34	82.9	475	1	GATA_THEMA	Q9x0z9 thermotoga
54	34	82.9	481	2	Q2XDU3_PSEPU	Q2xdu3 pseudomonas
55	34	82.9	501	2	Q3ALH4_SYNSC	Q3alh4 synechococc
56	34	82.9	507	1	LCK_CHICK	P42683 gallus gall
57	34	82.9	754	1	BGLB_CLOTM	P14002 clostridium
58	34	82.9	755	2	Q4CJZ5_CLOTM	Q4cjz5 clostridium
59	34	82.9	757	2	Q3MWR9_9DELT	Q3mwr9 syntrophoba
60	33	80.5	159	2	Q3PN21_NITHA	Q3pn21 nitrobacter
61	33	80.5	166	2	Q478X9_DECAR	Q478x9 dechloromon
62	33	80.5	174	2	Q3F2I8_9BURK	Q3f2i8 burkholderi
63	33	80.5	175	2	Q3J1S3_RHOS4	Q3j1s3 rhodobacter
64	33	80.5	179	1	APT_SILPO	Q5lny7 silicibacte
65	33	80.5	181	1	APT1_WHEAT	Q43199 triticum ae
66	33	80.5	181	2	Q9LW89_HORVU	Q9lw89 hordeum vul
67	33	80.5	204	2	Q3PN85_NITHA	Q3pn85 nitrobacter
68	33	80.5	213	2	Q3SH84_THIDA	Q3sh84 thiobacillu
69	33	80.5	226	1	RPIA_BORBR	Q7wh03 bordetella
70	33	80.5	226	1	RPIA_BORPA	Q7w9q5 bordetella
71	33	80.5	226	1	RPIA_BORPE	Q7vwc1 bordetella
72	33	80.5	238	2	Q6XXM6_PIG	Q6xxm6 sus scrofa
73	33	80.5	238	2	Q6XZB6_PIG	Q6xzb6 sus scrofa
74	33	80.5	240	2	Q40W58_KINRA	Q40w58 kineococcus
75	33	80.5	278	2	Q60CE7_METCA	Q60ce7 methylococc
76	33	80.5	285	2	Q2IIF7_9DELT	Q2iif7 anaeromyxob
77	33	80.5	302	2	Q3JQ91_BURP1	Q3jq91 burkholderi
78	33	80.5	302	2	Q62LR8_BURMA	Q62lr8 burkholderi
79	33	80.5	302	2	Q63SA7_BURPS	Q63sa7 burkholderi
80	33	80.5	340	2	Q36ZD2_RHOPA	Q36zd2 rhodopseudo
81	33	80.5	345	2	Q46UQ4_RALEJ	Q46uq4 ralstonia e
82	33	80.5	355	2	Q5WXF8_LEGPL	Q5wxf8 legionella
83	33	80.5	358	2	Q3VXE2_9ACTO	Q3vxe2 frankia sp.
84	33	80.5	358	2	Q3W0S5_9ACTO	Q3w0s5 frankia sp.
85	33	80.5	359	2	Q9Y9P9_AERPE	Q9y9p9 aeropyrum p
86	33	80.5	362	2	Q4BN29_BURVI	Q4bn29 burkholderi
87	33	80.5	375	2	Q2RYI7_RHORU	Q2ryi7 rhodospiril
88	33	80.5	375	2	Q8V1P2_SHV1	Q8v1p2 saimiriine
89	33	80.5	381	2	Q4SHF5_TETNG	Q4shf5 tetraodon n
90	33	80.5	382	2	Q2W0P3_MAGSA	Q2w0p3 magnetospir
91	33	80.5	394	2	Q3WZ07_9ACTN	Q3wz07 rubrobacter
92	33	80.5	400	1	PCAF_PSEPU	Q51956 pseudomonas
93	33	80.5	400	2	Q2XCG5_PSEPU	Q2xcg5 pseudomonas
94	33	80.5	401	2	Q3KGU4_PSEPF	Q3kgu4 pseudomonas
95	33	80.5	413	2	Q3WCD7_9ACTO	Q3wcd7 frankia sp.
96	33	80.5	418	2	Q3F5I4_9BURK	Q3f5i4 burkholderi
97	33	80.5	419	1	NEMO_HUMAN	Q9y6k9 h nf-kappa-
98	33	80.5	419	2	Q7LBY6_HUMAN	Q7lby6 homo sapien
99	33	80.5	426	2	Q37XJ1_SPHAR	Q37xj1 novosphingo
100	33	80.5	430	2	Q6N3V5_RHOPA	Q6n3v5 rhodopseudo

ALIGNMENTS

```
RESULT 1
Q2S8X6_9GAMM
ID   Q2S8X6_9GAMM   PRELIMINARY;   PRT;   559 AA.
AC   Q2S8X6;
DT   24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT   24-JAN-2006, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Uncharacterized protein conserved in bacteria.
GN   ORFNames=HCH_06251;
OS   Hahella chejuensis KCTC 2396.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
OC   Hahellaceae; Hahella.
OX   NCBI_TaxID=349521;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=KCTC 2396;
RX   PubMed=16352867; DOI=10.1093/nar/gki1016;
RA   Jeong H., Yim J.H., Lee C., Choi S.-H., Park Y.K., Yoon S.H.,
RA   Hur C.-G., Kang H.-Y., Kim D., Lee H.H., Park K.H., Park S.-H.,
RA   Park H.-S., Lee H.K., Oh T.K., Kim J.F.;
RT   "Genomic blueprint of Hahella chejuensis, a marine microbe producing
RT   an algicidal agent.";
RL   Nucleic Acids Res. 33:7066-7073(2005).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CP000155; ABC32898.1; -; Genomic_DNA.
SQ   SEQUENCE   559 AA;  64117 MW;  25D965C3322DF02F CRC64;

  Query Match             92.7%;  Score 38;  DB 2;  Length 559;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              |||:|||||
Db        551 KLVQRLGAA 559


RESULT 2
Q4K6W6_PSEF5
ID   Q4K6W6_PSEF5   PRELIMINARY;   PRT;   173 AA.
AC   Q4K6W6;
DT   02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   02-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Hypothetical protein.
GN   OrderedLocusNames=PFL_4937;
OS   Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=220664;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15980861; DOI=10.1038/nbt1110;
RA   Paulsen I.T., Press C.M., Ravel J., Kobayashi D.Y., Myers G.S.A.,
RA   Mavrodi D.V., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA   Durkin A.S., Brinkac L.M., Daugherty S.C., Sullivan S.A.,
RA   Rosovitz M.J., Gwinn M.L., Zhou L., Schneider D.J., Cartinhour S.W.,
RA   Nelson W.C., Weidman J., Watkins K., Tran K., Khouri H., Pierson E.A.,
RA   Pierson L.S. III, Thomashow L.S., Loper J.E.;
RT   "Complete genome sequence of the plant commensal Pseudomonas
RT   fluorescens Pf-5.";
RL   Nat. Biotechnol. 23:873-878(2005).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CP000076; AAY94166.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   173 AA;  18500 MW;  010C421E02BD8E28 CRC64;

  Query Match             90.2%;  Score 37;  DB 2;  Length 173;
  Best Local Similarity   88.9%;  Pred. No. 90;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              :|||||||
Db         20 QLVERLGAA 28


RESULT 3
RPIA_METTH
ID   RPIA_METTH     STANDARD;      PRT;   226 AA.
AC   P72012;
DT   30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1997, sequence version 1.
DT   07-MAR-2006, entry version 43.
DE   Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)
DE   (PRI).
GN   Name=rpiA; OrderedLocusNames=MTH608;
OS   Methanobacterium thermoautotrophicum.
OC   Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC   Methanobacteriaceae; Methanothermobacter.
OX   NCBI_TaxID=187420;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC   STRAIN=Delta H;
RX   MEDLINE=98080610; PubMed=9419225;
RA   Koga Y., Kyuragi T., Nishihara M., Sone N.;
RT   "Did archaeal and bacterial cells arise independently from noncellular
RT   precursors? A hypothesis stating that the advent of membrane
RT   phospholipid with enantiomeric glycerophosphate backbones caused the
RT   separation of the two lines of descent.";
RL   J. Mol. Evol. 46:54-63(1998).
RN   [2]
RP   ERRATUM.
RX   PubMed=9797414;
RA   Koga Y., Kyuragi T., Nishihara M., Sone N.;
RL   J. Mol. Evol. 47:631-631(1998).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Delta H;
RX   MEDLINE=98037514; PubMed=9371463;
RA   Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA   Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA   Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA   Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA   Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA   McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA   Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT   "Complete genome sequence of Methanobacterium thermoautotrophicum
RT   deltaH: functional analysis and comparative genomics.";
RL   J. Bacteriol. 179:7135-7155(1997).
CC   -!- CATALYTIC ACTIVITY: D-ribose 5-phosphate = D-ribulose 5-phosphate.
CC   -!- PATHWAY: Carbohydrate degradation; pentose phosphate pathway.
CC   -!- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; D88555; BAA13646.1; -; Genomic_DNA.
DR   EMBL; AE000666; AAB85114.1; -; Genomic_DNA.
DR   PIR; G69180; G69180.
DR   HSSP; O50083; 1LK5.
DR   GenomeReviews; AE000666_GR; MTH608.
DR   BioCyc; MTHE187420:MTH608-MONOMER; -.
DR   LinkHub; P72012; -.
DR   HAMAP; MF_00170; -; 1.
DR   InterPro; IPR004788; RpiA.
DR   PANTHER; PTHR11934; RpiA; 1.
DR   Pfam; PF06026; Rib_5-P_isom_A; 1.
DR   ProDom; PD005813; RpiA; 1.
DR   TIGRFAMs; TIGR00021; rpiA; 1.
KW   Complete proteome; Isomerase.
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FT   CHAIN         1    226       Ribose-5-phosphate isomerase A.
FT                               /FTId=PRO_0000158513.
SQ   SEQUENCE   226 AA;  23785 MW;  F5EE6E929C08792B CRC64;

  Query Match             90.2%;  Score 37;  DB 1;  Length 226;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db        124 KLVERLGA 131


RESULT 4
Q43YL3_SOLUS
ID   Q43YL3_SOLUS   PRELIMINARY;   PRT;   331 AA.
AC   Q43YL3;
DT   13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   13-SEP-2005, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Phosphate acetyltransferase (EC 2.3.1.8).
GN   ORFNames=AcidDRAFT_3922;
OS   Solibacter usitatus Ellin6076.
OC   Bacteria; Acidobacteria; Solibacteres; Solibacterales;
OC   Solibacteraceae; Solibacter.
OX   NCBI_TaxID=234267;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Ellin6076;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome and assembly of Solibacter usitatus
RT   Ellin6076.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Ellin6076;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Solibacter usitatus.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AAIA01000019; EAM57936.1; -; Genomic_DNA.
DR   GO; GO:0008959; F:phosphate acetyltransferase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR012147; P_Ac_Bu_trans.
DR   InterPro; IPR004614; PhpActrans.
DR   Pfam; PF01515; PTA_PTB; 1.
DR   PIRSF; PIRSF000428; P_Ac_trans; 1.
DR   TIGRFAMs; TIGR00651; pta; 1.
KW   Acyltransferase; Transferase.
SQ   SEQUENCE   331 AA;  34576 MW;  4BF1DA6049A448E3 CRC64;

  Query Match             90.2%;  Score 37;  DB 2;  Length 331;
  Best Local Similarity   88.9%;  Pred. No. 1.5e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              ||||||| |
Db        283 KLVERLGGA 291


RESULT 5
Q3TLX4_MOUSE
ID   Q3TLX4_MOUSE   PRELIMINARY;   PRT;   368 AA.
AC   Q3TLX4;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched
DE   library, clone:G830026O06 product:lymphocyte protein tyrosine kinase,
DE   full insert sequence. (Fragment).
GN   Name=Lck;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
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RC   TISSUE=Mammary gland;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK166263; BAE38668.1; -; mRNA.
DR   MGI; MGI:96756; Lck.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   368 AA;  42018 MW;  7AB6AE53AF1A5059 CRC64;

  Query Match             90.2%;  Score 37;  DB 2;  Length 368;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db        105 KLVERLGA 112


RESULT 6
Q4FZR6_RAT
ID   Q4FZR6_RAT     PRELIMINARY;   PRT;   379 AA.
AC   Q4FZR6;
DT   30-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   30-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Lck_mapped protein (Fragment).
GN   Name=Lck_mapped;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC099218; AAH99218.1; -; mRNA.
DR   SMR; Q4FZR6; 2-379.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1       1
SQ   SEQUENCE   379 AA;  43336 MW;  7CDEB573BAFB53AB CRC64;

  Query Match             90.2%;  Score 37;  DB 2;  Length 379;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db        116 KLVERLGA 123


RESULT 7
LCK_AOTNA
ID   LCK_AOTNA      STANDARD;      PRT;   508 AA.
AC   Q5PXS1;
DT   08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT   08-NOV-2005, sequence version 3.
DT   07-MAR-2006, entry version 13.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Aotus nancymaae (Ma's night monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=37293;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Perez-Quintero L.A., Vernot J.P.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways. Association of the TCR with a peptide
CC       antigen-bound MHC complex facilitates the interaction of CD4 and
CC       CD8 with MHC class II and class I molecules, respectively, and
CC       thereby recruits the associated LCK to the vicinity of the TCR/CD3
CC       complex. LCK then phosphorylates tyrosines residues within the
CC       immunoreceptor tyrosines-based activation motifs (ITAMs) in the
CC       cytoplasmic tails of the TCRgamma chains and CD3 subunits,
CC       initiating the TCR/CD3 signaling pathway. In addition, contributes
CC       to signaling by other receptor molecules. Associates directly with
CC       the cytoplasmic tail of CD2, and upon engagement of the CD2
CC       molecule, LCK undergoes hyperphosphorylation and activation. Also
CC       plays a role in the IL2 receptor-linked signaling pathway that
CC       controls T-cell proliferative response. Binding of IL2 to its
CC       receptor results in increased activity of LCK. Is expressed at all
CC       stages of thymocyte development and is required for the regulation
CC       of maturation events that are governed by both pre-TCR and mature
CC       alpha beta TCR (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also
CC       binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to
CC       other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds
CC       to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes
CC       through its SH3 domain and to the tyrosine phosphorylated form of
CC       KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.
CC       Interacts with phosphorylated LIME1. Interacts with CBLB (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.
CC       Present in lipid rafts in an unactive form (By similarity).
CC   -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.
CC       Interaction is regulated by Ser-58 phosphorylation (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY821852; AAV70114.2; -; mRNA.
DR   SMR; Q5PXS1; 64-508.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
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DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    508       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088123.
FT   DOMAIN       60    120       SH3.
FT   DOMAIN      126    223       SH2.
FT   DOMAIN      244    497       Protein kinase.
FT   NP_BIND     250    258       ATP (By similarity).
FT   REGION        1     71       Interactions with CD4 and CD8 (By
FT                                similarity).
FT   ACT_SITE    363    363       Proton acceptor (By similarity).
FT   BINDING     272    272       ATP (By similarity).
FT   MOD_RES     393    393       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     504    504       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   508 AA;  58041 MW;  8B61951BC192A3A4 CRC64;

  Query Match             90.2%;  Score 37;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db        245 KLVERLGA 252


RESULT 8
LCK_HUMAN
ID   LCK_HUMAN      STANDARD;      PRT;   508 AA.
AC   P06239; P07100; Q12850; Q13152; Q5TDH8; Q5TDH9; Q96DW4; Q9NYT8;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1994, sequence version 5.
DT   07-MAR-2006, entry version 87.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase) (LSK) (T cell-
DE   specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=87133831; PubMed=3493153;
RA   Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
RA   Mak T.W.;
RT   "A human T cell-specific cDNA clone (YT16) encodes a protein with
RT   extensive homology to a family of protein-tyrosine kinases.";
RL   Eur. J. Immunol. 16:1643-1646(1986).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=89123626; PubMed=3265417;
RA   Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F.,
RA   Wilson C.B.;
RT   "Structure and expression of lck transcripts in human lymphoid
RT   cells.";
RL   J. Cell. Biochem. 38:117-126(1988).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=90108697; PubMed=2558056; DOI=10.1016/0378-1119(89)90144-3;
RA   Rouer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
RA   Benarous R.;
RT   "Structure of the human lck gene: differences in genomic organisation
RT   within src-related genes affect only N-terminal exons.";
RL   Gene 84:105-113(1989).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA], VARIANTS LEU-27; GLN-LYS-PRO-231 INS;
RP   VAL-352 AND LEU-446, AND PHOSPHORYLATION SITES TYR-393 AND TYR-504.
RC   TISSUE=Leukemia;
RX   MEDLINE=94187714; PubMed=8139546;
RA   Wright D.D., Sefton B.M., Kamps M.P.;
RT   "Oncogenic activation of the Lck protein accompanies translocation of
RT   the LCK gene in the human HSB2 T-cell leukemia.";
RL   Mol. Cell. Biol. 14:2429-2437(1994).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM SHORT), AND ALTERNATIVE SPLICING.
RC   TISSUE=Leukemic T-cell;
RX   MEDLINE=96085119; PubMed=7495859; DOI=10.1016/0167-4781(95)00162-A;
RA   Vogel L.B., Arthur R., Fujita D.J.;
RT   "An aberrant lck mRNA in two human T-cell lines.";
RL   Biochim. Biophys. Acta 1264:168-172(1995).
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG   Human chromosome 1 international sequencing consortium;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX   MEDLINE=89096891; PubMed=2850479;
RA   Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT   "Structure of the murine lck gene and its rearrangement in a murine
RT   lymphoma cell line.";
RL   Mol. Cell. Biol. 8:3058-3064(1988).
RN   [9]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX   MEDLINE=89313764; PubMed=2787474;
RA   Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
RA   Miyamoto N.G., Mak T.W.;
RT   "Structure of the two promoters of the human lck gene: differential
RT   accumulation of two classes of lck transcripts in T cells.";
RL   Mol. Cell. Biol. 9:2173-2180(1989).
RN   [10]
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```
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 13-508.
RC   TISSUE=Peripheral blood lymphocyte;
RX   MEDLINE=20462621; PubMed=11009097;
RX   DOI=10.1002/1521-4141(200009)30:9<2632::AID-IMMU2632>3.0.CO;2-C;
RA   Boncristiano M., Majolini M.B., D'Elios M.M., Pacini S., Valensin S.,
RA   Ulivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,
RA   Baldari C.T.;
RT   "Defective recruitment and activation of ZAP-70 in common variable
RT   immunodeficiency patients with T cell defects.";
RL   Eur. J. Immunol. 30:2632-2638(2000).
RN   [11]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 367-508.
RX   MEDLINE=88217332; PubMed=2835736;
RA   Veillette A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.;
RT   "Expression of the lck tyrosine kinase gene in human colon carcinoma
RT   and other non-lymphoid human tumor cell lines.";
RL   Oncogene Res. 1:357-374(1987).
RN   [12]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 374-508.
RX   MEDLINE=87000726; PubMed=3489486; DOI=10.1016/0167-4889(86)90228-4;
RA   Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
RA   Linna T.J.;
RT   "Human T lymphocytes express a protein-tyrosine kinase homologous to
RT   p56LSTRA.";
RL   Biochim. Biophys. Acta 888:286-295(1986).
RN   [13]
RP   PHOSPHORYLATION SITE TYR-504.
RX   MEDLINE=92347326; PubMed=1639064;
RA   Bergman M., Mustelin T., Oetken C., Partanen J., Flint N.A.,
RA   Amrein K.E., Autero M., Burn P., Alitalo K.;
RT   "The human p50csk tyrosine kinase phosphorylates p56lck at Tyr-505 and
RT   down regulates its catalytic activity.";
RL   EMBO J. 11:2919-2924(1992).
RN   [14]
RP   INTERACTION WITH PI3K.
RX   MEDLINE=94067101; PubMed=7504174;
RA   Vogel L.B., Fujita D.J.;
RT   "The SH3 domain of p56lck is involved in binding to
RT   phosphatidylinositol 3'-kinase from T lymphocytes.";
RL   Mol. Cell. Biol. 13:7408-7417(1993).
RN   [15]
RP   INTERACTION WITH KHDRBS1.
RX   MEDLINE=95155308; PubMed=7852312; DOI=10.1074/jbc.270.6.2506;
RA   Vogel L.B., Fujita D.J.;
RT   "p70 phosphorylation and binding to p56lck is an early event in
RT   interleukin-2-induced onset of cell cycle progression in T-
RT   lymphocytes.";
RL   J. Biol. Chem. 270:2506-2511(1995).
RN   [16]
RP   INTERACTION WITH SQSTM1, AND MUTAGENESIS OF SER-58 AND ARG-153.
RX   PubMed=8618896;
RA   Park I., Chung J., Walsh C.T., Yun Y., Strominger J.L., Shin J.;
RT   "Phosphotyrosine-independent binding of a 62-kDa protein to the src
RT   homology 2 (SH2) domain of p56lck and its regulation by
RT   phosphorylation of Ser-59 in the lck unique N-terminal region.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:12338-12342(1995).
RN   [17]
RP   INTERACTION WITH HIV-1 NEF.
RX   MEDLINE=96386556; PubMed=8794306;
RA   Greenway A.L., Azad A., Mills J., McPhee D.A.;
RT   "Human immunodeficiency virus type 1 Nef binds directly to LCK and
RT   mitogen-activated protein kinase, inhibiting kinase activity.";
RL   J. Virol. 70:6701-6708(1996).
RN   [18]
RP   REVIEW.
RX   PubMed=10848956;
RA   Isakov N., Biesinger B.;
RT   "Lck protein tyrosine kinase is a key regulator of T-cell activation
RT   and a target for signal intervention by Herpesvirus saimiri and other
RT   viral gene products.";
RL   Eur. J. Biochem. 267:3413-3421(2000).
RN   [19]
RP   SUBCELLULAR LOCATION.
RX   PubMed=12218089;
RA   Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA   Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT   "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT   protein/phosphoprotein associated with glycolipid-enriched
RT   microdomains in lipid rafts in resting T cells.";
RL   J. Immunol. 169:2813-2817(2002).
RN   [20]
RP   MASS SPECTROMETRY.
RC   TISSUE=Mammary cancer;
RX   MEDLINE=21829512; PubMed=11840567;
RX   DOI=10.1002/1615-9861(200202)2:2<212::AID-PROT212>3.0.CO;2-H;
RA   Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
RA   Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
RA   Zvelebil M.J.;
RT   "Cluster analysis of an extensive human breast cancer cell line
RT   protein expression map database.";
RL   Proteomics 2:212-223(2002).
RN   [21]
RP   INTERACTION WITH LIME1.
RX   PubMed=14610046; DOI=10.1084/jem.20031484;
RA   Brdickova N., Brdicka T., Angelisova P., Horvath O., Spicka J.,
RA   Hilgert I., Paces J., Simeoni L., Kliche S., Merten C., Schraven B.,
RA   Horejsi V.;
RT   "LIME: a new membrane raft-associated adaptor protein involved in CD4
RT   and CD8 coreceptor signaling.";
RL   J. Exp. Med. 198:1453-1462(2003).
RN   [22]
RP   INTERACTION WITH LIME1.

  Query Match             90.2%;  Score 37;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db        245 KLVERLGA 252


RESULT 9
LCK_MOUSE
ID   LCK_MOUSE      STANDARD;      PRT;   508 AA.
AC   P06240; Q61794; Q61795; Q62320; Q91X65;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   25-OCT-2005, sequence version 3.
DT   07-MAR-2006, entry version 74.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase) (LSK).
GN   Name=Lck; Synonyms=Lsk-t;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86079521; PubMed=2416464; DOI=10.1016/0092-8674(85)90169-2;
RA   Marth J.D., Peet R., Krebs E.G., Perlmutter R.M.;
RT   "A lymphocyte-specific protein-tyrosine kinase gene is rearranged and
RT   overexpressed in the murine T cell lymphoma LSTRA.";
RL   Cell 43:393-404(1985).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86146842; PubMed=3081813;
RA   Voronova A.F., Sefton B.M.;
RT   "Expression of a new tyrosine protein kinase is stimulated by
RT   retrovirus promoter insertion.";
RL   Nature 319:682-685(1986).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=NOD; TISSUE=Thymus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
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RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX MEDLINE=89096891; PubMed=2850479;
RA Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT "Structure of the murine lck gene and its rearrangement in a murine
RT lymphoma cell line.";
RL Mol. Cell. Biol. 8:3058-3064(1988).
RN [6]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-10.
RX MEDLINE=88142832; PubMed=3501824;
RA Voronova A.F., Adler H.T., Sefton B.M.;
RT "Two lck transcripts containing different 5' untranslated regions are
RT present in T cells.";
RL Mol. Cell. Biol. 7:4407-4413(1987).
RN [7]
RP MUTAGENESIS OF TYR-504.
RX MEDLINE=88248001; PubMed=3380790;
RA Amrein K.E., Sefton B.M.;
RT "Avian reovirus mRNAs are nonfunctional in infected mouse cells:
RT translational basis for virus host-range restriction.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:4257-4261(1988).
RN [8]
RP INTERACTIONS WITH CD4 AND CD8, AND MUTAGENESIS OF 2-CYS--CYS-4; CYS-19
RP AND CYS-22.
RX MEDLINE=90182665; PubMed=2107025; DOI=10.1016/0092-8674(90)90090-2;
RA Turner J.M., Brodsky M.H., Irving B.A., Levin S.D., Perlmutter R.M.,
RA Littman D.R.;
RT "Interaction of the unique N-terminal region of tyrosine kinase p56lck
RT with cytoplasmic domains of CD4 and CD8 is mediated by cysteine
RT motifs.";
RL Cell 60:755-765(1990).
RN [9]
RP MUTAGENESIS.
RX MEDLINE=93059694; PubMed=1279202;
RA Hurley T.R., Amrein K.E., Sefton B.M.;
RT "Creation and characterization of temperature-sensitive mutants of the
RT lck tyrosine protein kinase.";
RL J. Virol. 66:7406-7413(1992).
RN [10]
RP MUTAGENESIS OF LYS-272.
RX MEDLINE=91163633; PubMed=1706070; DOI=10.1038/350062a0;
RA Abraham N., Miceli M.C., Parnes J.C., Veillette A.;
RT "Enhancement of T-cell responsiveness by the lymphocyte-specific
RT tyrosine protein kinase p56lck.";
RL Nature 350:62-66(1991).
RN [11]
RP MUTAGENESIS OF TYR-504.
RX MEDLINE=91219495; PubMed=1708890;
RA Abraham K.M., Levin S.D., Marth J.D., Forbush K.A., Perlmutter R.M.;
RT "Thymic tumorigenesis induced by overexpression of p56lck.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981(1991).
RN [12]
RP PHOSPHORYLATION BY CSK.
RX PubMed=8371758; DOI=10.1038/365156a0;
RA Chow L.M., Fournel M., Davidson D., Veillette A.;
RT "Negative regulation of T-cell receptor signalling by tyrosine protein
RT kinase p50csk.";
RL Nature 365:156-160(1993).
RN [13]
RP MUTAGENESIS.
RX MEDLINE=93133805; PubMed=8421674;
RA Carrera A.C., Alexandrov K., Roberts T.M.;
RT "The conserved lysine of the catalytic domain of protein kinases is
RT actively involved in the phosphotransfer reaction and not required for
RT anchoring ATP.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:442-446(1993).
RN [14]
RP PALMITOYLATION.
RX MEDLINE=94019312; PubMed=8413237;
RA Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;
RT "Palmitylation of an amino-terminal cysteine motif of protein tyrosine
RT kinases p56lck and p59fyn mediates interaction with glycosyl-
RT phosphatidylinositol-anchored proteins.";
RL Mol. Cell. Biol. 13:6385-6392(1993).
RN [15]
RP PALMITOYLATION.
RX MEDLINE=95071286; PubMed=7980442;
RA Koegl M., Zlatkine P., Ley S.C., Courtneidge S.A., Magee A.I.;
RT "Palmitoylation of multiple Src-family kinases at a homologous N-
RT terminal motif.";
RL Biochem. J. 303:749-753(1994).
RN [16]
RP INTERACTION WITH CBLB.
RX PubMed=10646608; DOI=10.1038/35003228;

```
RA   Bachmaier K., Krawczyk C., Kozieradzki I., Kong Y.-Y., Sasaki T.,
RA   Oliveira-dos-Santos A., Mariathasan S., Bouchard D., Wakeham A.,
RA   Itie A., Le J., Ohashi P.S., Sarosi I., Nishina H., Lipkowitz S.,
RA   Penninger J.M.;
RT   "Negative regulation of lymphocyte activation and autoimmunity by the
RT   molecular adaptor Cbl-b.";
RL   Nature 403:211-216(2000).
RN   [17]
RP   SUBCELLULAR LOCATION.
RX   PubMed=12218089;
RA   Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA   Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT   "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT   protein/phosphoprotein associated with glycolipid-enriched
RT   microdomains in lipid rafts in resting T cells.";
RL   J. Immunol. 169:2813-2817(2002).
RN   [18]
RP   PHOSPHORYLATION SITE TYR-393, AND MASS SPECTROMETRY.
RX   PubMed=15592455; DOI=10.1038/nbt1046;
RA   Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
RA   Zha X.-M., Polakiewicz R.D., Comb M.J.;
RT   "Immunoaffinity profiling of tyrosine phosphorylation in cancer

  Query Match             90.2%;  Score 37;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db        245 KLVERLGA 252


RESULT 10
LCK_SAISC
ID   LCK_SAISC      STANDARD;      PRT;   508 AA.
AC   Q95KR7;
DT   08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT   08-NOV-2005, sequence version 2.
DT   07-MAR-2006, entry version 26.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], ENZYME REGULATION, AND INTERACTION WITH
RP   SAIMIRINE HERPESVIRUS 2 TIP.
RC   TISSUE=T-cell;
RX   MEDLINE=21424508; PubMed=11533187;
RX   DOI=10.1128/JVI.75.19.9252-9261.2001;
RA   Greve T., Tamgueney G., Fleischer B., Fickenscher H., Broeker B.M.;
RT   "Downregulation of p56Lck tyrosine kinase activity in T cells of
RT   squirrel monkeys (Saimiri sciureus) correlates with the non-
RT   transforming and apathogenic properties of herpesvirus saimiri in its
RT   natural host.";
RL   J. Virol. 75:9252-9261(2001).
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways. Association of the TCR with a peptide
CC       antigen-bound MHC complex facilitates the interaction of CD4 and
CC       CD8 with MHC class II and class I molecules, respectively, and
CC       thereby recruits the associated LCK to the vicinity of the TCR/CD3
CC       complex. LCK then phosphorylates tyrosines residues within the
CC       immunoreceptor tyrosines-based activation motifs (ITAMs) in the
CC       cytoplasmic tails of the TCRgamma chains and CD3 subunits,
CC       initiating the TCR/CD3 signaling pathway. In addition, contributes
CC       to signaling by other receptor molecules. Associates directly with
CC       the cytoplasmic tail of CD2, and upon engagement of the CD2
CC       molecule, LCK undergoes hyperphosphorylation and activation. Also
CC       plays a role in the IL2 receptor-linked signaling pathway that
CC       controls T-cell proliferative response. Binding of IL2 to its
CC       receptor results in increased activity of LCK. Is expressed at all
CC       stages of thymocyte development and is required for the regulation
CC       of maturation events that are governed by both pre-TCR and mature
CC       alpha beta TCR (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- ENZYME REGULATION: Regulated by phosphatases.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also
CC       binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to
CC       other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds
CC       to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes
CC       through its SH3 domain and to the tyrosine phosphorylated form of
CC       KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.
CC       Interacts with phosphorylated LIME1. Interacts with CBLB (By
CC       similarity). Interacts with saimirine herpesvirus 2 TIP.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.
CC       Present in lipid rafts in an unactive form (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed specificaly in lymphoid cells.
CC   -!- DEVELOPMENTAL STAGE: Levels remain relatively constant throughout
CC       T-cell ontogeny.
CC   -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.
CC       Interaction is regulated by Ser-58 phosphorylation (By
CC       similarity).
CC   -!- PTM: Phosphorylated on Tyr-504 presumably by CSK. This
CC       phosphorylation downregulates catalytic activity. Phosphorylated
CC       on Tyr-393 either by itself or another kinase, leading to
CC       increased enzymatic activity.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   -!- CAUTION: LCK seems to be active in all vertebrates, except in
CC       squirrel monkey T-cells, in which it is inactivated. The reason
CC       seems to be that squirrel monkey are the natural host for
CC       Saimiriine herpesvirus 2, which is able to efficiently transform
CC       T-cells through a mecanism involving viral Tip/ host LCK
CC       interaction. Its inactivation may a mecanism that specificaly
CC       counteracts the transformation effects of viral Tip.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ277921; CAC38871.1; -; mRNA.
DR   HSSP; P06239; 1LKK.
DR   SMR; Q95KR7; 64-508.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
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KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    508       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088127.
FT   DOMAIN       60    120       SH3.
FT   DOMAIN      126    223       SH2.
FT   DOMAIN      244    497       Protein kinase.
FT   NP_BIND     250    258       ATP (By similarity).
FT   REGION        1     71       Interactions with CD4 and CD8 (By
FT                                similarity).
FT   ACT_SITE    363    363       Proton acceptor (By similarity).
FT   BINDING     272    272       ATP (By similarity).
FT   MOD_RES     393    393       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     504    504       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   508 AA;  58122 MW;  5088C64061853819 CRC64;

  Query Match             90.2%;  Score 37;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db        245 KLVERLGA 252


RESULT 11
Q7RTZ3_HUMAN
ID   Q7RTZ3_HUMAN   PRELIMINARY;   PRT;   509 AA.
AC   Q7RTZ3;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Protein tyrosine kinase.
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22289034; PubMed=12401726;
RA   Nervi S., Nicodeme S., Gartioux C., Atlan C., Lathrop M., Reviron D.,
RA   Naquet P., Matsuda F., Imbert J., Vialettes B.;
RT   "No association between lck gene polymorphisms and protein level in
RT   type 1 diabetes.";
RL   Diabetes 51:3326-3330(2002).
CC   -!- MISCELLANEOUS: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ third party annotation (TPA) entry.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BN000073; CAD55807.1; -; Genomic_DNA.
DR   HSSP; P06239; 1BHF.
DR   SMR; Q7RTZ3; 65-509.
DR   Ensembl; ENSG00000182866; Homo sapiens.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   509 AA;  58001 MW;  44BFF0D43FFB420D CRC64;

  Query Match             90.2%;  Score 37;  DB 2;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
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Qy          1 KLVERLGA 8
              ||||||||
Db        246 KLVERLGA 253


RESULT 12
Q95M32_9PRIM
ID   Q95M32_9PRIM   PRELIMINARY;   PRT;   509 AA.
AC   Q95M32;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Lck protein.
GN   Name=lck;
OS   Hylobates sp. (gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Hylobatidae; Hylobates.
OX   NCBI_TaxID=9581;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22031236; PubMed=12033791; DOI=10.1006/viro.2002.1381;
RA   Picard C., Greenway A., Holloway G., Olive D., Collette Y.;
RT   "Interaction with simian Hck tyrosine kinase reveals convergent
RT   evolution of the Nef protein from simian and human immunodeficiency
RT   viruses despite differential molecular surface usage.";
RL   Virology 295:320-327(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Picard C.;
RL   Thesis (2001), Department of Experimental Oncology laboratory, U.
CC   ---------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AJ320182; CAC44027.1; -; mRNA.
DR   HSSP; P06239; 1LCK.
DR   SMR; Q95M32; 65-509.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   509 AA;  57947 MW;  F1BFE5C237C8DB7E CRC64;

  Query Match             90.2%;  Score 37;  DB 2;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db        246 KLVERLGA 253


RESULT 13
Q3ZCM0_BOVIN
ID   Q3ZCM0_BOVIN   PRELIMINARY;   PRT;   509 AA.
AC   Q3ZCM0;
DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
DT   07-MAR-2006, entry version 6.
DE   Hypothetical protein MGC126900.
GN   Name=MGC126900;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Crossbred x Angus; TISSUE=Ileum;
RA   Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA   Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA   Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA   Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA   Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA   Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ----------------------------------------------------------------------
DR   EMBL; BC102046; AAI02047.1; -; mRNA.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   509 AA;  58116 MW;  CE0E80DCD6D0F2F8 CRC64;

  Query Match             90.2%;  Score 37;  DB 2;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||||||||
Db        246 KLVERLGA 253


RESULT 14
Q40AH8_9RHOB
ID   Q40AH8_9RHOB   PRELIMINARY;   PRT;   179 AA.
AC   Q40AH8;
DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
DT   21-FEB-2006, entry version 6.
DE   Adenine phosphoribosyl transferase (EC 2.4.2.7).
```

```
GN   ORFNames=JannDRAFT_1465;
OS   Jannaschia sp. CCS1.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC   Rhodobacteraceae; Jannaschia.
OX   NCBI_TaxID=290400;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CCS1;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome and assembly of Jannaschia sp. CCS1.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CCS1;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Jannaschia sp. CCS1.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- FUNCTION: Catalyzes a salvage reaction resulting in the formation
CC       of AMP, that is energically less costly than de novo synthesis (By
CC       similarity).
CC   -!- CATALYTIC ACTIVITY: AMP + diphosphate = adenine + 5-phospho-alpha-
CC       D-ribose 1-diphosphate.
CC   -!- PATHWAY: Purine salvage.
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC   -!- SIMILARITY: Belongs to the purine/pyrimidine
CC       phosphoribosyltransferase family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AAIG01000005; EAM66858.1; -; Genomic_DNA.
DR   GO; GO:0003999; F:adenine phosphoribosyltransferase activity; IEA.
DR   GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR   GO; GO:0006168; P:adenine salvage; IEA.
DR   GO; GO:0009116; P:nucleoside metabolism; IEA.
DR   GO; GO:0006166; P:purine ribonucleoside salvage; IEA.
DR   InterPro; IPR005764; Ade_phspho_trans.
DR   InterPro; IPR002375; Pr/py_rp_transf.
DR   InterPro; IPR000836; PRtransferase.
DR   Pfam; PF00156; Pribosyltran; 1.
DR   TIGRFAMs; TIGR01090; apt; 1.
DR   PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW   Glycosyltransferase; Purine salvage; Transferase.
SQ   SEQUENCE   179 AA;  19083 MW;  B3A502DE0F6813C2 CRC64;

  Query Match             87.8%;  Score 36;  DB 2;  Length 179;
  Best Local Similarity   87.5%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||:|||||
Db        136 KLIERLGA 143


RESULT 15
Q48EP0_PSE14
ID   Q48EP0_PSE14   PRELIMINARY;   PRT;   399 AA.
AC   Q48EP0;
DT   13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   13-SEP-2005, sequence version 1.
DT   21-FEB-2006, entry version 6.
DE   Beta-ketoadipyl CoA thiolase (EC 2.3.1.-).
GN   Name=pcaF; OrderedLocusNames=PSPPH_4017;
OS   Pseudomonas syringae pv. phaseolicola (strain 1448A / Race 6).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=264730;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=16159782; DOI=10.1128/JB.187.18.6488-6498.2005;
RA   Joardar V., Lindeberg M., Jackson R., Selengut J., Dodson R.,
RA   Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA   Gwinn Giglio M., Madupu R., Nelson W.C., Rosovitz M.J., Sullivan S.A.,
RA   Crabtree J., Creasy T., Davidsen T.M., Haft D.H., Zafar N., Zhou L.,
RA   Halpin R., Holley T., Khouri H.M., Feldblyum T.V., White O.,
RA   Fraser C.M., Chatterjee A.K., Cartinhour S., Schneider D.,
RA   Mansfield J., Collmer A., Buell R.;
RT   "Whole-genome sequence analysis of Pseudomonas syringae pv.
RT   phaseolicola 1448A reveals divergence among pathovars in genes
RT   involved in virulence and transposition.";
RL   J. Bacteriol. 187:6488-6498(2005).
CC   -!- SIMILARITY: Belongs to the thiolase family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; CP000058; AAZ33439.1; -; Genomic_DNA.
DR   GO; GO:0008415; F:acyltransferase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   InterPro; IPR012793; PcaF.
DR   InterPro; IPR002155; Thiolase.
DR   Pfam; PF02803; Thiolase_C; 1.
DR   Pfam; PF00108; Thiolase_N; 1.
DR   TIGRFAMs; TIGR01930; AcCoA-C-Actrans; 1.
DR   TIGRFAMs; TIGR02430; pcaF; 1.
DR   PROSITE; PS00098; THIOLASE_1; 1.
DR   PROSITE; PS00737; THIOLASE_2; 1.
DR   PROSITE; PS00099; THIOLASE_3; 1.
KW   Acyltransferase; Complete proteome; Transferase.
SQ   SEQUENCE   399 AA;  41771 MW;  7F275F72A9B1DE25 CRC64;

  Query Match             87.8%;  Score 36;  DB 2;  Length 399;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              |||||| |
Db        304 KLVERLGLA 312


RESULT 16
Q4ZP81_PSEU2
ID   Q4ZP81_PSEU2   PRELIMINARY;   PRT;   399 AA.
AC   Q4ZP81;
DT   07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT   07-JUN-2005, sequence version 1.
DT   21-FEB-2006, entry version 8.
DE   Thiolase (EC 2.3.1.16).
GN   OrderedLocusNames=Psyr_4011;
OS   Pseudomonas syringae pv. syringae (strain B728a).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=205918;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=16043691; DOI=10.1073/pnas.0504930102;
RA   Feil H., Feil W.S., Chain P., Larimer F., Dibartolo G., Copeland A.,
RA   Lykidis A., Trong S., Nolan M., Goltsman E., Thiel J., Malfatti S.,
RA   Loper J.E., Lapidus A., Detter J.C., Land M., Richardson P.M.,
RA   Kyrpides N.C., Ivanova N., Lindow S.E.;
RT   "Comparison of the complete genome sequences of Pseudomonas syringae
RT   pv. syringae B728a and pv. tomato DC3000.";
RL   Proc. Natl. Acad. Sci. U.S.A. 102:11064-11069(2005).
CC   -!- SIMILARITY: Belongs to the thiolase family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; CP000075; AAY39041.1; -; Genomic_DNA.
```

```
DR   GO; GO:0003988; F:acetyl-CoA C-acyltransferase activity; IEA.
DR   GO; GO:0008415; F:acyltransferase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   InterPro; IPR012793; PcaF.
DR   InterPro; IPR002155; Thiolase.
DR   PANTHER; PTHR18919; Thiolase; 1.
DR   Pfam; PF02803; Thiolase_C; 1.
DR   Pfam; PF00108; Thiolase_N; 1.
DR   TIGRFAMs; TIGR01930; AcCoA-C-Actrans; 1.
DR   TIGRFAMs; TIGR02430; pcaF; 1.
DR   PROSITE; PS00098; THIOLASE_1; 1.
DR   PROSITE; PS00737; THIOLASE_2; 1.
DR   PROSITE; PS00099; THIOLASE_3; 1.
KW   Acyltransferase; Complete proteome; Transferase.
SQ   SEQUENCE   399 AA;  41836 MW;  6293DF28605A901E CRC64;

  Query Match             87.8%;  Score 36;  DB 2;  Length 399;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              ||||||| |
Db        304 KLVERLGLA 312


RESULT 17
Q87X81_PSESM
ID   Q87X81_PSESM   PRELIMINARY;   PRT;   399 AA.
AC   Q87X81;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   21-FEB-2006, entry version 16.
DE   3-oxoadipyl-CoA thiolase.
GN   Name=catF; OrderedLocusNames=PSPTO4307; ORFNames=PSPTO_4307;
OS   Pseudomonas syringae pv. tomato.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=323;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=DC3000;
RX   MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA   Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
RA   Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA   Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA   Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA   Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA   Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
RA   Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
RA   Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA   Bender C.L., White O., Fraser C.M., Collmer A.;
RT   "The complete genome sequence of the Arabidopsis and tomato pathogen
RT   Pseudomonas syringae pv. tomato DC3000.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
CC   -!- SIMILARITY: Belongs to the thiolase family.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AE016853; AAO57758.1; -; Genomic_DNA.
DR   HSSP; P27796; 1AFW.
DR   TIGR; PSPTO4307; -.
DR   BioCyc; PSYR223283:PSPTO4307-MONOMER; -.
DR   GO; GO:0008415; F:acyltransferase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   InterPro; IPR012793; PcaF.
DR   InterPro; IPR002155; Thiolase.
DR   PANTHER; PTHR18919; Thiolase; 1.
DR   Pfam; PF02803; Thiolase_C; 1.
DR   Pfam; PF00108; Thiolase_N; 1.
DR   TIGRFAMs; TIGR01930; AcCoA-C-Actrans; 1.
DR   TIGRFAMs; TIGR02430; pcaF; 1.
DR   PROSITE; PS00098; THIOLASE_1; 1.
DR   PROSITE; PS00737; THIOLASE_2; 1.
DR   PROSITE; PS00099; THIOLASE_3; 1.
KW   Acyltransferase; Complete proteome; Transferase.
SQ   SEQUENCE   399 AA;  41798 MW;  348D9656362D4129 CRC64;

  Query Match             87.8%;  Score 36;  DB 2;  Length 399;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              ||||||| |
Db        304 KLVERLGLA 312


RESULT 18
Q4KH35_PSEF5
ID   Q4KH35_PSEF5   PRELIMINARY;   PRT;   400 AA.
AC   Q4KH35;
DT   02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   02-AUG-2005, sequence version 1.
DT   21-FEB-2006, entry version 6.
DE   Beta-ketoadipyl CoA thiolase (EC 2.3.1.-).
GN   Name=pcaF; OrderedLocusNames=PFL_1319;
OS   Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=220664;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15980861; DOI=10.1038/nbt1110;
RA   Paulsen I.T., Press C.M., Ravel J., Kobayashi D.Y., Myers G.S.A.,
RA   Mavrodi D.V., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA   Durkin A.S., Brinkac L.M., Daugherty S.C., Sullivan S.A.,
RA   Rosovitz M.J., Gwinn M.L., Zhou L., Schneider D.J., Cartinhour S.W.,
RA   Nelson W.C., Weidman J., Watkins K., Tran K., Khouri H., Pierson E.A.,
RA   Pierson L.S. III, Thomashow L.S., Loper J.E.;
RT   "Complete genome sequence of the plant commensal Pseudomonas
RT   fluorescens Pf-5.";
RL   Nat. Biotechnol. 23:873-878(2005).
CC   -!- SIMILARITY: Belongs to the thiolase family.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; CP000076; AAY90604.1; -; Genomic_DNA.
DR   GO; GO:0008415; F:acyltransferase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   InterPro; IPR012793; PcaF.
DR   InterPro; IPR002155; Thiolase.
DR   PANTHER; PTHR18919; Thiolase; 1.
DR   Pfam; PF02803; Thiolase_C; 1.
DR   Pfam; PF00108; Thiolase_N; 1.
DR   TIGRFAMs; TIGR01930; AcCoA-C-Actrans; 1.
DR   TIGRFAMs; TIGR02430; pcaF; 1.
DR   PROSITE; PS00098; THIOLASE_1; 1.
DR   PROSITE; PS00737; THIOLASE_2; 1.
DR   PROSITE; PS00099; THIOLASE_3; 1.
KW   Acyltransferase; Complete proteome; Transferase.
SQ   SEQUENCE   400 AA;  41641 MW;  97167FB14DC2639D CRC64;

  Query Match             87.8%;  Score 36;  DB 2;  Length 400;
  Best Local Similarity   77.8%;  Pred. No. 2.8e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              ||:|||| |
Db        304 KLIERLGVA 312


RESULT 19
Y906_CHLMU
ID   Y906_CHLMU     STANDARD;      PRT;   419 AA.
AC   Q9PJC5;
```

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DT   06-JUN-2003, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-2000, sequence version 1.
DT   07-MAR-2006, entry version 20.
DE   Hypothetical UPF0242 protein TC0906.
GN   OrderedLocusNames=TC0906;
OS   Chlamydia muridarum.
OC   Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX   NCBI_TaxID=83560;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=MoPn / Nigg;
RX   MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
RA   Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA   White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,
RA   Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
RA   Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
RA   McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
RT   "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT   pneumoniae AR39.";
RL   Nucleic Acids Res. 28:1397-1406(2000).
CC   -!- SIMILARITY: Belongs to the UPF0242 family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE002357; AAF39699.1; -; Genomic_DNA.
DR   PIR; A81651; A81651.
DR   GenomeReviews; AE002160_GR; TC0906.
DR   TIGR; TC0906; -.
DR   BioCyc; CMUR83560:TC0906-MONOMER; -.
DR   InterPro; IPR009623; UPF0242.
DR   Pfam; PF06785; UPF0242; 1.
KW   Complete proteome; Hypothetical protein.
FT   CHAIN         1    419       Hypothetical UPF0242 protein TC0906.
FT                                /FTId=PRO_0000216821.
SQ   SEQUENCE   419 AA;  48901 MW;  0B813066FEAC1E06 CRC64;

  Query Match             87.8%;  Score 36;  DB 1;  Length 419;
  Best Local Similarity   88.9%;  Pred. No. 2.9e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              |||||||  |
Db        125 KLVERLGQA 133


RESULT 20
Q44GN0_CHRSL
ID   Q44GN0_CHRSL   PRELIMINARY;   PRT;   467 AA.
AC   Q44GN0;
DT   13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   13-SEP-2005, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Phosphomannomutase (EC 5.4.2.8).
GN   ORFNames=CsalDRAFT_1845;
OS   Chromohalobacter salexigens DSM 3043.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
OC   Halomonadaceae; Chromohalobacter.
OX   NCBI_TaxID=290398;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=DSM 3043;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome assembly of Chromohalobacter
RT   salexigens DSM 3043.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=DSM 3043;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Chromohalobacter
RT   salexigens DSM 3043.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AAHZ01000008; EAM23978.1; -; Genomic_DNA.
DR   GO; GO:0016853; F:isomerase activity; IEA.
DR   GO; GO:0004615; F:phosphomannomutase activity; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   InterPro; IPR005841; PG/PMM_mutase.
DR   Pfam; PF02878; PGM_PMM_I; 1.
DR   Pfam; PF02879; PGM_PMM_II; 1.
DR   Pfam; PF02880; PGM_PMM_III; 1.
DR   Pfam; PF00408; PGM_PMM_IV; 1.
DR   PRINTS; PR00509; PGMPMM.
DR   PROSITE; PS00710; PGM_PMM; 1.
KW   Isomerase.
SQ   SEQUENCE   467 AA;  50576 MW;  7E4AE5CF0C52B4CA CRC64;

  Query Match             87.8%;  Score 36;  DB 2;  Length 467;
  Best Local Similarity   87.5%;  Pred. No. 3.2e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGA 8
              ||:|||||
Db        189 KLIERLGA 196


RESULT 21
Q4CPA3_TRYCR
ID   Q4CPA3_TRYCR   PRELIMINARY;   PRT;   508 AA.
AC   Q4CPA3;
DT   13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   13-SEP-2005, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Hypothetical protein (Fragment).
GN   ORFNames=Tc00.1047053510721.10;
OS   Trypanosoma cruzi.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
OC   Schizotrypanum.
OX   NCBI_TaxID=5693;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CL Brener;
RA   El-Sayed N.M.A., Myler P.J., Bartholomeu D.C., Nilsson D.,
RA   Aggarwal G., Tran A.-N., Ghedin E., Worthey E.A., Delcher A.L.,
RA   Blandin G., Westenberger S.J., Caler E., Cerqueira G.C., Branche C.,
RA   Haas B., Anapuma A., Arner E., Aslund L., Attipoe P., Bontempi E.,
RA   Bringaud F., Burton P., Cadag E., Campbell D.A., Carrington M.,
RA   Crabtree J., Darban H., da Silveira J.F., de Jong P., Edwards K.,
RA   Englund P.T., Fazelina G., Feldblyum T., Ferella M., Frasch A.C.,
RA   Gull K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,
RA   Kluge S., Koo H., Lacerda D., Levin M.J., Lorenzi H., Louie T.,
RA   Machado C.R., McCulloch R., McKenna A., Mizuno Y., Mottram J.C.,
RA   Nelson S., Ochaya S., Osoegawa K., Pai G., Parsons M., Pentony M.,
RA   Pettersson U., Pop M., Ramirez J.L., Rinta J., Robertson L.,
RA   Salzberg S.L., Sanchez D.O., Seyler A., Sharma R., Shetty J.,
RA   Simpson A.J., Sisk E., Tammi M.T., Tarleton R., Teixeira S.,
RA   Van Aken S., Vogt C., Ward P.N., Wickstead B., Wortman J., White O.,
RA   Fraser C.M., Stuart K.D., Andersson B.;
RT   "The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas'
RT   Disease.";
RL   Science 0:0-0(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CL Brener;
RA   El-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J.,
RA   Aggarwal G., Caler E., Renauld H., Worthey E.A., Hertz-Fowler C.,
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RA   Ghedin E., Peacock C., Bartholomeu D.C., Haas B.J., Tran A.-N.,
RA   Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A., Badger J.,
RA   Bringaud F., Cadag E., Carlton J.M., Cerqueira G.C., Creasy T.,
RA   Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivens A.C.,
RA   Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Peterson J.,
RA   Salzberg S.L., Shallom J., Silva J.C., Sundaram J., Westenberger S.,
RA   White O., Melville S.E., Donelson J.E., Andersson B., Stuart K.D.,
RA   Hall N.;
RT   "Comparative Genomics of Trypanosomatid Parasitic Protozoa.";
RL   Science 0:0-0(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CL Brener;
RA   El-Sayed N., Bartholomeu D., Haas B.;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
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CC   ---------------------------------------------------------------------
DR   EMBL; AAHK01002690; EAN82103.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   508 AA;  57226 MW;  8DCCBF424722CFC4 CRC64;

  Query Match             87.8%;  Score 36;  DB 2;  Length 508;
  Best Local Similarity   88.9%;  Pred. No. 3.4e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              ||||||| |
Db        409 KLVERLGRA 417


RESULT 22
Q4D4X4_TRYCR
ID   Q4D4X4_TRYCR   PRELIMINARY;   PRT;   597 AA.
AC   Q4D4X4;
DT   13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   13-SEP-2005, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Hypothetical protein.
GN   ORFNames=Tc00.1047053511909.10;
OS   Trypanosoma cruzi.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
OC   Schizotrypanum.
OX   NCBI_TaxID=5693;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CL Brener;
RA   El-Sayed N.M.A., Myler P.J., Bartholomeu D.C., Nilsson D.,
RA   Aggarwal G., Tran A.-N., Ghedin E., Worthey E.A., Delcher A.L.,
RA   Blandin G., Westenberger S.J., Caler E., Cerqueira G.C., Branche C.,
RA   Haas B., Anapuma A., Arner E., Aslund L., Attipoe P., Bontempi E.,
RA   Bringaud F., Burton P., Cadag E., Campbell D.A., Carrington M.,
RA   Crabtree J., Darban H., da Silveira J.F., de Jong P., Edwards K.,
RA   Englund P.T., Fazelina G., Feldblyum T., Ferella M., Frasch A.C.,
RA   Gull K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,
RA   Kluge S., Koo H., Lacerda D., Levin M.J., Lorenzi H., Louie T.,
RA   Machado C.R., McCulloch R., McKenna A., Mizuno Y., Mottram J.C.,
RA   Nelson S., Ochaya S., Osoegawa K., Pai G., Parsons M., Pentony M.,
RA   Pettersson U., Pop M., Ramirez J.L., Rinta J., Robertson L.,
RA   Salzberg S.L., Sanchez D.O., Seyler A., Sharma R., Shetty J.,
RA   Simpson A.J., Sisk E., Tammi M.T., Tarleton R., Teixeira S.,
RA   Van Aken S., Vogt C., Ward P.N., Wickstead B., Wortman J., White O.,
RA   Fraser C.M., Stuart K.D., Andersson B.;
RT   "The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas'
RT   Disease.";
RL   Science 0:0-0(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CL Brener;
RA   El-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J.,
RA   Aggarwal G., Caler E., Renauld H., Worthey E.A., Hertz-Fowler C.,
RA   Ghedin E., Peacock C., Bartholomeu D.C., Haas B.J., Tran A.-N.,
RA   Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A., Badger J.,
RA   Bringaud F., Cadag E., Carlton J.M., Cerqueira G.C., Creasy T.,
RA   Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivens A.C.,
RA   Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Peterson J.,
RA   Salzberg S.L., Shallom J., Silva J.C., Sundaram J., Westenberger S.,
RA   White O., Melville S.E., Donelson J.E., Andersson B., Stuart K.D.,
RA   Hall N.;
RT   "Comparative Genomics of Trypanosomatid Parasitic Protozoa.";
RL   Science 0:0-0(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CL Brener;
RA   El-Sayed N., Bartholomeu D., Haas B.;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AAHK01001015; EAN87570.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   597 AA;  67296 MW;  7D326736CF48E2B2 CRC64;

  Query Match             87.8%;  Score 36;  DB 2;  Length 597;
  Best Local Similarity   88.9%;  Pred. No. 3.9e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              ||||||| |
Db        498 KLVERLGRA 506


RESULT 23
Q4CY55_TRYCR
ID   Q4CY55_TRYCR   PRELIMINARY;   PRT;   791 AA.
AC   Q4CY55;
DT   13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   13-SEP-2005, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Hypothetical protein.
GN   ORFNames=Tc00.1047053510317.20;
OS   Trypanosoma cruzi.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
OC   Schizotrypanum.
OX   NCBI_TaxID=5693;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CL Brener;
RA   El-Sayed N.M.A., Myler P.J., Bartholomeu D.C., Nilsson D.,
RA   Aggarwal G., Tran A.-N., Ghedin E., Worthey E.A., Delcher A.L.,
RA   Blandin G., Westenberger S.J., Caler E., Cerqueira G.C., Branche C.,
RA   Haas B., Anapuma A., Arner E., Aslund L., Attipoe P., Bontempi E.,
RA   Bringaud F., Burton P., Cadag E., Campbell D.A., Carrington M.,
RA   Crabtree J., Darban H., da Silveira J.F., de Jong P., Edwards K.,
RA   Englund P.T., Fazelina G., Feldblyum T., Ferella M., Frasch A.C.,
RA   Gull K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,
RA   Kluge S., Koo H., Lacerda D., Levin M.J., Lorenzi H., Louie T.,
RA   Machado C.R., McCulloch R., McKenna A., Mizuno Y., Mottram J.C.,
RA   Nelson S., Ochaya S., Osoegawa K., Pai G., Parsons M., Pentony M.,
RA   Pettersson U., Pop M., Ramirez J.L., Rinta J., Robertson L.,
RA   Salzberg S.L., Sanchez D.O., Seyler A., Sharma R., Shetty J.,
RA   Simpson A.J., Sisk E., Tammi M.T., Tarleton R., Teixeira S.,
RA   Van Aken S., Vogt C., Ward P.N., Wickstead B., Wortman J., White O.,
RA   Fraser C.M., Stuart K.D., Andersson B.;
RT   "The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas'
RT   Disease.";
RL   Science 0:0-0(2005).
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RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CL Brener;
RA   El-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J.,
RA   Aggarwal G., Caler E., Renauld H., Worthey E.A., Hertz-Fowler C.,
RA   Ghedin E., Peacock C., Bartholomeu D.C., Haas B.J., Tran A.-N.,
RA   Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A., Badger J.,
RA   Bringaud F., Cadag E., Carlton J.M., Cerqueira G.C., Creasy T.,
RA   Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivens A.C.,
RA   Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Peterson J.,
RA   Salzberg S.L., Shallom J., Silva J.C., Sundaram J., Westenberger S.,
RA   White O., Melville S.E., Donelson J.E., Andersson B., Stuart K.D.,
RA   Hall N.;
RT   "Comparative Genomics of Trypanosomatid Parasitic Protozoa.";
RL   Science 0:0-0(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CL Brener;
RA   El-Sayed N., Bartholomeu D., Haas B.;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AAHK01001480; EAN85204.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   791 AA;  88644 MW;  355C4DEAA84FF882 CRC64;

  Query Match             87.8%;  Score 36;  DB 2;  Length 791;
  Best Local Similarity   77.8%;  Pred. No. 4.9e+02;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              ||:||:|||
Db        483 KLLERIGAA 491


RESULT 24
Q3S4S6_9MICC
ID   Q3S4S6_9MICC   PRELIMINARY;   PRT;   160 AA.
AC   Q3S4S6;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Putative Rieske non-heme iron oxygenase alpha subunit (Fragment).
OS   Arthrobacter sp. 3YC3.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Micrococcineae; Micrococcaceae; Arthrobacter.
OX   NCBI_TaxID=342827;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=3YC3;
RA   Witzig R., Junca H., Hecht H.-J., Pieper D.H.;
RT   "Toluene/biphenyl dioxygenase gene diversity in benzene-polluted
RT   soils: the environmental importance of the isopropylbenzene
RT   dioxygenase branch.";
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; DQ166965; AAZ95272.1; -; Genomic_DNA.
DR   GO; GO:0005506; F:iron ion binding; IEA.
DR   GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR001663; Rng_hydr_dOase_A.
DR   Pfam; PF00848; Ring_hydroxyl_A; 1.
FT   NON_TER       1      1
FT   NON_TER     160    160
SQ   SEQUENCE   160 AA;  17556 MW;  59A1206CBB88DDBA CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 160;
  Best Local Similarity   77.8%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              | :||||||
Db         81 KAIERLGAA 89


RESULT 25
Q2LC71_9MICC
ID   Q2LC71_9MICC   PRELIMINARY;   PRT;   252 AA.
AC   Q2LC71;
DT   21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT   21-FEB-2006, sequence version 1.
DT   21-FEB-2006, entry version 1.
DE   Putative Rieske non-heme iron oxygenase alpha subunit (Fragment).
OS   Arthrobacter sp. 3YC3.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Micrococcineae; Micrococcaceae; Arthrobacter.
OX   NCBI_TaxID=342827;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=3YC3;
RA   Witzig R., Junca H., Hecht H.-J., Pieper D.H.;
RT   "Toluene/biphenyl dioxygenase gene diversity in benzene-polluted
RT   soils: the environmental importance of the isopropylbenzene
RT   dioxygenase branch.";
RL   Submitted (DEC-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; DQ336942; ABC66291.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     252    252
SQ   SEQUENCE   252 AA;  27999 MW;  79BB168D2164D0D9 CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 252;
  Best Local Similarity   77.8%;  Pred. No. 3e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              | :||||||
Db        173 KAIERLGAA 181


RESULT 26
Q84H43_ALCDF
ID   Q84H43_ALCDF   PRELIMINARY;   PRT;   322 AA.
AC   Q84H43;
DT   01-JUN-2003, integrated into UniPrctKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Phosphotransacetylase.
GN   Name=pta;
OS   Alcaligenes defragrans.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Alcaligenaceae; Alcaligenes.
OX   NCBI_TaxID=75697;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NKNTAU;
RX   MEDLINE=22399517; PubMed=12358600; DOI=10.1042/BJ20021455;
RA   Ruff J., Denger K., Cook A.M.;
RT   "Sulphoacetaldehyde acetyltransferase yields acetyl phosphate:
RT   purification from Alcaligenes defragrans and gene clusters in taurine
RT   degradation.";
RL   Biochem. J. 369:275-285(2003).
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```

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CC   ---------------------------------------------------------------------
DR   EMBL; AY134843; AAN08490.1; -; Genomic_DNA.
DR   GO; GO:0016407; F:acetyltransferase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR012147; P_Ac_Bu_trans.
DR   InterPro; IPR004614; PhpActrans.
DR   InterPro; IPR002505; PTA_PTB.
DR   Pfam; PF01515; PTA_PTB; 1.
DR   PIRSF; PIRSF000428; P_Ac_trans; 1.
DR   TIGRFAMs; TIGR00651; pta; 1.
SQ   SEQUENCE   322 AA;  34524 MW;  229F7BD43B2965A6 CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 322;
  Best Local Similarity   88.9%;  Pred. No. 3.7e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              ||||||| |
Db        273 KLVERLGHA 281


RESULT 27
Q7MVH9_PORGI
ID   Q7MVH9_PORGI   PRELIMINARY;   PRT;   336 AA.
AC   Q7MVH9;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Phosphotransacetylase.
GN   Name=pta; OrderedLocusNames=PG1082; ORFNames=PG_1082;
OS   Porphyromonas gingivalis (Bacteroides gingivalis).
OC   Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC   Porphyromonadaceae; Porphyromonas.
OX   NCBI_TaxID=837;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=W83;
RX   MEDLINE=22829867; PubMed=12949112;
RX   DOI=10.1128/JB.185.18.5591-5601.2003;
RA   Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA   Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA   Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA   Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA   Dewhirst F.E., Fraser C.M.;
RT   "Complete genome sequence of the oral pathogenic bacterium
RT   Porphyromonas gingivalis strain W83.";
RL   J. Bacteriol. 185:5591-5601(2003).
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CC   ---------------------------------------------------------------------
DR   EMBL; AE015924; AAQ66196.1; -; Genomic_DNA.
DR   TIGR; PG1082; -.
DR   BioCyc; PGIN242619:PG1082-MONOMER; -.
DR   GO; GO:0016407; F:acetyltransferase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR012147; P_Ac_Bu_trans.
DR   InterPro; IPR004614; PhpActrans.
DR   InterPro; IPR002505; PTA_PTB.
DR   Pfam; PF01515; PTA_PTB; 1.
DR   PIRSF; PIRSF000428; P_Ac_trans; 1.
DR   TIGRFAMs; TIGR00651; pta; 1.
KW   Complete proteome.
SQ   SEQUENCE   336 AA;  35784 MW;  AD41C5B42B743DBF CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 336;
  Best Local Similarity   88.9%;  Pred. No. 3.8e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
              ||||||| |
Db        285 KLVERLGHA 293


RESULT 28
Q8BUD6_MOUSE
ID   Q8BUD6_MOUSE   PRELIMINARY;   PRT;   341 AA.
AC   Q8BUD6;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   10 days lactation, adult female mammary gland cDNA, RIKEN full-length
DE   enriched library, clone:D730033M24 product:similar to BCG INDUCED
DE   INTEGRAL MEMBRANE PROTEIN BIGMO-103 (UP-REGULATED BY BCG-CWS).
GN   Name=Slc39a8;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
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RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AK085740; BAC39526.1; -; mRNA.
DR   MGI; MGI:1914797; Slc39a8.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0046873; F:metal ion transporter activity; IEA.
DR   GO; GO:0030001; P:metal ion transport; IEA.
DR   InterPro; IPR003689; ZIP.
DR   Pfam; PF02535; Zip; 1.
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Db         50 RLLERLGAA 58


RESULT 29
Q4ZZL7_PSEU2
ID   Q4ZZL7_PSEU2   PRELIMINARY;   PRT;   393 AA.
AC   Q4ZZL7;
DT   07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT   07-JUN-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Hypothetical protein.
GN   OrderedLocusNames=Psyr_0333;
OS   Pseudomonas syringae pv. syringae (strain B728a).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=205918;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=16043691; DOI=10.1073/pnas.0504930102;
RA   Feil H., Feil W.S., Chain P., Larimer F., Dibartolo G., Copeland A.,
RA   Lykidis A., Trong S., Nolan M., Goltsman E., Thiel J., Malfatti S.,
RA   Loper J.E., Lapidus A., Detter J.C., Land M., Richardson P.M.,
RA   Kyrpides N.C., Ivanova N., Lindow S.E.;
RT   "Comparison of the complete genome sequences of Pseudomonas syringae
RT   pv. syringae B728a and pv. tomato DC3000.";
RL   Proc. Natl. Acad. Sci. U.S.A. 102:11064-11069(2005).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
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DR   EMBL; CP000075; AAY35405.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   393 AA;  43107 MW;  A784AC3154C1721E CRC64;

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  Best Local Similarity   77.8%;  Pred. No. 4.3e+02;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        337 RLVERLGAS 345


RESULT 30
Q5FVQ0_RAT
ID   Q5FVQ0_RAT     PRELIMINARY;   PRT;   462 AA.
AC   Q5FVQ0;
DT   01-MAR-2005, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2005, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Solute carrier family 39 (Metal ion transporter), member 8
DE   (Predicted).
GN   Name=Slc39a8;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RG   NIH MGC Project;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC089844; AAH89844.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0046873; F:metal ion transporter activity; IEA.
DR   GO; GO:0030001; P:metal ion transport; IEA.
DR   InterPro; IPR003689; ZIP.
DR   Pfam; PF02535; Zip; 1.
SQ   SEQUENCE   462 AA;  50171 MW;  954467170797180F CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 462;
  Best Local Similarity   77.8%;  Pred. No. 4.9e+02;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVERLGAA 9
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Db         50 RLLERLGAA 58


Search completed: June 29, 2006, 09:29:31
Job time : 110.942 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:14 ; Search time 97.5904 Seconds
(without alignments)
46.851 Million cell updates/sec

Title: US-10-062-257A-13
Perfect score: 49
Sequence: 1 QLQHQRLVRL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	100.0	10	4	AAB73129	Aab73129 Tumour an
2	49	100.0	11	5	ABJ04236	Abj04236 Kinase-as
3	49	100.0	11	6	ABU54283	Abu54283 Lck (K057
4	49	100.0	18	5	ABJ04174	Abj04174 Kinase-as
5	49	100.0	18	6	ABU54221	Abu54221 Lck prote
6	49	100.0	259	2	AAY43955	Aay43955 Human pro
7	49	100.0	263	8	ADR88385	Adr88385 LCK tyros
8	49	100.0	265	7	ABR56203	Abr56203 Mutant Ly
9	49	100.0	271	7	ABR56204	Abr56204 Mutant Ly
10	49	100.0	279	9	ADY85449	Ady85449 Catalytic
11	49	100.0	346	3	AAY76750	Aay76750 Human pro
12	49	100.0	346	4	AAE06208	Aae06208 Human pro
13	49	100.0	346	5	ABB84435	Abb84435 Human pro
14	49	100.0	355	8	ABM82980	Abm82980 Human dia
15	49	100.0	363	6	ABR59690	Abr59690 Human p56
16	49	100.0	363	8	ADP48375	Adp48375 Human lym
17	49	100.0	417	2	AAR14201	Aar14201 (Beta-gal
18	49	100.0	437	5	ABG79672	Abg79672 Tumour in
19	49	100.0	458	7	ADC99048	Adc99048 Human KPP
20	49	100.0	508	3	AAB37700	Aab37700 Human lym
21	49	100.0	508	7	ADE58802	Ade58802 Human Pro
22	49	100.0	508	7	ADE58799	Ade58799 Human Pro
23	49	100.0	508	7	ADF45072	Adf45072 Human kin
24	49	100.0	508	7	ADL34479	Adl34479 Human lym
25	49	100.0	508	8	ADS88148	Ads88148 Human pro
26	49	100.0	509	3	AAY49420	Aay49420 PKA subst
27	49	100.0	509	6	ABR58699	Abr58699 Human can
28	49	100.0	509	7	ABR56202	Abr56202 Human Lym
29	49	100.0	509	7	ADE40449	Ade40449 Human pro
30	49	100.0	509	8	ADL22907	Adl22907 Human MP2
31	49	100.0	509	8	ADP12458	Adp12458 Protein e
32	49	100.0	509	8	ADP48374	Adp48374 Human lym
33	49	100.0	509	9	ADZ51107	Adz51107 Amino aci
34	49	100.0	509	9	AEA35921	Aea35921 Human Lck
35	49	100.0	539	8	ABM82981	Abm82981 Human dia
36	49	100.0	539	8	ABM82982	Abm82982 Human dia
37	49	100.0	551	4	ABG22264	Abg22264 Novel hum
38	49	100.0	567	5	ABG79673	Abg79673 Tumour in
39	43	87.8	259	2	AAY43956	Aay43956 Mouse pro
40	41	83.7	454	8	ADH48367	Adh48367 Human KPP
41	41	83.7	503	8	ADQ97514	Adq97514 Mouse can
42	41	83.7	504	7	ADF45035	Adf45035 Human kin
43	41	83.7	505	8	ADK70442	Adk70442 Respirato
44	41	83.7	505	8	ADL22909	Adl22909 Human MP2
45	41	83.7	505	8	ADQ97517	Adq97517 Human can
46	41	83.7	505	9	AEA35922	Aea35922 Human Blk
47	41	83.7	558	8	ADQ97519	Adq97519 Human can
48	40	81.6	9	4	AAB73158	Aab73158 Tumour an
49	39	79.6	10	9	AEC97262	Aec97262 HLA-A03-b
50	39	79.6	260	2	AAY29671	Aay29671 Human src
51	39	79.6	260	4	AAU08733	Aau08733 Src-famil
52	39	79.6	496	2	AAY29668	Aay29668 Human src
53	39	79.6	496	4	AAU08734	Aau08734 Xenopus l
54	39	79.6	496	4	AAU08730	Aau08730 Xenopus l
55	39	79.6	496	4	AAU08735	Aau08735 Xenopus l
56	39	79.6	1237	3	AAY81609	Aay81609 Streptoco
57	39	79.6	4365	6	ABU02252	Abu02252 S. pneumo
58	38	77.6	550	3	AAG33471	Aag33471 Arabidops
59	38	77.6	575	8	ADT56884	Adt56884 Plant pol
60	38	77.6	601	3	AAG33470	Aag33470 Arabidops
61	38	77.6	608	3	AAG33469	Aag33469 Arabidops
62	37	75.5	111	4	AAU59093	Aau59093 Propionib
63	37	75.5	111	6	ABM55612	Abm55612 Propionib
64	37	75.5	327	6	ABP79308	Abp79308 N. gonorr
65	37	75.5	335	3	AAB51795	Aab51795 Human sec
66	37	75.5	685	7	ABM86145	Abm86145 Rice abio
67	37	75.5	696	7	ABM86276	Abm86276 Rice abio
68	36	73.5	11	5	ABJ04234	Abj04234 Kinase-as
69	36	73.5	11	6	ABU54281	Abu54281 Lyn (K055
70	36	73.5	18	5	ABJ04172	Abj04172 Kinase-as
71	36	73.5	18	6	ABU54219	Abu54219 Lyn prote
72	36	73.5	18	7	ABW00283	Abw00283 Lyn-kinas
73	36	73.5	18	8	ADQ91826	Adq91826 Human pro
74	36	73.5	126	4	AAM80055	Aam80055 Human pro
75	36	73.5	162	4	ADM20141	Adm20141 Protein e
76	36	73.5	215	8	ABM83910	Abm83910 Human dia
77	36	73.5	215	8	ABM83906	Abm83906 Human dia
78	36	73.5	251	9	ADY52569	Ady52569 Human onc
79	36	73.5	260	2	AAY43954	Aay43954 Human pro
80	36	73.5	271	8	ADX77981	Adx77981 Plant ful
81	36	73.5	272	8	ADX89611	Adx89611 Plant ful
82	36	73.5	288	8	ADY12890	Ady12890 Plant ful
83	36	73.5	302	9	AEB27101	Aeb27101 Pinus rad
84	36	73.5	303	8	ABM83905	Abm83905 Human dia
85	36	73.5	303	8	ABM83907	Abm83907 Human dia
86	36	73.5	303	8	ABM83903	Abm83903 Human dia
87	36	73.5	303	8	ABM83904	Abm83904 Human dia
88	36	73.5	303	8	ABM83909	Abm83909 Human dia
89	36	73.5	303	8	ABM83908	Abm83908 Human dia
90	36	73.5	315	3	AAG58897	Aag58897 Arabidops
91	36	73.5	318	8	ADY24656	Ady24656 Plant ful
92	36	73.5	320	3	AAB50379	Aab50379 Human unc
93	36	73.5	320	3	AAG60193	Aag60193 Arabidops
94	36	73.5	320	4	AAM93892	Aam93892 Human pol
95	36	73.5	320	4	AAM79071	Aam79071 Human pro
96	36	73.5	320	4	AAM39031	Aam39031 Human pol

97	36	73.5	320	5	ABP65101	Abp65101 Hypoxia-i
98	36	73.5	320	7	ABU62101	Abu62101 Human mit
99	36	73.5	320	7	ADD18694	Add18694 Human dis
100	36	73.5	320	7	ABM85767	Abm85767 Human pro

ALIGNMENTS

RESULT 1
AAB73129
ID AAB73129 standard; peptide; 10 AA.
XX
AC AAB73129;
XX
DT 09-MAY-2001 (first entry)
XX
DE Tumour antigen peptide #13.
XX
KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS Homo sapiens.
XX
PN WO200111044-A1.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-JP005220.
XX
PR 05-AUG-1999; 99JP-00222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT polynucleotides encoding them for treatment of cancer.
XX
PS Claim 1; Page 70; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 1 QLQHQRLVRL 10

RESULT 2
ABJ04236
ID ABJ04236 standard; peptide; 11 AA.
XX
AC ABJ04236;
XX
DT 24-OCT-2002 (first entry)
XX
DE Kinase-associated signal transduction modulating peptide 69.
XX
KW Kinase-associated signal transduction; diabetes; cancer; obesity;
KW restenosis; bone healing; alopecia; osteoporosis;
KW neurodegenerative disease; autoimmune disease; inflammation;
KW atherosclerosis; skin disorder; central nervous system disease;
KW inflammatory disorder; autoimmune disease; cardiovascular disease.
XX
OS Unidentified.
XX
PN WO200248336-A2.
XX
PD 20-JUN-2002.
XX
PF 11-DEC-2001; 2001WO-US047443.
XX
PR 11-DEC-2000; 2000US-00734520.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.
XX
PI Ben-Sasson S;
XX
DR WPI; 2002-583508/62.
XX
PT Identifying compounds for modulating kinase-associated signal
PT transduction and treating cancer, by synthesizing compounds having short
PT sequences identical to native sequences appearing in specific region of a
PT kinase.
XX
PS Claim 14; Fig 3; 143pp; English.
XX
CC The invention comprises a method for identifying compounds for the
CC modulation of kinase-associated signal transduction. The invention also
CC comprises a number of peptides which modulate kinase-associated signal
CC transduction. The method of the invention is useful for identifying
CC compounds for the modulation of kinase-associated signal transduction.
CC The kinase-associated signal transduction modulating peptides of the
CC invention are useful for treating: diabetes; cancer; obesity; bone
CC healing; alopecia; osteoporosis; neurodegenerative disease; autoimmune
CC disease; inflammation; restenosis; atherosclerosis; skin disorders;
CC central nervous system disease; inflammatory disorders; autoimmune
CC diseases; and cardiovascular diseases. The peptides ABJ04168 - ABJ04300
CC represent the kinase-associated signal transduction modulating peptides
CC of the invention
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 49; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 2 QLQHQRLVRL 11

RESULT 3
ABU54283
ID ABU54283 standard; peptide; 11 AA.
XX
AC ABU54283;
XX
DT 06-MAR-2003 (first entry)
XX
DE Lck (K057A100) protein kinase A-region peptide.
XX
KW Kinase; A-region; PKA; PKA-Calpha; signal transduction; inhibitor;
KW stimulator; proliferation; differentiation; oncogenesis; cancer;
KW arteriosclerosis; psoriasis; septic shock; therapeutic; diabetes;
KW obesity; restenosis; tissue remodeling; bone healing; alopecia; scarring;
KW osteoporosis; neurodegenerative disease; autoimmune disease;
KW inflammation; atherosclerosis; skin disorder; central nervous system;
KW cardiovascular disease; dermatological; neuroprotective;
KW immunosuppressive.
XX
OS Unidentified.
OS Synthetic.
XX
PN US2002137141-A1.

XX
PD 26-SEP-2002.
XX
PF 11-DEC-2001; 2001US-00012034.
XX
PR 11-DEC-2000; 2000US-00734520.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Ben-Sasson S;
XX
DR WPI; 2003-110601/10.
XX
PT Identifying candidate compounds for the modulation of kinase-associated
PT signal transduction, useful for treating diabetes, cancer, obesity,
PT osteoporosis, autoimmune disorders, atherosclerosis and cardiovascular
PT diseases.
XX
PS Claim 14; Fig 3; 79pp; English.
XX
CC The invention discloses compounds, or variants of them, and methods for
CC identifying and synthesising the candidate compounds which comprise a
CC peptide region in the protein kinase A-region (PKA). This region is
CC determined by aligning catalytic subunits of the kinase and PKA-Calpha
CC and determining the sequence of the kinase corresponding to positions 92-
CC 109 of PKA-Calpha. The capacity of the compound to modulate the signal
CC transduction associated with the kinase (as a kinase inhibitor or
CC stimulator) is then determined. Protein kinases mediate signal
CC transduction in a wide variety of cellular events, such as cell
CC proliferation, differentiation, oncogenesis and immune/inflammatory
CC responses. Enhanced stimulation can lead to proliferative diseases, such
CC as cancer, arteriosclerosis, psoriasis and septic shock. The methods and
CC compositions are useful for detecting A-region ligands and for treating a
CC disease where a therapeutically beneficial effect may be evident by the
CC modulation of a signal transduction associated with a kinase, where the
CC kinase from which the A-region is determined is the kinase associated
CC with the signal transduction, and where the disease is diabetes, cancer,
CC obesity, restenosis, tissue remodeling including improved bone healing,
CC prevention of alopecia, reduced scarring, osteoporosis, neurodegenerative
CC disease, autoimmune disease, inflammation, atherosclerosis, skin
CC disorders, diseases of the central nervous system and cardiovascular
CC diseases. The sequences presented in ABU54215-ABU54336 are the A-region
CC peptides disclosed in the invention which are N-myristylated and C-
CC amidated
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 49; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 2 QLQHQRLVRL 11

RESULT 4
ABJ04174
ID ABJ04174 standard; peptide; 18 AA.
XX
AC ABJ04174;
XX
DT 24-OCT-2002 (first entry)
XX
DE Kinase-associated signal transduction modulating peptide 7.
XX
KW Kinase-associated signal transduction; diabetes; cancer; obesity;
KW restenosis; bone healing; alopecia; osteoporosis;
KW neurodegenerative disease; autoimmune disease; inflammation;
KW atherosclerosis; skin disorder; central nervous system disease;
KW inflammatory disorder; autoimmune disease; cardiovascular disease.
XX
OS Unidentified.

XX
PN WO200248336-A2.
XX
PD 20-JUN-2002.
XX
PF 11-DEC-2001; 2001WO-US047443.
XX
PR 11-DEC-2000; 2000US-00734520.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS) YISSUM RES & DEV CO.
XX
PI Ben-Sasson S;
XX
DR WPI; 2002-583508/62.
XX
PT Identifying compounds for modulating kinase-associated signal
PT transduction and treating cancer, by synthesizing compounds having short
PT sequences identical to native sequences appearing in specific region of a
PT kinase.
XX
PS Claim 18; Fig 1; 143pp; English.
XX
CC The invention comprises a method for identifying compounds for the
CC modulation of kinase-associated signal transduction. The invention also
CC comprises a number of peptides which modulate kinase-associated signal
CC transduction. The method of the invention is useful for identifying
CC compounds for the modulation of kinase-associated signal transduction.
CC The kinase-associated signal transduction modulating peptides of the
CC invention are useful for treating: diabetes; cancer; obesity; bone
CC healing; alopecia; osteoporosis; neurodegenerative disease; autoimmune
CC disease; inflammation; restenosis; atherosclerosis; skin disorders;
CC central nervous system disease; inflammatory disorders; autoimmune
CC diseases; and cardiovascular diseases. The peptides ABJ04168 - ABJ04300
CC represent the kinase-associated signal transduction modulating peptides
CC of the invention
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 49; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 6 QLQHQRLVRL 15

RESULT 5
ABU54221
ID ABU54221 standard; peptide; 18 AA.
XX
AC ABU54221;
XX
DT 06-MAR-2003 (first entry)
XX
DE Lck protein kinase A-region peptide.
XX
KW Kinase; A-region; PKA; PKA-Calpha; signal transduction; inhibitor;
KW stimulator; proliferation; differentiation; oncogenesis; cancer;
KW arteriosclerosis; psoriasis; septic shock; therapeutic; diabetes;
KW obesity; restenosis; tissue remodeling; bone healing; alopecia; scarring;
KW osteoporosis; neurodegenerative disease; autoimmune disease;
KW inflammation; atherosclerosis; skin disorder; central nervous system;
KW cardiovascular disease; dermatological; neuroprotective;
KW immunosuppressive.
XX
OS Unidentified.
OS Synthetic.
XX
PN US2002137141-A1.
XX
PD 26-SEP-2002.

XX
PF 11-DEC-2001; 2001US-00012034.
XX
PR 11-DEC-2000; 2000US-00734520.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Ben-Sasson S;
XX
DR WPI; 2003-110601/10.
XX
PT Identifying candidate compounds for the modulation of kinase-associated
PT signal transduction, useful for treating diabetes, cancer, obesity,
PT osteoporosis, autoimmune disorders, atherosclerosis and cardiovascular
PT diseases.
XX
PS Claim 18; Fig 1; 79pp; English.
XX
CC The invention discloses compounds, or variants of them, and methods for
CC identifying and synthesising the candidate compounds which comprise a
CC peptide region in the protein kinase A-region (PKA). This region is
CC determined by aligning catalytic subunits of the kinase and PKA-Calpha
CC and determining the sequence of the kinase corresponding to positions 92-
CC 109 of PKA-Calpha. The capacity of the compound to modulate the signal
CC transduction associated with the kinase (as a kinase inhibitor or
CC stimulator) is then determined. Protein kinases mediate signal
CC transduction in a wide variety of cellular events, such as cell
CC proliferation, differentiation, oncogenesis and immune/inflammatory
CC responses. Enhanced stimulation can lead to proliferative diseases, such
CC as cancer, arteriosclerosis, psoriasis and septic shock. The methods and
CC compositions are useful for detecting A-region ligands and for treating a
CC disease where a therapeutically beneficial effect may be evident by the
CC modulation of a signal transduction associated with a kinase, where the
CC kinase from which the A-region is determined is the kinase associated
CC with the signal transduction, and where the disease is diabetes, cancer,
CC obesity, restenosis, tissue remodeling including improved bone healing,
CC prevention of alopecia, reduced scarring, osteoporosis, neurodegenerative
CC disease, autoimmune disease, inflammation, atherosclerosis, skin
CC disorders, diseases of the central nervous system and cardiovascular
CC diseases. The sequences presented in ABU54215-ABU54336 are the A-region
CC peptides disclosed in the invention which are N-myristylated and C-
CC amidated
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 49; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 6 QLQHQRLVRL 15

RESULT 6
AAY43955
ID AAY43955 standard; protein; 259 AA.
XX
AC AAY43955;
XX
DT 21-DEC-1999 (first entry)
XX
DE Human protein kinase #15.
XX
KW Prediction; secondary structure; alignment; evolutionary conservation;
KW homology; periodicity; co-variation analysis; antigenic site;
KW site directed mutagenesis; interaction.
XX
OS Homo sapiens.
XX
PN US5958784-A.
XX
PD 28-SEP-1999.
XX
PF 25-MAR-1992; 92US-00857224.
XX
PR 25-MAR-1992; 92US-00857224.
XX
PA (BENN/) BENNER S A.
XX
PI Benner SA;
XX
DR WPI; 1999-570766/48.
XX
PT Predicting the folded structure of proteins.
XX
PS Disclosure; Col 253-256; 113pp; English.
XX
CC Sequences AAY43902-Y44015 represent proteins used in a novel method of
CC predicting the folded structure of proteins, by aligning sequences of
CC homologous proteins and using patterns of evolutionarily conserved and
CC varied sequences to assign positions. Positions in the alignment are
CC assigned to the surface or inside of the folded structure, active sites,
CC and parsing segments. Secondary structural units are assigned by
CC identifying periodicity in the assignments, and assembled into globular
CC form using distance constraints imposed by disulfide bridges, active site
CC assignments and co-variation analysis. The predicted secondary structures
CC are useful for identifying antigenic sites on a protein molecule, as
CC guides for site directed mutagenesis studies, and for understanding the
CC interaction of a protein with other molecules
XX
SQ Sequence 259 AA;

Query Match 100.0%; Score 49; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 52 QLQHQRLVRL 61

RESULT 7
ADR88385
ID ADR88385 standard; protein; 263 AA.
XX
AC ADR88385;
XX
DT 18-NOV-2004 (first entry)
XX
DE LCK tyrosine kinase protein.
XX
KW Molecular scaffold; nuclear hormone receptor; TNF receptor;
KW G-protein coupled receptor; methyl transferase; ligase;
KW LCK tyrosine kinase; enzyme.
XX
OS Unidentified.
XX
PN US2004171062-A1.
XX
PD 02-SEP-2004.
XX
PF 28-FEB-2003; 2003US-00377268.
XX
PR 28-FEB-2002; 2002US-0360651P.
PR 16-SEP-2002; 2002US-0411398P.
PR 20-SEP-2002; 2002US-0412341P.
PR 02-JAN-2003; 2003US-0437929P.
XX
PA (PLEX-) PLEXXIKON INC.
XX
PI Hirth K, Milburn MV;
XX
DR WPI; 2004-642017/62.
XX
PT Designing a ligand binding to a target molecule, comprises identifying as

PT molecular scaffolds compounds binding to members of a molecular family,
PT detecting orientation of scaffolds at a binding site of target, and
PT synthesizing ligand.
XX
PS Disclosure; SEQ ID NO 24; 186pp; English.
XX
CC The present invention relates to a method of designing a ligand binding
CC to a target molecule. The method involves identifying as molecular
CC scaffolds compounds binding to members of a molecular family, detecting
CC orientation of scaffolds at a binding site of target, and synthesising
CC ligand. The invention is useful for designing drug products and for
CC designing ligand binding to target molecules such as nuclear hormone
CC receptors, TNF receptors, G-protein coupled receptors, methyl
CC transferases, ligases, etc. The present sequence is the LCK tyrosine
CC kinase protein. This sequence is used to illustrate the method of
CC invention.
XX
SQ Sequence 263 AA;

Query Match 100.0%; Score 49; DB 8; Length 263;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 56 QLQHQRLVRL 65

RESULT 8
ABR56203
ID ABR56203 standard; protein; 265 AA.
XX
AC ABR56203;
XX
DT 18-DEC-2003 (first entry)
XX
DE Mutant Lymphocyte Cell Kinase, Lck, fragment (237-501, D364N).
XX
KW Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW Src-family protein tyrosine kinase; T-cell; immune response; mutein;
KW mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 128
FT /note= "Wild-type D substituted with N. This position is
FT 364 in the full-length sequence (see ABR56202 for the
FT wild-type full length sequence"
FT Modified-site 158
FT /note= "Phosphorylation site"
XX
PN WO2003020880-A2.
XX
PD 13-MAR-2003.
XX
PF 02-AUG-2002; 2002WO-US024546.
XX
PR 03-AUG-2001; 2001US-0310051P.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Borhani DW, Calderwood D, Dixon RW, Hirst GC, Hrnciar P, Loew A;
PI Leung A, Ritter K;
XX
DR WPI; 2003-300872/29.
XX
PT New crystalline polypeptide comprising ligand binding domain or catalytic
PT domain of Lck protein, for determining three-dimensional structure of
PT catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS Claim 12; Fig 2; 994pp; English.
XX
CC The present invention relates to a crystalline polypeptide (I),
CC comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC in T-cells and plays an essential role in immune response. (I) is useful
CC for identifying a compound which is an inhibitor of human Lck protein.
CC The present sequence is a mutated fragment of the human Lck sequence,
CC which approximately comprises the catalytic domain
XX
SQ Sequence 265 AA;

Query Match 100.0%; Score 49; DB 7; Length 265;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 58 QLQHQRLVRL 67

RESULT 9
ABR56204
ID ABR56204 standard; protein; 271 AA.
XX
AC ABR56204;
XX
DT 18-DEC-2003 (first entry)
XX
DE Mutant Lymphocyte Cell Kinase, Lck, fragment (231-501, D364N).
XX
KW Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW Src-family protein tyrosine kinase; T-cell; immune response; mutein;
KW mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 134
FT /note= "Wild-type D substituted with N. This position is
FT 364 in the full-length sequence (see ABR56202 for the
FT wild-type full length sequence"
FT Modified-site 164
FT /note= "Phosphorylation site"
XX
PN WO2003020880-A2.
XX
PD 13-MAR-2003.
XX
PF 02-AUG-2002; 2002WO-US024546.
XX
PR 03-AUG-2001; 2001US-0310051P.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Borhani DW, Calderwood D, Dixon RW, Hirst GC, Hrnciar P, Loew A;
PI Leung A, Ritter K;
XX
DR WPI; 2003-300872/29.
XX
PT New crystalline polypeptide comprising ligand binding domain or catalytic
PT domain of Lck protein, for determining three-dimensional structure of
PT catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS Example 1; Fig 3; 994pp; English.
XX
CC The present invention relates to a crystalline polypeptide (I),
CC comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC in T-cells and plays an essential role in immune response. (I) is useful
CC for identifying a compound which is an inhibitor of human Lck protein.
CC The present sequence is a mutated fragment of the human Lck sequence,
CC which approximately comprises the catalytic domain

XX
SQ Sequence 271 AA;

Query Match 100.0%; Score 49; DB 7; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 64 QLQHQRLVRL 73

RESULT 10
ADY85449
ID ADY85449 standard; protein; 279 AA.
XX
AC ADY85449;
XX
DT 16-JUN-2005 (first entry)
XX
DE Catalytic domain of PIM kinase-like protein LCK.
XX
KW Kinase; protein co-ordinate data; protein structure; cancer; cytostatic;
KW neoplasm; inflammation; antiinflammatory.
XX
OS Unidentified.
XX
PN WO2005028624-A2.
XX
PD 31-MAR-2005.
XX
PF 15-SEP-2004; 2004WO-US030360.
XX
PR 15-SEP-2003; 2003US-0503277P.
XX
PA (PLEX-) PLEXXIKON INC.
XX
PI Artis DR, Bremer RE, Gillette SJ, Hurt CR, Ibrahim PL;
PI Zuckerman RL;
XX
DR WPI; 2005-273155/28.
XX
PT New scaffold library used for identifying and developing ligands for
PT protein kinases and treating kinase associated disorders e.g. cancer,
PT comprises set of compounds comprising N-heterocyclic compounds.
XX
PS Disclosure; Page 170-174; 236pp; English.
XX
CC The invention relates to a new kinase scaffold library comprises at least
CC 1 set of compounds, each set comprising at least 1 N-heterocyclic
CC compound of formulae (I)-(VII) given in the specification. Also included
CC are a system for fitting compounds in binding sites of protein kinases
CC (comprising an electronic kinase scaffold, and a scaffold library
CC comprising at least 1 collection of electronic representations of (I)-
CC (VII), where the scaffold library is embedded in a computer device and
CC the electronic representations of the compounds can be selectively
CC retrieved and functionally connected with computer software adapted to
CC fit electronic representations of compounds in an electronic
CC representation of a binding site of a kinase), obtaining improved ligands
CC binding to a protein kinase (which comprises determining if a derivative
CC of (I)-(VII) binds to the kinase with greater affinity and/or specificity
CC than (I)-(VII)), developing ligands specific for a particular kinase
CC (which comprises determining if a derivative of (I)-(VII) that binds to
CC kinases has greater for specificity for the particular kinase than (I)-
CC (VII), developing ligands binding to a kinase (which comprises
CC determining the orientation of at least 1 molecular scaffold of (I)-(VII)
CC in co-crystals with the kinase, identifying chemical structures of the
CC scaffolds, that, when modified, change the binding affinity and/or
CC specificity between the scaffold and kinase and synthesizing a ligand in
CC which at least 1 chemical structure of the scaffold is modified),
CC developing ligands with increased specificity on a kinase (which
CC comprises testing a derivative of a kinase binding compound (I)-(VII) for
CC increased specificity on the kinase), identifying a ligand binding to a
CC kinase (which comprises determining if a derivative compound including a
CC core structure (I)-(VII) binds to the kinase with changed binding
CC affinity and/or specificity), a co-crystal of a kinase and a binding
CC compound (I)-(VII), preparation of co-crystals of Pim-1 with (I)-(VII),
CC identifying potential kinase binding compounds (which comprises fitting
CC electronic representations of (I)-(VII) in an electronic representation
CC of a kinase binding site), attaching a kinase binding compound to an
CC attachment component (which comprises identifying energetically allowed
CC sites for attachment of the component on a kinase binding compound (I)-
CC (VII) and attaching the compound or derivative to the attachment
CC component at the allowed site), modified compounds (comprising (I)-(VIII)
CC with an attached linker group, and developing a ligand for a kinase
CC comprising conserved residues matching at least on of Pim-1 residues 49,
CC 52, 67, 121, 128 and 186 which comprises determining if (I)-(VII) binds
CC to the kinase. The kinases comprise Pim-1, Pyk2, c-Abl, Her2, cMet,
CC vascular endothelial growth factor receptor, endothelial growth factor
CC receptor, cKit, Pkcbeta, p38, Cdk2, Akt or Gsk3beta. The kinase scaffold
CC library is used for identifying and developing ligands binding to
CC kinases, for modulating kinase activity and for treating disease
CC condition associated with abnormal kinase activity e.g. cancer,
CC inflammatory disease. The method identifies improved ligands binding to a
CC kinase resulting in ligands having high affinity and specificity towards
CC kinase. The co-crystals of kinase and the binding compound are of
CC sufficient size and quality to allow structural determination of at least
CC 2 Angstroms. The present sequence is a catalytic domain from a PIM-like
CC kinase. NOTE: It is not clear whether the sequence as presented
CC represents a continuous amino acid sequence.
XX
SQ Sequence 279 AA;

Query Match 100.0%; Score 49; DB 9; Length 279;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 64 QLQHQRLVRL 73

RESULT 11
AAY76750
ID AAY76750 standard; protein; 346 AA.
XX
AC AAY76750;
XX
DT 17-APR-2000 (first entry)
XX
DE Human protein kinase homologue, PKH-3.
XX
KW Protein kinase homologue; human; PKH; diagnosis; therapy; cancer; AIDS;
KW autoimmune disorder; inflammatory disorder; reproductive defect; asthma;
KW diabetes mellitus; infertility; ovulatory defect; endometriosis;
KW polycystic ovary syndrome.
XX
OS Homo sapiens.
XX
PN US6013455-A.
XX
PD 11-JAN-2000.
XX
PF 15-OCT-1998; 98US-00173581.
XX
PR 15-OCT-1998; 98US-00173581.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Hillman JL, Yue H, Yang YT, Corley NC, Gorgone GA, Azimzai Y;
PI Lu DAM, Bandman O, Guegler KJ;
XX
DR WPI; 2000-136321/12.
DR N-PSDB; AAZ86794.
XX
PT Nucleic acids encoding a human protein kinase homolog useful for

PT preventing, diagnosing and treating cancer, autoimmune/inflammatory
PT disorders and reproductive defects.
XX
PS Claim 1; Col 47-50; 38pp; English.
XX
CC This sequence represents a human protein kinase homolog (PKH) of the
CC invention. The PKH sequences may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate PKH expression such
CC as cancers, autoimmune/inflammatory disorders and reproductive defects.
CC They may be used to treat disorders associated with decreased PKH
CC expression such as cancers (e.g. lymphoma, melanoma and cancers of the
CC breast lung and prostate), autoimmune/inflammatory disorders (e.g. AIDS,
CC asthma and diabetes mellitus), and reproductive defects (e.g.
CC infertility, ovulatory defects, endometriosis and polycystic ovary
CC syndrome). The DNA may be administered to treat diseases by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC PKH by expressing inactive proteins or to supplement the patients own
CC production of PKH polypeptides. Additionally, the DNA may be used to
CC produce PKH, according to standard recombinant DNA methodology, by
CC inserting the nucleic acids into a host cell and culturing the cell to
CC express the protein. Conversely, antisense nucleic acid molecules may be
CC administered to down regulate PKH expression by binding with the cells
CC own PKH genes and preventing their expression. The DNA, and antisense
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acid sequences in samples,
CC and hence which patients may be in need of restorative therapy. They may
CC also be used to study the expression and function of PKH polypeptides and
CC their role in metabolism. The PKH polypeptides may be used as antigens in
CC the production of antibodies against PKH and in assays to identify
CC modulators (agonists and antagonists) of PKH expression and activity. The
CC anti-PKH antibodies and PKH antagonists may also be used to down regulate
CC PKH expression and activity. The anti-PKH antibodies may also be used as
CC diagnostic agents for detecting the presence of PKH polypeptides in
CC samples
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 49; DB 3; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 131 QLQHQRLVRL 140

RESULT 12
AAE06208
ID AAE06208 standard; protein; 346 AA.
XX
AC AAE06208;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human protein kinase homolog-3 (PKH-3).
XX
KW Human; protein kinase homolog-3; PKH-3; cytostatic; protein therapy;
KW vaccine; immunosuppressive; antisclerotic; antiabortive; adenocarcinoma;
KW Acquired Immune deficiency Syndrome; AIDS; melanoma; cancer; bone; liver;
KW breast; autoimmune disorder; multiple sclerosis; drug screening; anaemia;
KW Crohn's disease; ectopic pregnancy; tubal disease; inflammatory disorder;
KW reproductive disorder; polycystic ovary syndrome; asthma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 125. .333
FT /note= "Signature sequence"
XX
PN US6264947-B1.
XX
PD 24-JUL-2001.
XX
PF 20-OCT-1999; 99US-00420915.
XX
PR 15-OCT-1998; 98US-00173581.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Bandman O, Tang YT, Hillman JL, Yue H, Guegler KJ, Corley NC;
PI Gorgone GA, Azimzai Y, Lu DAM;
XX
DR WPI; 2001-450728/48.
DR N-PSDB; AAD11845.
XX
PT Human protein kinase proteins and homologs, useful for preventing,
PT diagnosing and treating cancers, autoimmune/inflammatory disorders and
PT reproductive disorders.
XX
PS Claim 1; Col 47-50; 38pp; English.
XX
CC The present sequence is human protein kinase homolog-3 (PKH-3). Human
CC protein kinase homologs (PKH) and their cDNA molecules are used in the
CC prevention, diagnosis and treatment of diseases associated with increased
CC or decreased expression of PKH. Examples of such disorders include,
CC cancer (e.g. adenocarcinoma, melanoma and bone, breast and liver cancer),
CC autoimmune/inflammatory disorders (e.g. Acquired Immune deficiency
CC Syndrome (AIDS), anaemia, asthma, Crohn's disease and multiple sclerosis)
CC and reproductive disorders (e.g. tubal disease, ectopic pregnancy and
CC polycystic ovary syndrome). PKH, its catalytic or immunogenic fragment
CC are used for screening libraries of compounds in any of the drug
CC screening techniques. PKH nucleic acids are used to generate
CC hybridisation probes useful in mapping the naturally occurring genomic
CC sequences. PKH are also used as antigens in the production of antibodies
CC against protein kinases (PK) and in assays to identify modulators of PK
CC expression and activity. PKH is also used in protein therapy
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 49; DB 4; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 131 QLQHQRLVRL 140

RESULT 13
ABB84435
ID ABB84435 standard; protein; 346 AA.
XX
AC ABB84435;
XX
DT 08-NOV-2002 (first entry)
XX
DE Human protein kinase homologue from clone 507669.
XX
KW Protein kinase homologue; PKH; cytostatic; immunosuppressive; antifungal;
KW antiinflammatory; antiallergic; antiasthmatic; antianaemic; antidiabetic;
KW antiarteriosclerotic; antithyroid; dermatological; nephrotropic; human;
KW antigout; thyromimetic; nootropic; osteopathic; antiarthritic; allergy;
KW antirheumatic; ophthalmological; antiulcer; antiviral; antibacterial;
KW antiprotozoal; antiparasitic; antihelmintic; ankylosing spondylitis;
KW acquired immunodeficiency syndrome; AIDS; Addison's disease; amyloidosis;
KW adult respiratory distress syndrome; anaemia; asthma; atherosclerosis;
KW autoimmune haemolytic anaemia; autoimmune thyroiditis; bronchitis;
KW cholecystitis; contact dermatitis; Crohn's disease; atopic dermatitis;
KW dermatomyositis; diabetes mellitus; emphysema; atrophic gastritis; gout;
KW glomerulonephritis; Goodpasture's syndrome; Graves' disease; psoriasis;
KW Hashimoto's thyroiditis; hypereosinophilia; irritable bowel syndrome;
KW multiple sclerosis; myasthenia gravis; myocardial inflammation; uveitis;
KW pericardial inflammation; osteoarthritis; osteoporosis; pancreatitis;
KW polymyositis; Reiter's syndrome; rheumatoid arthritis; scleroderma; SLE;
KW Sjogren's syndrome; systemic lupus erythematosus; systemic sclerosis;
KW thrombocytopenic purpura; ulcerative colitis; Werner syndrome; infection;

KW haemodialysis; extracorporeal circulation; infertility; tubal disease;
KW ovulatory defect; endometriosis; oestrous; menstrual cycle; gene therapy;
KW uterine fibroid; autoimmune disorder; polycystic ovary syndrome; enzyme;
KW ovarian hyperstimulation syndrome; ectopic pregnancy; teratogenesis;
KW cancer.
XX
OS Homo sapiens.
XX
PN US2002081290-A1.
XX
PD 27-JUN-2002.
XX
PF 30-MAY-2001; 2001US-00870962.
XX
PR 15-OCT-1998; 98US-00173581.
PR 20-OCT-1999; 99US-00420915.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Tang YT, Hillman JL, Yue H, Guegler KJ, Corley NC;
PI Gorgone GA, Azimzai Y, Lu DAM;
XX
DR WPI; 2002-655433/70.
DR N-PSDB; ABQ76288.
XX
PT Nucleic acids encoding a human protein kinase homolog useful for
PT preventing, diagnosing and treating cancer, autoimmune/inflammatory
PT disorders and reproductive defects.
XX
PS Claim 47; Page 27; 43pp; English.
XX
CC This invention describes a novel protein kinase homologue (PKH)
CC polypeptides which have cytostatic, immunosuppressive, antiinflammatory,
CC antiallergic, antiasthmatic, antianaemic, antiarteriosclerotic,
CC antithyroid, dermatological, antidiabetic, nephrotropic, antigout,
CC thyromimetic, nootropic, osteopathic, antiarthritic, antirheumatic,
CC ophthalmological, antiulcer, antiviral, antibacterial, antifungal,
CC antiprotozoal, antiparasitic and antihelmintic activity. The polypeptide
CC is used for treating a disease or condition associated with decreased
CC expression of functional PKH. The polypeptide is used to screen for
CC agonists and antagonists of PKH which can also be used in disease
CC treatment. The polypeptide and polynucleotide are used for treating
CC acquired immunodeficiency syndrome (AIDS), Addison's disease, adult
CC respiratory distress syndrome, allergies, ankylosing spondylitis,
CC amyloidosis, anaemia, asthma, atherosclerosis, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, bronchitis, cholecystitis, cancer,
CC contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis,
CC diabetes mellitus, emphysema, atrophic gastritis, glomerulonephritis,
CC Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis,
CC hypereosinophilia, irritable bowel syndrome, multiple sclerosis,
CC myasthenia gravis, myocardial or pericardial inflammation,
CC osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis,
CC Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's syndrome,
CC systemic lupus erythematosus (SLE), systemic sclerosis, thrombocytopenic
CC purpura, ulcerative colitis, uveitis, Werner syndrome, complications of
CC cancer, haemodialysis, and extracorporeal circulation, viral, bacterial,
CC fungal, parasitic, protozoal, and helminthic infections, infertility,
CC including tubal disease, ovulatory defects, and endometriosis,
CC disruptions of the oestrous cycle, disruptions of the menstrual cycle,
CC polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial
CC and ovarian tumours, uterine fibroids, autoimmune disorders, ectopic
CC pregnancies, and teratogenesis. The polypeptides of the invention can be
CC used for gene therapy. This sequence represents a PKH from clone ID
CC 507669 isolated from TMLR3DT02, a library constructed using RNA isolated
CC from non-adherent peripheral blood mononuclear cells collected from a
CC pool of male and female donors
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 49; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 131 QLQHQRLVRL 140

RESULT 14
ABM82980
ID ABM82980 standard; protein; 355 AA.
XX
AC ABM82980;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3229.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN41632.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 355 AA;

Query Match 100.0%; Score 49; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10

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                ||||||||||
Db        140 QLQHQRLVRL 149


RESULT 15
ABR59690
ID   ABR59690 standard; protein; 363 AA.
XX
AC   ABR59690;
XX
DT   25-JUL-2003  (first entry)
XX
DE   Human p56lck.
XX
KW   Human; T lymphocyte activation; T-cell; A-raf-1; TCPTP/PTPN2; asthma;
KW   immunosuppressive; antiasthmatic; antiallergic; antiinflammatory;
KW   lymphocyte activation; lymphocyte migration; cytokine production;
KW   cell surface marker expression; antibody production; apoptosis; allergy;
KW   antibody proliferation; antibody differentiation; hypersensitivity;
KW   graft versus host disease; inflammation; p56lck.
XX
OS   Homo sapiens.
XX
PN   WO2003029277-A2.
XX
PD   10-APR-2003.
XX
PF   02-OCT-2002; 2002WO-US031618.
XX
PR   03-OCT-2001; 2001US-0327212P.
XX
PA   (RIGE-) RIGEL PHARM INC.
XX
PI   Chu P,  Li C,  Liao XC,  Masuda E,  Pardo J,  Zhao H;
XX
DR   WPI; 2003-363276/34.
DR   N-PSDB; ACC81082.
XX
PT   Identifying a compound that modulates T lymphocyte activation, useful for
PT   monitoring changes in cell surface marker expression, comprises
PT   contacting a T cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with
PT   a compound.
XX
PS   Disclosure; Page 64; 126pp; English.
XX
CC   The invention relates to a novel method for identifying a compound that
CC   modulates T lymphocyte activation. The method comprises contacting a T
CC   cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with a compound,
CC   where the A-raf- 1 or TCPTP/PTPN2 polypeptide is encoded by a nucleic
CC   acid that hybridises to a nucleic acid encoding a polypeptide having a
CC   sequence selected from two 606-amino acid sequence and a 415-amino acid
CC   sequence given in the specification. The method of the invention has
CC   immunosuppressive, antiasthmatic, antiallergic, and antiinflammatory
CC   activity. The method is useful for identifying compounds that modulate
CC   lymphocyte activation and migration, and for monitoring changes in cell
CC   surface marker expression, cytokine production, antibody production,
CC   proliferation and differentiation, and apoptosis, using either cell lines
CC   or primary cells. The A-raf- 1 or TCPTP/PTPN2 proteins may be used as
CC   drug targets for compounds that suppress or activate lymphocyte
CC   activation and migration, e.g. for the treatment of diseases in which
CC   modulation of the immune response is desired such as delayed type
CC   hypersensitivity reactions, asthma, allergies, graft versus host disease,
CC   and acute and chronic inflammation. Modulators of lymphocyte activation
CC   are useful for treating disorders related T and B cell activation and
CC   migration. The present sequence is used in the exemplification of the
CC   invention
XX
SQ   Sequence 363 AA;

  Query Match             100.0%;  Score 49;  DB 6;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
              ||||||||||
Db        294 QLQHQRLVRL 303


RESULT 16
ADP48375
ID   ADP48375 standard; protein; 363 AA.
XX
AC   ADP48375;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human lymphocyte specific tyrosine kinase (Lck) polypeptide #2.
XX
KW   Human; lymphocyte specific tyrosine kinase; Lck;
KW   antisense oligonucleotide; phosphorothioate linkage;
KW   2'-O-methoxyethyl sugar moiety; 5-methylcytosine;
KW   hyperproliferative disorder; cancer; cytostatic; enzyme.
XX
OS   Homo sapiens.
XX
PN   US2004116365-A1.
XX
PD   17-JUN-2004.
XX
PF   10-DEC-2002; 2002US-00316515.
XX
PR   10-DEC-2002; 2002US-00316515.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Borchers AH,  Freier SM;
XX
DR   WPI; 2004-498280/47.
DR   N-PSDB; ADP48372.
XX
PT   New antisense oligonucleotide compounds, useful for diagnosing,
PT   preventing and/or treating diseases or conditions associated with
PT   aberrant expression or activity of Lck, such as hyperproliferative
PT   disorders.
XX
PS   Example 17; SEQ ID NO 75; 40pp; English.
XX
CC   The invention relates to a compound targeted to a nucleic acid molecule
CC   encoding the human lymphocyte specific tyrosine kinase (Lck) polypeptide.
CC   The compound is an antisense oligonucleotide that specifically hybridises
CC   with the nucleic acid and inhibits expression of the polypeptide. The
CC   antisense oligonucleotide comprises at least one modified internucleoside
CC   linkage i.e. a phosphorothioate linkage, at least one modified sugar
CC   moiety, preferably a 2'-O-methoxyethyl sugar moiety, or at least one
CC   modified nucleobase comprising a 5-methylcytosine. The antisense
CC   compounds are useful for modulating the expression of the human Lck
CC   polypeptide and in preparation of a composition for treating
CC   hyperproliferative disorders, e.g. cancer. This sequence represents a
CC   human Lck polypeptide of the invention.
XX
SQ   Sequence 363 AA;

  Query Match             100.0%;  Score 49;  DB 8;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
              ||||||||||
Db        294 QLQHQRLVRL 303


RESULT 17
AAR14201
ID   AAR14201 standard; protein; 417 AA.
XX
AC   AAR14201;
```

XX
DT 13-DEC-1991 (first entry)
XX
DE (Beta-galactosidase N-terminal)-(lck gene prod.) fusion protein.
XX
KW Multi-cloning site.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .26
FT /note= "beta-galactosidase fragment"
FT Region 27. .417
FT /note= "lck gene polypeptide"
XX
PN JP03201994-A.
XX
PD 03-SEP-1991.
XX
PF 28-DEC-1989; 89JP-00338268.
XX
PR 28-DEC-1989; 89JP-00338268.
XX
PA (TOKU) TOKUYAMA SODA KK.
XX
DR WPI; 1991-300980/41.
DR N-PSDB; AAQ14201.
XX
PT Fused polypeptide - has amino acid sequence of beta-galactosidase with a
PT LCK gene conjugated to the N-terminal via DNA having multi-cloning site.
XX
PS Claim 1; Fig 4,2; 15pp; Japanese.
XX
CC The sequence consists of the N-terminal amino acids of the beta-
CC galactosidase gene fused with the lck gene. It is produced by E.coli
CC transformed with a recombinant vector (see AAQ13983). It is useful for
CC producing an antibody specifically immunoreactive with only a lck gene-
CC derived polypeptide in T cells. The antibody may recognise lck gene-
CC derived polypeptides in human cells
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 49; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 202 QLQHQRLVRL 211

RESULT 18
ABG79672
ID ABG79672 standard; protein; 437 AA.
XX
AC ABG79672;
XX
DT 15-NOV-2002 (first entry)
XX
DE Tumour involved gene (TIG) splice variant protein, NV-3.
XX
KW Human; splice variant; tumour-involved gene; TIG;
KW pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;
KW endothelial cell; cell differentiation; cell proliferation; apoptosis;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US2002086384-A1.
XX
PD 04-JUL-2002.
XX
PF 13-MAR-2001; 2001US-00805020.
XX
PR 14-MAR-2000; 2000IL-00135402.
PR 16-MAY-2000; 2000IL-00136154.
XX
PA (LEVI/) LEVINE Z.
PA (DAVI/) DAVID A.
PA (ROMA/) ROMANO C.
PA (BERN/) BERNSTEIN J.
XX
PI Levine Z, David A, Romano C, Bernstein J;
XX
DR WPI; 2002-635679/68.
DR N-PSDB; ABS65202.
XX
PT Novel nucleic acid sequence, which is an alternative splicing variant of
PT tumor involved genes, useful for detecting cancer, predisposition to
PT cancer, for evaluating cancer state and in gene therapy for treating
PT cancer.
XX
PS Claim 4; Page 68-69; 180pp; English.
XX
CC The invention discloses isolated human nucleic acid alternative splicing
CC variants that are all tumour-involved genes (TIGs). The nucleic acids and
CC polypeptides are useful for determining the level of a nucleic acid or
CC polypeptide in a biological sample, for detecting a variant nucleic acid
CC or polypeptide sequence in a biological sample, for determining the level
CC of variant nucleic acid or polypeptide sequences in a biological sample
CC and for determining the ratio between the level of variant sequence in a
CC first biological sample and the level of the original sequence from which
CC the variant has been varied by alternative splicing in a second
CC biological sample and for raising antibodies. A pharmaceutical
CC composition comprising a carrier and the nucleic acid, is useful for
CC treating diseases (e.g. cancer) that can be ameliorated or cured by
CC increasing or decreasing the level of the encoded protein. The nucleic
CC acids are also useful for diagnostic purposes, especially for detecting
CC cancer or a predisposition to cancer, for evaluating the state or
CC aggressiveness of cancer disease, in basic research, for understanding
CC the physiological function of the original TIG, in targeting or
CC developing pharmaceuticals, for distinguishing various stages in the life
CC cycle of the same type of cells which may be helpful for the development
CC of pharmaceuticals for various cancer stages in which cell cycle is non-
CC normal, for determining mutations in tumour-involved genes and in gene
CC therapy. The polypeptides are useful for identifying compounds capable of
CC binding to the variant product and modulating its activity and for
CC modulating endothelial differentiation and proliferation, as well as to
CC modulate apoptosis either ex vivo or in vivo. The sequences presented in
CC ABG796700-ABG79705 are the new variants (NV) 1-36 proteins of the TIGs
CC disclosed
XX
SQ Sequence 437 AA;

Query Match 100.0%; Score 49; DB 5; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 294 QLQHQRLVRL 303

RESULT 19
ADC99048
ID ADC99048 standard; protein; 458 AA.
XX
AC ADC99048;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human KPP protein - SEQ ID 1.
XX
KW anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian;
KW nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;

KW antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;
KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;
KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;
KW virucide; protozoacide; fungicide; kinase; phosphatase; KPP;
KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;
KW cancer; developmental; mental retardation; neurological;
KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;
KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
KW helminthic infection; transgenic; gene therapy; human; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003033680-A2.
XX
PD 24-APR-2003.
XX
PF 17-OCT-2002; 2002WO-US033723.
XX
PR 19-OCT-2001; 2001US-0345474P.
PR 02-NOV-2001; 2001US-0343910P.
PR 13-NOV-2001; 2001US-0333098P.
PR 16-NOV-2001; 2001US-0332424P.
PR 30-NOV-2001; 2001US-0334288P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;
PI Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;
PI Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;
PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;
PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;
PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;
PI Zebarjadian Y;
XX
DR WPI; 2003-403214/38.
DR N-PSDB; ADC99100.
XX
PT New human kinases and phosphatases and polynucleotides, useful for
PT diagnosing, treating or preventing autoimmune or inflammatory disorders
PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
PT cancer or hepatitis.
XX
PS Claim 1; SEQ ID NO 1; 424pp; English.
XX
CC The invention relates to a novel isolated polypeptide which is a human
CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,
CC agonists and antagonists are useful for diagnosing, treating or
CC preventing cell proliferative disorders such as atherosclerosis,
CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental
CC retardation, neurological disorders including Alzheimer's disease and
CC Parkinson's disease, autoimmune and inflammatory disorders such as
CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,
CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the
CC polynucleotides encoding KPP may be useful for creating transgenic
CC animals to model human disease, as well as during gene therapy
CC procedures. The current sequence is that of the human KPP protein of the
CC invention.
XX
SQ Sequence 458 AA;

```
  Query Match             100.0%;  Score 49;  DB 7;  Length 458;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
              ||||||||||
Db        243 QLQHQRLVRL 252
```

RESULT 20
AAB37700
ID AAB37700 standard; protein; 508 AA.
XX
AC AAB37700;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human lymphocyte kinase.
XX
KW Human; lymphocyte kinase; protein co-ordinate data; lck; crystal.
XX
OS Homo sapiens.
XX
PN WO200070030-A1.
XX
PD 23-NOV-2000.
XX
PF 19-MAY-2000; 2000WO-US013881.
XX
PR 19-MAY-1999; 99US-0134965P.
XX
PA (KINE-) KINETIX PHARM INC.
XX
PI Zhu X;
XX
DR WPI; 2000-687708/67.
XX
PT Crystal of a protein-ligand complex for identifying kinase inhibitors,
PT comprises a truncated lymphocyte kinase and a ligand, and diffracts X-
PT rays to determine atomic coordinates at a resolution greater than 5
PT angstroms.
XX
PS Claim 1; Page 434-5; 438pp; English.
XX
CC The present invention relates to a crystal of a protein-ligand complex
CC comprising a truncated lymphocyte kinase (lck) and a ligand. The crystal
CC diffracts X-rays so that the atomic coordinates of the protein-ligand
CC complex can be determined to a resolution of greater than 5.0 Angstroms.
CC The truncated lck used in the present invention comprises the globular
CC core of the corresponding full-length lck. The present sequence is the
CC full-length human lck protein. The crystal of the present invention may
CC be used to identify kinase inhibitors in screening assays, in drug
CC screening and drug design processes, to design, select or test inhibitors
CC of kinase enzymes, where the inhibitors are used as therapeutics for the
CC treatment and modulation of diseases, disease symptoms or the effect of
CC other physiological events mediated by kinases, having one or more kinase
CC enzymes involved in their pathology
XX
SQ Sequence 508 AA;

```
  Query Match             100.0%;  Score 49;  DB 3;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.7;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
              ||||||||||
Db        293 QLQHQRLVRL 302
```

RESULT 21
ADE58802
ID ADE58802 standard; protein; 508 AA.
XX
AC ADE58802;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P06239, SEQ ID NO 4689.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.

```
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P06239.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 508 AA;

  Query Match             100.0%;  Score 49;  DB 7;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.7;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
              ||||||||||
Db        293 QLQHQRLVRL 302


RESULT 22
ADE58799
ID   ADE58799 standard; protein; 508 AA.
XX
AC   ADE58799;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein P06239, SEQ ID NO 4686.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P06239.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 508 AA;

  Query Match             100.0%;  Score 49;  DB 7;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.7;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
              ||||||||||
Db        293 QLQHQRLVRL 302


RESULT 23
ADF45072
ID   ADF45072 standard; protein; 508 AA.
XX
AC   ADF45072;
XX
DT   12-FEB-2004  (first entry)
```

XX
DE Human kinase LCK.
XX
KW Human; protein kinase; enzyme; inhibitor; LCK.
XX
OS Homo sapiens.
XX
PN WO2003081210-A2.
XX
PD 02-OCT-2003.
XX
PF 20-MAR-2003; 2003WO-US008725.
XX
PR 21-MAR-2002; 2002US-0366892P.
XX
PA (SUNE-) SUNESIS PHARM INC.
XX
PI Prescott JC, Braisted A;
XX
DR WPI; 2003-865136/80.
XX
PT Identifying ligand binding to inactive conformation of target protein
PT kinase (T) comprises contacting the conformation modified (T) which
PT contains reactive group at binding site, with ligands and detecting
PT kinase-ligand conjugate formation.
XX
PS Disclosure; SEQ ID NO 41; 260pp; English.
XX
CC The present invention relates to a method for identifying a ligand (L),
CC which binds to an inactive conformation of target protein kinase (T). The
CC method involves contacting inactive conformation of (T), which contains
CC or is modified to contain a reactive group at or near a binding site of
CC interest, with one or more ligand candidates capable of covalently
CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC The method is useful for identifying protein kinase inhibitors that
CC preferentially bind to inactive conformation of a target protein kinase.
CC The present sequence is a protein kinase which may be modified via an
CC amino acid substitution, for use in the method of the invention.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 49; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 293 QLQHQRLVRL 302

RESULT 24
ADL34479
ID ADL34479 standard; peptide; 508 AA.
XX
AC ADL34479;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human lymphocyte kinase (Lck) globular core.
XX
KW cytostatic; immunosuppressive; antiinflammatory; antibacterial; virucide;
KW fungicide; nootropic; neuroprotective; kinase inhibitor; crystal;
KW protein-ligand complex; lymphocyte kinase; Lck; Lck ligand;
KW kinase inhibitor; therapeutic; kinase-mediated physiological event;
KW cancer; autoimmunological; metabolic; inflammatory; infection;
KW central nervous system degenerative disease; transplant rejection; human;
KW globular core; protein co-ordinate data.
XX
OS Homo sapiens.
XX
PN US6589758-B1.
XX
PD 08-JUL-2003.
XX
PF 21-MAY-2001; 2001US-00862154.
XX
PR 19-MAY-2000; 2000US-0205510P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zhu X;
XX
DR WPI; 2003-810380/76.
XX
PT Crystal of protein-ligand complex useful for identifying an inhibitor of
PT lymphocyte kinase (Lck), comprises truncated Lck and a ligand.
XX
PS Claim 1; SEQ ID NO 1; 295pp; English.
XX
CC The invention describes a crystal (I) of a protein-ligand complex (C)
CC comprising a truncated lymphocyte kinase (Lck) and a ligand, where (I)
CC effectively diffracts X-rays for determination of atomic coordinates of
CC (C) to a resolution of greater than 5.0 angstroms, and truncated Lck
CC comprises a sequence (S1) of residues 225-508 of a 508 amino acid
CC sequence, given in specification and retains the globular core of full-
CC length Lck. (I) is useful in an inhibitor screening assay and to
CC identify, design, select, and evaluate potential inhibitors of kinases
CC that would be useful as therapeutics for diseases or symptoms of diseases
CC that are associated with kinase-mediated physiological events. The
CC inhibitors identified by the methods may also be useful for inhibition of
CC kinase activity of one or more enzymes. The inhibitors are also useful
CC for inhibiting the biological activity of any enzyme comprising greater
CC than 90%, alternatively greater than 85%, or alternatively greater than
CC 70% sequence homology with a kinase sequence. The inhibitors are useful
CC for inhibiting the biological activity of any enzyme that binds ATP and
CC thus for treating disease or disease symptoms mediated by any enzyme that
CC binds ATP. The inhibitors are useful in inhibiting kinase activity and
CC are useful in treating kinase-mediated disease or disease symptoms in a
CC mammal, particularly a human e.g., cancer, autoimmunological, metabolic,
CC inflammatory, infection, (bacterial, viral, yeast, fungal, etc.), central
CC nervous system degenerative disease etc. The inhibitors are useful in
CC treating or preventing diseases, including, transplant rejection etc.
CC This is the amino acid sequence of a human lymphocyte kinase (Lck)
CC polypeptide comprising the Lck globular core.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 49; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 293 QLQHQRLVRL 302

RESULT 25
ADS88148
ID ADS88148 standard; protein; 508 AA.
XX
AC ADS88148;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human protein of a TNF-alpha signalling pathway protein complex SeqID 3.
XX
KW protein complex; tumour necrosis factor-alpha signalling pathway;
KW TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
KW inflammatory bowel disease; infectious disease; septic shock;
KW bacterial infection; neurological disease; stroke-induced inflammation;
KW neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
KW antirheumatic; cytostatic; antibacterial; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004035783-A2.

XX
PD 29-APR-2004.
XX
PF 24-SEP-2003; 2003WO-EP050655.
XX
PR 26-SEP-2002; 2002EP-00021809.
PR 10-FEB-2003; 2003EP-00100274.
XX
PA (CELL-) CELLZOME AG.
XX
PI Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
PI Superti-Furga G, Kruse U;
XX
DR WPI; 2004-348460/32.
XX
PT New protein complex comprising at least one first and second protein of
PT the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
PT diagnosing or treating inflammation, neurological diseases, infectious
PT diseases or cancer.
XX
PS Example; SEQ ID NO 3; 1980pp; English.
XX
CC This invention relates to novel protein complexes of the tumour necrosis
CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
CC methods for preparing these complexes comprising at least two component
CC proteins, as well as screening methods to identify modulators of the
CC pathway, which include antibodies, agonists and antagonists thereof. The
CC present invention describes a protein complex and kit that are useful for
CC diagnosing, prognosing or treating chronic inflammatory diseases such as
CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases
CC such as septic shock and bacterial infections; neurological diseases such
CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
CC cancer. Accordingly, these complexes can be used for the development of
CC pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
CC antirheumatic, cytostatic and antibacterial activities and can be used
CC for gene therapy purposes. In particular, the invention further provides
CC siRNA-oligonucleotides useful for inhibiting protein expression for in
CC vitro or cell culture assays. This polypeptide is a human protein that
CC can be used in combination with other proteins provided in the
CC specification to form novel complexes of the TNF-alpha signalling pathway
CC of the invention.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 49; DB 8; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 293 QLQHQRLVRL 302

RESULT 26
AAY49420
ID AAY49420 standard; protein; 509 AA.
XX
AC AAY49420;
XX
DT 13-MAR-2000 (first entry)
XX
DE PKA substrate, Src-family protein.
XX
KW Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer;
KW kinase substrate; immunosuppressive disorder; proliferative disease;
KW HIV infection; AIDS; immunodeficiency; autoimmune disease;
KW systemic lupus erythematosus; Src-family.
XX
OS Homo sapiens.
XX
PN WO9962315-A2.
XX
PD 02-DEC-1999.
XX
PF 27-MAY-1999; 99WO-GB001680.
XX
PR 27-MAY-1998; 98NO-00002419.
PR 30-DEC-1998; 98US-0114240P.
XX
PA (LAUR-) LAURAS AS.
PA (JONE/) JONES E L.
XX
PI Hansson V, Levy FO, Mustelin T, Skalhegg BS, Sundvold V;
PI Tasken K, Vang T, Altman A, Munshi A;
XX
DR WPI; 2000-086801/07.
DR N-PSDB; AAZ46491.
XX
PT Altering the activity of protein kinase signaling pathways, used for
PT treating immunosuppressive disorders, e.g. AIDS, proliferative disorders,
PT e.g. cancers or autoimmune diseases.
XX
PS Claim 23; Page 95-96; 111pp; English.
XX
CC The invention provides a novel method of altering the activity of the
CC protein kinase A (PKA) signaling pathway in a cell that comprises
CC altering the extent of phosphorylation of one or more PKA substrates, or
CC kinase substrates downstream in the PKA signaling pathway. Pharmaceutical
CC compositions containing a nucleic acid molecule that encodes a PKA
CC substrate, or fragment, precursor or functionally equivalent variant,
CC where the sequence is modified to alter its susceptibility to
CC phosphorylation by PKA can be used for treating a disorder exhibiting
CC abnormal PKA signaling activity, immunosuppressive disorders or
CC proliferative diseases. They can be used for treating e.g. HIV infection,
CC AIDS, common variable immunodeficiency or cancers. Conditions in which
CC upregulation of the PKA pathway is required, such as autoimmune disease,
CC e.g. systemic lupus erythematosus, may also be treated. The present
CC sequence represents a PKA substrate, wherein the substrate is in the Src-
CC family, preferably Lck, Fyn, Src, Yes, Fgr, Lyn, Hck Blk, Yrk, c-tkl,
CC Fyk, Src-1 or Src-2
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 49; DB 3; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 294 QLQHQRLVRL 303

RESULT 27
ABR58699
ID ABR58699 standard; protein; 509 AA.
XX
AC ABR58699;
XX
DT 09-JUL-2003 (first entry)
XX
DE Human cancer related protein SEQ ID NO:356.
XX
KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.
XX
OS Homo sapiens.
XX
PN WO2003025138-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-US029560.
XX
PR 17-SEP-2001; 2001US-0323469P.
PR 20-SEP-2001; 2001US-0323887P.
PR 13-NOV-2001; 2001US-0350666P.

PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI Zlotnik A;
XX
DR WPI; 2003-354600/33.
DR N-PSDB; ACC72850.
XX
PT New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX
PS Claim 12; Page 762; 767pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 49; DB 6; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 294 QLQHQRLVRL 303

RESULT 28
ABR56202
ID ABR56202 standard; protein; 509 AA.
XX
AC ABR56202;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human Lymphocyte Cell Kinase, Lck.
XX
KW Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW Src-family protein tyrosine kinase; T-cell; immune response.
XX
OS Homo sapiens.
XX
PN WO2003020880-A2.
XX
PD 13-MAR-2003.
XX
PF 02-AUG-2002; 2002WO-US024546.
XX
PR 03-AUG-2001; 2001US-0310051P.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Borhani DW, Calderwood D, Dixon RW, Hirst GC, Hrnciar P, Loew A;
PI Leung A, Ritter K;
XX
DR WPI; 2003-300872/29.
XX
PT New crystalline polypeptide comprising ligand binding domain or catalytic
PT domain of Lck protein, for determining three-dimensional structure of
PT catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS Claim 5; Fig 1; 994pp; English.
XX
CC The present invention relates to a crystalline polypeptide (I),
CC comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC in T-cells and plays an essential role in immune response. The present
CC sequence is the full-length sequence of human Lck (1-509). (I) is useful
CC for identifying a compound which is an inhibitor of human Lck protein
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 49; DB 7; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 294 QLQHQRLVRL 303

RESULT 29
ADE40449
ID ADE40449 standard; protein; 509 AA.
XX
AC ADE40449;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human proto-oncogene Tyr protein kinase LCK (gene ID 1611) protein.
XX
KW AIDS; acquired immunodeficiency syndrome; human immunodeficiency virus;
KW HIV-related disorder; differential expression; drug screening;
KW viral replication modulation; diagnosis; prognosis; predisposition;
KW anti-HIV; gene therapy; antisense therapy; human;
KW proto-oncogene Tyr protein kinase LCK; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003070883-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004246.
XX
PR 15-FEB-2002; 2002US-0357391P.
PR 13-MAY-2002; 2002US-0380249P.
PR 25-JUN-2002; 2002US-0391306P.
PR 27-AUG-2002; 2002US-0406297P.
PR 19-SEP-2002; 2002US-0412007P.
PR 10-OCT-2002; 2002US-0417508P.
PR 10-DEC-2002; 2002US-0432318P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Powell DM, Weich NS;
XX
DR WPI; 2003-671808/63.
DR N-PSDB; ADE40448.
XX
PT Identifying a compound capable of diagnosing, preventing or treating AIDS
PT or an HIV-related disorder comprises assaying the ability of the compound
PT to modulate e.g. 1414, 1481 or 1553 nucleic acid expression or

PT polypeptide activity.
XX
PS Claim 1; SEQ ID NO 28; 167pp; English.
XX
CC The invention relates to a method of identifying a compound useful in the
CC treatment of AIDS (acquired immunodeficiency syndrome) or an HIV (human
CC immunodeficiency virus)-related disorder. The invention involves assaying
CC the ability of a test compound to modulate the activity or expression of
CC 26 human proteins. These proteins and nucleic acids encoding them
CC (ADE40422-ADE40473) are differentially expressed in tissues relating to
CC AIDS or an HIV-related disorder compared to their expression in normal
CC tissues. The invention also relates to the use of the compounds
CC identified to modulate viral replication in a cell and to treat a patient
CC with AIDS or an HIV-related disorder. The invention further discloses
CC methods for the diagnostic evaluation and prognosis of various HIV-
CC related disorders, and for the identification of individuals exhibiting a
CC predisposition to such conditions. The modulatory compounds identified
CC using the method of the invention may be small organic molecules,
CC peptides, antibodies or antisense nucleic acid molecules. The methods of
CC the invention are useful in diagnosing, preventing or treating AIDS or
CC HIV-related disorders. The present sequence represents a human protein
CC which is differentially expressed in AIDS or HIV-related disorders.
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 49; DB 7; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 294 QLQHQRLVRL 303

RESULT 30
ADL22907
ID ADL22907 standard; protein; 509 AA.
XX
AC ADL22907;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human MP2153 polypeptide sequence SEQ ID NO: 27.
XX
KW human; MP2153; p21; p53; cancer.
XX
OS Homo sapiens.
XX
PN WO2004015069-A2.
XX
PD 19-FEB-2004.
XX
PF 06-AUG-2003; 2003WO-US024505.
XX
PR 07-AUG-2002; 2002US-0401701P.
PR 16-SEP-2002; 2002US-0411017P.
PR 30-DEC-2002; 2002US-0437107P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Francis-Lang H, Friedman L, Kidd T, Roche S, Belvin M;
PI Plowman GD, Lickteig K, Zhang H, Amundsen CD;
XX
DR WPI; 2004-180653/17.
DR N-PSDB; ADL22890.
XX
PT Identifying a candidate p21 or p53 pathway modulating agent using an
PT assay system having a modulator of p21 or p53 (MP2153) polypeptide or
PT nucleic acid, useful for diagnosing or treating cancer, such as colon or
PT breast cancer.
XX
PS Example 3; Page 94-96; 110pp; English.
XX
CC The present invention relates to a method of identifying a candidate p21
CC or p53 pathway modulating agent. This comprises providing an assay system
CC comprising a modulator of p21 or p53 (MP2153) polypeptide or nucleic
CC acid, contacting the assay system with a test agent, where in its
CC presence the system provides a reference activity, and detecting a test
CC agent-biased activity of the assay system, wherein a difference between
CC the test agent-biased activity and the reference activity identifies the
CC test agent as a candidate p21 or p53 pathway modulating agent. The
CC methods and compositions of the present invention are useful for the
CC diagnosis and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of the p21 or p53 pathway, such as
CC cancer, preferably colon or head and neck cancer. The present sequence is
CC a human MP2153 protein sequence of the invention.
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 49; DB 8; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
||||||||||
Db 294 QLQHQRLVRL 303

Search completed: June 29, 2006, 09:13:03
Job time : 100.59 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 09:13:45 ; Search time 14.8193 Seconds
(without alignments)
64.927 Million cell updates/sec

Title: US-10-062-257A-13
Perfect score: 49
Sequence: 1 QLQHQRLVRL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	100.0	509	1	OKHULK	protein-tyrosine k
2	43	87.8	509	1	I48845	protein-tyrosine k
3	41	83.7	499	1	A40092	protein-tyrosine k
4	41	83.7	505	2	I37206	protein-tyrosine k
5	38	77.6	507	1	A39939	protein-tyrosine k
6	38	77.6	535	2	T51736	mitogen-activated
7	38	77.6	560	2	D85084	probable mitogen-a
8	38	77.6	572	2	T01836	serine/threonine-s
9	38	77.6	608	2	T01833	serine/threonine-s
10	38	77.6	1895	2	T06609	disease resistance
11	37	75.5	219	2	S43107	orf2 protein - Yer
12	37	75.5	260	2	T14971	probable transposa
13	37	75.5	260	2	AB0031	insertion sequence
14	37	75.5	260	2	AH0078	insertion sequence
15	37	75.5	260	2	AI0197	insertion sequence
16	37	75.5	260	2	AH0356	insertion sequence
17	37	75.5	260	2	AF0065	insertion sequence
18	37	75.5	260	2	AC0395	insertion sequence
19	37	75.5	260	2	AH0047	insertion sequence
20	37	75.5	260	2	AC0185	insertion sequence
21	37	75.5	260	2	AD0450	insertion sequence
22	37	75.5	260	2	AF0254	insertion sequence
23	37	75.5	260	2	AE0174	insertion sequence
24	37	75.5	260	2	AC0070	insertion sequence
25	37	75.5	260	2	AH0231	insertion sequence
26	37	75.5	260	2	AH0436	insertion sequence
27	37	75.5	260	2	AE0124	insertion sequence
28	37	75.5	260	2	AC0139	insertion sequence
29	37	75.5	260	2	AD0113	insertion sequence
30	37	75.5	260	2	AE0459	insertion sequence
31	37	75.5	260	2	AC0206	insertion sequence
32	37	75.5	260	2	AE0133	insertion sequence
33	37	75.5	260	2	AI0095	insertion sequence
34	37	75.5	260	2	AH0389	insertion sequence
35	37	75.5	260	2	AF0307	insertion sequence
36	37	75.5	260	2	AB0332	insertion sequence
37	37	75.5	260	2	AD0322	insertion sequence
38	37	75.5	260	2	AF0292	insertion sequence
39	37	75.5	260	2	AG0004	insertion sequence
40	37	75.5	260	2	AH0101	insertion sequence
41	37	75.5	260	2	AB0247	insertion sequence
42	37	75.5	260	2	AB0211	insertion sequence
43	37	75.5	260	2	AD0342	insertion sequence
44	37	75.5	260	2	AI0398	insertion sequence
45	37	75.5	260	2	AI0487	insertion sequence
46	37	75.5	260	2	AG0213	insertion sequence
47	37	75.5	260	2	AC0457	insertion sequence
48	37	75.5	260	2	AE0288	insertion sequence
49	37	75.5	260	2	AH0430	insertion sequence
50	37	75.5	260	2	AH0012	insertion sequence
51	37	75.5	260	2	AI0021	insertion sequence
52	37	75.5	260	2	AF0163	insertion sequence
53	37	75.5	260	2	AE0265	insertion sequence
54	37	75.5	260	2	AE0417	insertion sequence
55	36	73.5	330	2	T01016	hypothetical prote
56	36	73.5	352	2	T04841	protein kinase hom
57	36	73.5	372	2	T01551	receptor kinase ho
58	36	73.5	429	2	T01550	receptor kinase ho
59	36	73.5	465	2	I48926	protein-tyrosine k
60	36	73.5	467	2	I56579	protein-tyrosine k
61	36	73.5	485	2	T04840	hypothetical prote
62	36	73.5	496	2	A56040	protein-tyrosine k
63	36	73.5	505	2	I59296	protein-tyrosine k
64	36	73.5	512	1	A39719	protein-tyrosine k
65	36	73.5	512	1	I56160	protein-tyrosine k
66	36	73.5	512	1	TVHULY	protein-tyrosine k
67	36	73.5	517	2	T04838	probable serine/th
68	36	73.5	570	2	T04836	probable serine/th
69	36	73.5	633	2	T04835	probable serine/th
70	36	73.5	656	2	T10568	probable serine/th
71	36	73.5	658	2	D84869	probable receptor
72	36	73.5	658	2	T04831	probable serine/th
73	36	73.5	664	2	B85122	serine/threonine k
74	36	73.5	664	2	T10573	probable serine/th
75	36	73.5	666	2	T10567	probable serine/th
76	36	73.5	676	2	T47526	protein kinase-lik
77	36	73.5	683	2	T05149	protein kinase hom
78	36	73.5	700	2	T10566	probable serine/th
79	36	73.5	711	2	T05148	protein kinase hom
80	36	73.5	815	1	T05754	S-receptor kinase
81	36	73.5	820	2	G86246	hypothetical prote
82	36	73.5	828	2	C96639	protein T1F9.14 [i
83	36	73.5	830	2	T04848	protein kinase hom
84	36	73.5	831	2	D96639	protein T1F9.12 [i
85	36	73.5	842	2	E96641	hypothetical prote
86	36	73.5	848	1	T02053	S-receptor kinase
87	36	73.5	849	1	T05181	S-receptor kinase
88	36	73.5	849	1	T09349	S-receptor kinase
89	36	73.5	850	2	T14450	serine/threonine k
90	36	73.5	852	2	A85041	probable receptor
91	36	73.5	1240	2	T04833	hypothetical prote
92	35	71.4	328	2	H84548	hypothetical prote
93	35	71.4	333	2	T02690	hypothetical prote
94	35	71.4	507	2	A55625	protein-tyrosine k
95	35	71.4	527	2	A49865	protein-tyrosine k
96	35	71.4	568	1	TVFVS1	protein-tyrosine k
97	35	71.4	595	1	QRHUE	estrogen receptor
98	35	71.4	701	2	S64737	80K estrogen recep
99	35	71.4	854	2	T14377	S-receptor kinase
100	35	71.4	1695	2	T19823	hypothetical prote

ALIGNMENTS

RESULT 1
OKHULK
protein-tyrosine kinase (EC 2.7.1.112) lck - human
N;Alternate names: kinase-related transforming protein (lck)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 05-Oct-2004
C;Accession: JQ0152; S07822; S07200; S01879; S07143; A32797; I57636
R;Rouer, E.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R.
Gene 84, 105-113, 1989
A;Title: Structure of the human lck gene: differences in genomic organisation within src
A;Reference number: JQ0152; MUID:90108697; PMID:2558056
A;Accession: JQ0152
A;Molecule type: DNA
A;Residues: 1-509 <ROU>
A;Cross-references: UNIPROT:P06239; UNIPARC:UPI0000151F17; EMBL:X14053
R;Perlmutter, R.M.; Marth, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, C.B.
J. Cell. Biochem. 38, 117-126, 1988
A;Title: Structure and expression of lck transcripts in human lymphoid cells.
A;Reference number: S07822; MUID:89123626; PMID:3265417
A;Accession: S07822
A;Molecule type: mRNA
A;Residues: 1-86,'P',88-509 <PER>
A;Cross-references: UNIPARC:UPI0000163BD5; EMBL:X13529; NID:g34294; PIDN:CAA31884.1; PID
R;Koga, Y.; Caccia, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikai, Y.; Mak, T.W.
Eur. J. Immunol. 16, 1643-1646, 1986
A;Title: A human T cell-specific cDNA clone (YT16) encodes a protein with extensive homo
A;Reference number: S07200; MUID:87133831; PMID:3493153
A;Accession: S07200
A;Molecule type: mRNA
A;Residues: 1-205,'ASAITPI',212-257,'RCGW',262,'TTT',266,'T',268-281,'AGRLP',287-503,'ST
A;Cross-references: UNIPARC:UPI000016B09E; EMBL:X05027; NID:g36807; PIDN:CAA28691.1; PID
R;Veillette, A.; Foss, F.M.; Sausville, E.A.; Bolen, J.B.; Rosen, N.
Oncogene Res. 1, 357-374, 1987
A;Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other r
A;Reference number: S01879; MUID:88217332; PMID:2835736
A;Accession: S01879
A;Molecule type: mRNA
A;Residues: 368-471,'H',473-509 <VEI>
A;Cross-references: UNIPARC:UPI000016ABFC; EMBL:X06369; NID:g34288; PIDN:CAA29667.1; PID
R;Trevillyan, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Linna, T.J.
Biochim. Biophys. Acta 888, 286-295, 1986
A;Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56(LSTRA).
A;Reference number: S07143; MUID:87000726; PMID:3489486
A;Accession: S07143
A;Molecule type: mRNA
A;Residues: 'A',376-509 <TRE>
A;Cross-references: UNIPARC:UPI000016AF39; EMBL:X04476; NID:g35779; PIDN:CAA28165.1; PID
R;Takadera, T.; Leung, S.; Gernone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.W
Mol. Cell. Biol. 9, 2173-2180, 1989
A;Title: Structure of the two promoters of the human lck gene: differential accumulation
A;Reference number: A32797; MUID:89313764; PMID:2787474
A;Accession: A32797
A;Molecule type: DNA
A;Residues: 1-35 <TAK>
A;Cross-references: UNIPARC:UPI000016ABFF; GB:M26692; NID:g341523; PIDN:AAA59503.1; PID:
R;Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
Mol. Cell. Biol. 8, 3058-3064, 1988
A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel
A;Reference number: I57636; MUID:89096891; PMID:2850479
A;Accession: I57636
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-35,'VR' <RES>
A;Cross-references: UNIPARC:UPI000016ABFD; GB:M21510; NID:g187031; PIDN:AAA59501.1; PID:
C;Comment: Protein tyrosine kinases play important roles in the control of cell growth a
C;Genetics:
A;Gene: GDB:LCK
A;Cross-references: GDB:119360; OMIM:153390
A;Map position: 1p35-1p34.3
A;Introns: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;2-509/Product: protein-tyrosine kinase lck #status predicted <MAT>
F;68-116/Domain: SH3 homology <SH3>
F;127-224/Domain: SH2 homology <SH2>
F;243-501/Domain: protein kinase homology <KIN>
F;251-259/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3,5/Binding site: palmitate (Cys) (covalent) #status predicted
F;273/Active site: Lys #status predicted
F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 100.0%; Score 49; DB 1; Length 509;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
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Db 294 QLQHQRLVRL 303

RESULT 2
I48845
protein-tyrosine kinase (EC 2.7.1.112) lck, lymphocyte - mouse
N;Alternate names: p56; protein-tyrosine kinase tck
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: I48845; A23639; I57629; I77452
R;Voronova, A.F.; Sefton, B.M.
Nature 319, 682-685, 1986
A;Title: Expression of a new tyrosine protein kinase is stimulated by retrovirus promote
A;Reference number: I48845; MUID:86146842; PMID:3081813
A;Accession: I48845
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-509 <VOR1>
A;Cross-references: UNIPROT:Q91X65; UNIPARC:UPI000000418D; EMBL:X03533; NID:g54813; PIDN
R;Marth, J.D.; Peet, R.; Krebs, E.G.; Perlmutter, R.M.
Cell 43, 393-404, 1985
A;Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpres
A;Reference number: A23639; MUID:86079521; PMID:2416464
A;Accession: A23639
A;Molecule type: mRNA
A;Residues: 1-282,'VP',285-509 <MAR>
A;Cross-references: UNIPARC:UPI0000172586; GB:M12056; NID:g198763
A;Note: the sequence is revised in GenBank entry MUSLCK, release 116.0, (PIDN:AAB59674.1
R;Voronova, A.F.; Adler, H.T.; Sefton, B.M.
Mol. Cell. Biol. 7, 4407-4413, 1987
A;Title: Two lck transcripts containing different 5' untranslated regions are present in
A;Reference number: I57629; MUID:88142832; PMID:3501824
A;Accession: I57629
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <VOR>
A;Cross-references: UNIPARC:UPI000016CE9D; GB:M18098; NID:g198766; PIDN:AAA39421.1; PID:
R;Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
Mol. Cell. Biol. 8, 3058-3064, 1988
A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel
A;Reference number: I57636; MUID:89096891; PMID:2850479
A;Accession: I77452
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-35,'VR' <GAR>
A;Cross-references: UNIPARC:UPI000016CE9E; GB:M21511; NID:g198768; PIDN:AAA39422.1; PID:
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro
F;68-116/Domain: SH3 homology <SH3>
F;127-224/Domain: SH2 homology <SH2>
F;243-501/Domain: protein kinase homology <KIN>
F;251-259/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

```
F;273/Active site: Lys #status predicted
F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match          87.8%;  Score 43;  DB 1;  Length 509;
  Best Local Similarity   90.0%;  Pred. No. 2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
              |||| |||||
Db        294 QLQHPRLVRL 303


RESULT 3
A40092
protein-tyrosine kinase (EC 2.7.1.112) blk [validated] - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C;Accession: A40092
R;Dymecki, S.M.; Niederhuber, J.E.; Desiderio, S.V.
Science 247, 332-336, 1990
A;Title: Specific expression of a tyrosine kinase gene, blk, in B lymphoid cells.
A;Reference number: A40092; MUID:90117147; PMID:2404338
A;Accession: A40092
A;Molecule type: mRNA
A;Residues: 1-499 <DYM>
A;Cross-references: UNIPROT:P16277; UNIPARC:UPI0000151F18; GB:M30903; NID:g202076; PIDN:
C;Genetics:
A;Gene: MGI:Blk
A;Cross-references: MGI:88169
A;Map position: 14:28.0
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;59-107/Domain: SH3 homology <SH3>
F;118-214/Domain: SH2 homology <SH2>
F;233-491/Domain: protein kinase homology <KIN>
F;241-249/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;263/Active site: Lys #status predicted

  Query Match          83.7%;  Score 41;  DB 1;  Length 499;
  Best Local Similarity   88.9%;  Pred. No. 4.6;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LQHQRLVRL 10
              |||:|||||
Db        285 LQHERLVRL 293


RESULT 4
I37206
protein-tyrosine kinase (EC 2.7.1.112) blk - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Oct-2004
C;Accession: I37206; S51647
R;Islam, K.B.; Rabbani, H.; Larsson, C.; Sanders, R.; Smith, C.I.
J. Immunol. 154, 1265-1272, 1995
A;Title: Molecular cloning, characterization, and chromosomal localization of a human ly
A;Reference number: I37206; MUID:95123078; PMID:7822795
A;Accession: I37206
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-505 <RES>
A;Cross-references: UNIPROT:P51451; UNIPARC:UPI0000163B22; EMBL:Z33998; NID:g601951; PID
C;Genetics:
A;Gene: GDB:BLK
A;Cross-references: GDB:454114; OMIM:191305
A;Map position: 8p23-8p22
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; tyro
F;65-113/Domain: SH3 homology <SH3>
F;124-220/Domain: SH2 homology <SH2>
F;239-497/Domain: protein kinase homology <KIN>
F;247-255/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;269/Active site: Lys #status predicted

  Query Match          83.7%;  Score 41;  DB 2;  Length 505;
  Best Local Similarity   88.9%;  Pred. No. 4.6;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LQHQRLVRL 10
              |||:|||||
Db        291 LQHERLVRL 299


RESULT 5
A39939
protein-tyrosine kinase (EC 2.7.1.112) tkl [similarity] - chicken
N;Alternate names: kinase-related transforming protein (tkl); T-cell surface antigen ass
C;Species: Gallus gallus (chicken)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C;Accession: A42126; A39939
R;Chow, L.M.; Ratcliffe, M.J.; Veillette, A.
Mol. Cell. Biol. 12, 1226-1233, 1992
A;Title: tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene.
A;Reference number: A42126; MUID:92186854; PMID:1545804
A;Accession: A42126
A;Molecule type: mRNA
A;Residues: 1-88 <CHO>
A;Cross-references: UNIPARC:UPI0000172587; GB:M85043
A;Experimental source: thymus, spleen
A;Note: sequence extracted from NCBI backbone (NCBIN:88831, NCBIP:88833)
R;Strebhardt, K.; Mullins, J.I.; Bruck, C.; Ruebsamen-Waigmann, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987
A;Title: Additional member of the protein-tyrosine kinase family: the src-and lck-relate
A;Reference number: A39939; MUID:88097370; PMID:3321053
A;Accession: A39939
A;Molecule type: mRNA
A;Residues: 52-507 <STR>
A;Cross-references: UNIPARC:UPI00001713B3; GB:J03579; NID:g212712; PIDN:AAA49081.1; PID:
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;66-114/Domain: SH3 homology <SH3>
F;125-222/Domain: SH2 homology <SH2>
F;241-499/Domain: protein kinase homology <KIN>
F;249-257/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match          77.6%;  Score 38;  DB 1;  Length 507;
  Best Local Similarity   88.9%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LQHQRLVRL 10
              ||| |||||
Db        293 LQHPRLVRL 301


RESULT 6
T51736
mitogen-activated protein kinase MAP3K beta [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 05-Oct-2004
C;Accession: T51736
R;Jouannic, S.
submitted to the EMBL Data Library, August 1998
A;Reference number: Z25444
A;Accession: T51736
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-535 <JOU>
A;Cross-references: UNIPROT:O82650; UNIPARC:UPI00000A949D; EMBL:AJ010092; PIDN:CAA08996.
C;Genetics:
A;Gene: MAP3K beta 3

  Query Match          77.6%;  Score 38;  DB 2;  Length 535;
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  Best Local Similarity   77.8%;  Pred. No. 18;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVR 9
              ||||| :||
Db        333 QLQHQNIVR 341


RESULT 7
D85084
probable mitogen-activated protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C;Accession: D85084
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: D85084
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-560 <STO>
A;Cross-references: UNIPROT:Q9M0T3; UNIPARC:UPI00000A5165; GB:NC_001268; NID:g7267488; P
C;Genetics:
A;Gene: AT4g08470
A;Map position: 4

  Query Match             77.6%;  Score 38;  DB 2;  Length 560;
  Best Local Similarity   77.8%;  Pred. No. 19;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVR 9
              ||||| :||
Db        358 QLQHQNIVR 366


RESULT 8
T01836
serine/threonine-specific protein kinase ARA.KIN homolog T15F16.2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 05-Oct-2004
C;Accession: T01836
R;Antoniou, B.; Le, T.
submitted to the EMBL Data Library, August 1998
A;Description: The sequence of A. thaliana T15F16.
A;Reference number: Z14443
A;Accession: T01836
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-572 <ANT>
A;Cross-references: UNIPROT:O81473; UNIPARC:UPI000009F5CA; EMBL:AF076275; NID:g3293582;
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4
A;Introns: 156/2; 241/2; 323/2; 351/3; 372/3; 425/2; 449/3; 481/3; 519/3
A;Note: T15F16.2

  Query Match             77.6%;  Score 38;  DB 2;  Length 572;
  Best Local Similarity   77.8%;  Pred. No. 19;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVR 9
              ||||| :||
Db        358 QLQHQNIVR 366


RESULT 9
T01833
serine/threonine-specific protein kinase ARA.KIN (EC 2.7.1.-) - Arabidopsis thaliana
N;Alternate names: protein T15F16.5
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 05-Oct-2004
C;Accession: T01833; S65789
R;Antoniou, B.; Le, T.
submitted to the EMBL Data Library, August 1998
A;Description: The sequence of A. thaliana T15F16.
A;Reference number: Z14443
A;Accession: T01833
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-608 <ANT>
A;Cross-references: UNIPROT:O81470; UNIPARC:UPI00000A1A9F; EMBL:AF076275; NID:g3293582;
A;Experimental source: cultivar Columbia
R;Covic, L.; Lew, R.R.
Biochim. Biophys. Acta 1305, 125-129, 1996
A;Title: Arabidopsis thaliana cDNA isolated by functional complementation shows homology
A;Reference number: S65789; MUID:96180314; PMID:8597596
A;Accession: S65789
A;Molecule type: mRNA
A;Residues: 'YVRE',119-236,'LDPLLIIGDRLG',248-338,'V',340-358,'G',360-369,'EVEALKNPYNREG
A;Cross-references: UNIPARC:UPI000017A45B; EMBL:L43125; NID:g871811; PIDN:AAA99196.1; PI
C;Genetics:
A;Map position: 4
A;Introns: 353/2; 381/3; 402/3; 455/2; 479/3; 499/3; 537/3
A;Note: T15F16.5
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;331-587/Domain: protein kinase homology <KIN>
F;339-347/Region: protein kinase ATP-binding motif

  Query Match             77.6%;  Score 38;  DB 2;  Length 608;
  Best Local Similarity   77.8%;  Pred. No. 21;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVR 9
              ||||| :||
Db        388 QLQHQNIVR 396


RESULT 10
T06609
disease resistance protein homolog F16J13.90 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
C;Accession: T06609
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,
submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15789
A;Accession: T06609
A;Molecule type: DNA
A;Residues: 1-1895 <BEV>
A;Cross-references: UNIPROT:Q9SZ67; UNIPARC:UPI000009F5B5; EMBL:AL049638; GSPDB:GN00062;
A;Experimental source: cultivar Columbia; BAC clone F16J13
C;Genetics:
A;Gene: ATSP:F16J13.90
A;Map position: 4
A;Introns: 67/2; 340/2; 391/3; 607/2; 661/2; 791/2; 1148/3; 1255/3; 1646/2; 1674/3; 1695
C;Superfamily: DNA-binding protein WRKY1

  Query Match             77.6%;  Score 38;  DB 2;  Length 1895;
  Best Local Similarity   77.8%;  Pred. No. 65;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVR 9
              ||||| :||
Db       1681 QLQHQNIVR 1689


RESULT 11
S43107
orf2 protein - Yersinia pestis
C;Species: Yersinia pestis
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S43107
R;Filippov, A.A.; Oleinikov, P.V.; Vladimir, M.L.; Protsenko, O.A.; Smirnov, G.B.
submitted to the EMBL Data Library, March 1994
A;Description: Sequencing of IS285, a Novel IS element of Yersinia pestis.
```

A;Reference number: S43106
A;Accession: S43107
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <FIL>
A;Cross-references: UNIPROT:Q56968; UNIPARC:UPI00000B43AB; EMBL:X78302; NID:g467611; PID
C;Superfamily: DNA replication protein dnaC

Query Match 75.5%; Score 37; DB 2; Length 219;
Best Local Similarity 70.0%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:|||||: |
Db 3 ELQHQRLMAL 12

RESULT 12
T14971
probable transposase - Yersinia pestis plasmid pMT1 and pCD1 insertion sequence
C;Species: Yersinia pestis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14971; T15009; T42855; T14648; T43560; T47059; T46991; T17450
R;Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A;Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIM5 plasmid
A;Reference number: Z18268; MUID:99043898; PMID:9826348
A;Accession: T14971
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-260 <LIN>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; EMBL:AF074611; NID:g3883003;
A;Experimental source: plasmid pMT1
A;Accession: T15009
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 2-260 <LI2>
A;Cross-references: UNIPARC:UPI00000DCDC0; EMBL:AF074611; NID:g3883003; PID:g3883092; PI
R;Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R.
Infect. Immun. 66, 4611-4623, 1998
A;Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia p
A;Reference number: Z22273; MUID:98427122; PMID:9746557
A;Accession: T42855
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-260 <PER>
A;Cross-references: UNIPARC:UPI0000003DEC; EMBL:AF074612; NID:g3822037; PIDN:AAC69770.1;
A;Experimental source: strain KIM5, plasmid pCD1
R;Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Carrano,
submitted to the EMBL Data Library, March 1998
A;Description: Structural organization of virulence determinants in three Yersinia pesti
A;Reference number: Z18168
A;Accession: T14648
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 2-260 <HUP>
A;Cross-references: UNIPARC:UPI00000DCDC0; EMBL:AF053947; NID:g2996286; PID:g2996299; PI
A;Experimental source: plasmid pMT1
R;Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubaker
J. Bacteriol. 180, 5192-5202, 1998
A;Title: Structural organization of virulence-associated plasmids of Yersinia pestis.
A;Reference number: Z22578; MUID:98422474; PMID:9748454
A;Accession: T43560
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 2-260 <HU2>
A;Cross-references: UNIPARC:UPI00000DCDC0; EMBL:AF053946; PIDN:AAC62557.1
A;Experimental source: strain KIM, plasmid pCD1
R;Buchrieser, C.; Rusniok, C.; Couve, E.; Frangeul, L.; Billault, A.; Kunst, F.; Carniel
submitted to the EMBL Data Library, October 1998
A;Description: DNA sequence of the 102 kbases unstable region of Yersinia pestis.
A;Reference number: Z24348
A;Accession: T47059
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 2-260 <BUC>
A;Cross-references: UNIPARC:UPI00000DCDC0; EMBL:AL031866; PIDN:CAA21402.1
A;Experimental source: strain 6/69
A;Accession: T46991
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 2-260 <BU2>
A;Cross-references: UNIPARC:UPI00000DCDC0; EMBL:AL031866; PIDN:CAA21334.1
A;Experimental source: strain 6/69
R;Fetherston, J.D.; Bertolino, V.J.; Perry, R.D.
Mol. Microbiol. 32, 289-299, 1999
A;Title: YbtP and YbtQ: two ABC transporters required for iron uptake in Yersinia pestis
A;Reference number: Z18782; MUID:99248409; PMID:10231486
A;Accession: T17450
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 164-260 <FET>
A;Cross-references: UNIPARC:UPI00000B10E8; EMBL:AF091251; NID:g3818595; PID:g3818610; PI
C;Genetics:
A;Gene: Y1054; Y0016; Y1094
A;Genome: plasmid
A;Mobile element: insertion sequence
A;Note: plasmids pMT1 and pCD1
C;Superfamily: DNA replication protein dnaC

Query Match 75.5%; Score 37; DB 2; Length 260;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:|||||: |
Db 4 ELQHQRLMAL 13

RESULT 13
AB0031
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0031
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0031
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC89109.1;
C;Genetics:
A;Gene: YPO0248
C;Superfamily: DNA replication protein dnaC

Query Match 75.5%; Score 37; DB 2; Length 260;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:|||||: |
Db 4 ELQHQRLMAL 13

RESULT 14
AH0078
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH0078
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AH0078
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC89491.1;
C;Genetics:
A;Gene: YPO0638
C;Superfamily: DNA replication protein dnaC

Query Match 75.5%; Score 37; DB 2; Length 260;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:||||||: |
Db 4 ELQHQRLMAL 13

RESULT 15
AI0197
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AI0197
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AI0197
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC90444.1;
C;Genetics:
A;Gene: YPO1622
C;Superfamily: DNA replication protein dnaC

Query Match 75.5%; Score 37; DB 2; Length 260;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:||||||: |
Db 4 ELQHQRLMAL 13

RESULT 16
AH0356
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH0356
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AH0356
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC92179.1;
C;Genetics:
A;Gene: YPO2931
C;Superfamily: DNA replication protein dnaC

Query Match 75.5%; Score 37; DB 2; Length 260;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:||||||: |
Db 4 ELQHQRLMAL 13

RESULT 17
AF0065
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AF0065
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AF0065
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC89385.1;
C;Genetics:
A;Gene: YPO0527
C;Superfamily: DNA replication protein dnaC

Query Match 75.5%; Score 37; DB 2; Length 260;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:||||||: |
Db 4 ELQHQRLMAL 13

RESULT 18
AC0395
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0395
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AC0395
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC92487.1;
C;Genetics:
A;Gene: YPO3252
C;Superfamily: DNA replication protein dnaC

Query Match 75.5%; Score 37; DB 2; Length 260;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:||||||: |
Db 4 ELQHQRLMAL 13

RESULT 19
AH0047
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH0047
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AH0047
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC89243.1;
C;Genetics:
A;Gene: YPO0385
C;Superfamily: DNA replication protein dnaC

Query Match 75.5%; Score 37; DB 2; Length 260;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:||||||: |
Db 4 ELQHQRLMAL 13

RESULT 20
AC0185
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0185
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AC0185
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC90342.1;
C;Genetics:
A;Gene: YPO1519
C;Superfamily: DNA replication protein dnaC

Query Match 75.5%; Score 37; DB 2; Length 260;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:||||||: |
Db 4 ELQHQRLMAL 13

RESULT 21
AD0450
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD0450
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AD0450
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC93168.1;
C;Genetics:
A;Gene: YPO3700
C;Superfamily: DNA replication protein dnaC

Query Match 75.5%; Score 37; DB 2; Length 260;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:||||||: |
Db 4 ELQHQRLMAL 13

RESULT 22
AF0254
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AF0254
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AF0254
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC90898.1;
C;Genetics:
A;Gene: YPO2086
C;Superfamily: DNA replication protein dnaC

Query Match 75.5%; Score 37; DB 2; Length 260;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:||||||: |
Db 4 ELQHQRLMAL 13

RESULT 23
AE0174
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE0174
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AE0174
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC90256.1;
C;Genetics:
A;Gene: YPO1426
C;Superfamily: DNA replication protein dnaC

Query Match 75.5%; Score 37; DB 2; Length 260;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:||||||: |
Db 4 ELQHQRLMAL 13

RESULT 24
AC0070
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0070
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AC0070
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC89422.1;
C;Genetics:
A;Gene: YPO0566
C;Superfamily: DNA replication protein dnaC

  Query Match 75.5%; Score 37; DB 2; Length 260;
  Best Local Similarity 70.0%; Pred. No. 13;
  Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:||||||: |
Db 4 ELQHQRLMAL 13

RESULT 25
AH0231
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH0231
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AH0231
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC90716.1;
C;Genetics:
A;Gene: YPO1901
C;Superfamily: DNA replication protein dnaC

  Query Match 75.5%; Score 37; DB 2; Length 260;
  Best Local Similarity 70.0%; Pred. No. 13;
  Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:||||||: |
Db 4 ELQHQRLMAL 13

RESULT 26
AH0436
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH0436
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AH0436
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC92820.1;
C;Genetics:
A;Gene: YPO3592
C;Superfamily: DNA replication protein dnaC

  Query Match 75.5%; Score 37; DB 2; Length 260;
  Best Local Similarity 70.0%; Pred. No. 13;
  Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:||||||: |
Db 4 ELQHQRLMAL 13

RESULT 27
AE0124
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE0124
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AE0124
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC89856.1;
C;Genetics:
A;Gene: YPO1014
C;Superfamily: DNA replication protein dnaC

  Query Match 75.5%; Score 37; DB 2; Length 260;
  Best Local Similarity 70.0%; Pred. No. 13;
  Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLQHQRLVRL 10
:||||||: |
Db 4 ELQHQRLMAL 13

RESULT 28
AC0139
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0139
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AC0139
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC89974.1;
C;Genetics:
A;Gene: YPO1131
C;Superfamily: DNA replication protein dnaC

  Query Match 75.5%; Score 37; DB 2; Length 260;
  Best Local Similarity 70.0%; Pred. No. 13;
  Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 QLQHQRLVRL 10
              :||||||: |
Db          4 ELQHQRLMAL 13
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RESULT 29
AD0113
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD0113
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AD0113
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC89767.1;
C;Genetics:
A;Gene: YPO0923
C;Superfamily: DNA replication protein dnaC

  Query Match 75.5%; Score 37; DB 2; Length 260;
  Best Local Similarity 70.0%; Pred. No. 13;
  Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 QLQHQRLVRL 10
              :||||||: |
Db          4 ELQHQRLMAL 13
```

RESULT 30
AE0459
insertion sequence IS100, ATP-binding protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE0459
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AE0459
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q9R3L5; UNIPARC:UPI0000003DEC; GB:AL590842; PIDN:CAC93241.1;
C;Genetics:
A;Gene: YPO3773
C;Superfamily: DNA replication protein dnaC

  Query Match 75.5%; Score 37; DB 2; Length 260;
  Best Local Similarity 70.0%; Pred. No. 13;
  Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 QLQHQRLVRL 10
              :||||||: |
Db          4 ELQHQRLMAL 13
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Search completed: June 29, 2006, 09:31:30
Job time : 15.8193 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:39 ; Search time 117.59 Seconds
(without alignments)
78.664 Million cell updates/sec

Title: US-10-062-257A-13
Perfect score: 49
Sequence: 1 QLQHQRLVRL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	100.0	508	1	LCK_AOTNA	Q5pxs1 aotus nancy
2	49	100.0	508	1	LCK_HUMAN	P06239 homo sapien
3	49	100.0	509	2	Q7RTZ3_HUMAN	Q7rtz3 homo sapien
4	49	100.0	509	2	Q95M32_9PRIM	Q95m32 hylobates s
5	49	100.0	509	2	Q3ZCM0_BOVIN	Q3zcm0 bos taurus
6	49	100.0	516	2	Q573B4_HUMAN	Q573b4 homo sapien
7	46	93.9	322	2	Q4RR72_TETNG	Q4rr72 tetraodon n
8	45	91.8	508	1	LCK_SAISC	Q95kr7 saimiri sci
9	43	87.8	368	2	Q3TLX4_MOUSE	Q3tlx4 mus musculu
10	43	87.8	379	2	Q4FZR6_RAT	Q4fzr6 rattus norv
11	43	87.8	485	2	Q5TYU7_BRARE	Q5tyu7 brachydanio
12	43	87.8	508	1	LCK_MOUSE	P06240 mus musculu
13	41	83.7	490	2	Q6KA98_ORYSA	Q6ka98 oryza sativ
14	41	83.7	498	1	BLK_MOUSE	P16277 mus musculu
15	41	83.7	498	2	Q5FW27_XENTR	Q5fw27 xenopus tro
16	41	83.7	499	2	Q3TAT8_MOUSE	Q3tat8 mus musculu
17	41	83.7	499	2	Q4KM97_RAT	Q4km97 rattus norv
18	41	83.7	499	2	Q8K2M8_MOUSE	Q8k2m8 mus musculu
19	41	83.7	504	1	BLK_HUMAN	P51451 homo sapien
20	41	83.7	505	2	Q96IN1_HUMAN	Q96in1 homo sapien
21	40	81.6	320	2	Q3XC39_METFL	Q3xc39 methylobaci
22	40	81.6	511	2	Q4RL31_TETNG	Q4rl31 tetraodon n
23	39	79.6	249	2	Q9U8V6_EPTBU	Q9u8v6 eptatretus
24	39	79.6	371	2	Q6L576_ORYSA	Q6l576 oryza sativ
25	39	79.6	496	2	O93411_XENLA	O93411 xenopus lae
26	39	79.6	510	2	Q66I04_BRARE	Q66i04 brachydanio
27	39	79.6	646	2	Q7QS13_GIALA	Q7qs13 giardia lam
28	38	77.6	175	2	Q2IJL1_9DELT	Q2ijl1 anaeromyxob
29	38	77.6	327	2	Q6KAA1_ORYSA	Q6kaa1 oryza sativ
30	38	77.6	335	2	Q514Y0_ENTHI	Q514y0 entamoeba h
31	38	77.6	466	2	Q4RNX3_TETNG	Q4rnx3 tetraodon n
32	38	77.6	503	2	Q6TPQ4_BRARE	Q6tpq4 brachydanio
33	38	77.6	507	1	LCK_CHICK	P42683 gallus gall
34	38	77.6	511	2	Q3EEH6_ACTSC	Q3eeh6 actinobacil
35	38	77.6	535	2	O82650_ARATH	O82650 arabidopsis
36	38	77.6	560	2	Q84W26_ARATH	Q84w26 arabidopsis
37	38	77.6	560	2	Q9M0T3_ARATH	Q9m0t3 arabidopsis
38	38	77.6	572	2	O81473_ARATH	O81473 arabidopsis
39	38	77.6	575	2	O82668_BRANA	O82668 brassica na
40	38	77.6	608	2	O81470_ARATH	O81470 arabidopsis
41	38	77.6	608	2	Q39020_ARATH	Q39020 arabidopsis
42	38	77.6	608	2	Q8W4N5_ARATH	Q8w4n5 arabidopsis
43	38	77.6	1895	1	WRK19_ARATH	Q9sz67 arabidopsis
44	37	75.5	113	2	Q9S124_ECOLI	Q9s124 escherichia
45	37	75.5	127	2	Q2W5W9_MAGSA	Q2w5w9 magnetospir
46	37	75.5	219	2	Q56968_YERPE	Q56968 yersinia pe
47	37	75.5	259	2	P74994_ECOLI	P74994 escherichia
48	37	75.5	259	2	Q7BTY2_YERPE	Q7bty2 yersinia pe
49	37	75.5	259	2	Q83W92_ECOLI	Q83w92 escherichia
50	37	75.5	259	2	Q7ARN6_YERPE	Q7arn6 yersinia pe
51	37	75.5	259	2	Q7B1Z4_YERPS	Q7b1z4 yersinia ps
52	37	75.5	260	2	Q7BT15_YERPE	Q7bt15 yersinia pe
53	37	75.5	260	2	Q9R3L5_ECOLI	Q9r3l5 escherichia
54	37	75.5	260	2	Q2TTS5_ECOLI	Q2tts5 escherichia
55	37	75.5	260	2	Q8FG76_ECOL6	Q8fg76 escherichia
56	37	75.5	260	2	Q8VSN7_SHIFL	Q8vsn7 shigella fl
57	37	75.5	260	2	Q7ARK4_YERPE	Q7ark4 y insertion
58	37	75.5	357	2	Q38BZ0_9TRYP	Q38bz0 trypanosoma
59	37	75.5	463	2	Q9EZD9_ECOLI	Q9ezd9 escherichia
60	37	75.5	649	2	Q6YVV4_ORYSA	Q6yvv4 oryza sativ
61	37	75.5	649	2	Q6YVV7_ORYSA	Q6yvv7 oryza sativ
62	37	75.5	672	2	Q84SG8_ORYSA	Q84sg8 oryza sativ
63	37	75.5	712	2	Q47E45_DECAR	Q47e45 dechloromon
64	37	75.5	856	2	Q6APR6_DESPS	Q6apr6 desulfotale
65	36	73.5	117	2	Q4CDK4_CLOTM	Q4cdk4 clostridium
66	36	73.5	123	2	Q8DA02_VIBVU	Q8da02 vibrio vuln
67	36	73.5	127	2	Q6V493_SOYBN	Q6v493 glycine max
68	36	73.5	180	2	Q5XTM5_CARPA	Q5xtm5 carica papa
69	36	73.5	249	2	Q9PVV0_LAMRE	Q9pvv0 lampetra re
70	36	73.5	263	2	Q6V9R7_HUMAN	Q6v9r7 homo sapien
71	36	73.5	266	2	Q8GL69_9BACT	Q8gl69 uncultured
72	36	73.5	266	2	Q93T29_BURCE	Q93t29 burkholderi
73	36	73.5	281	2	Q2J7F3_9ACTO	Q2j7f3 frankia sp.
74	36	73.5	312	2	Q8H8P1_ORYSA	Q8h8p1 oryza sativ
75	36	73.5	320	1	DNC_HUMAN	Q9hc21 homo sapien
76	36	73.5	320	1	DNC_MACFA	Q5is35 macaca fasc
77	36	73.5	320	1	DNC_PONPY	Q5nvc1 pongo pygma
78	36	73.5	320	2	Q5JPC1_HUMAN	Q5jpc1 homo sapien
79	36	73.5	320	2	Q8NBT6_HUMAN	Q8nbt6 homo sapien
80	36	73.5	322	2	Q5H3U6_XANOR	Q5h3u6 xanthomonas
81	36	73.5	330	2	O04191_ARATH	O04191 arabidopsis
82	36	73.5	331	2	Q2M2N5_MOUSE	Q2m2n5 mus musculu
83	36	73.5	352	2	O65476_ARATH	O65476 arabidopsis
84	36	73.5	362	2	Q2R2U4_ORYSA	Q2r2u4 oryza sativ
85	36	73.5	370	2	Q4TC30_TETNG	Q4tc30 tetraodon n
86	36	73.5	372	2	O23082_ARATH	O23082 arabidopsis
87	36	73.5	393	2	Q8BQI4_MOUSE	Q8bqi4 mus musculu
88	36	73.5	426	2	Q6ZFY2_ORYSA	Q6zfy2 oryza sativ
89	36	73.5	429	2	O23081_ARATH	O23081 arabidopsis
90	36	73.5	434	2	Q654J4_ORYSA	Q654j4 oryza sativ
91	36	73.5	437	2	Q948D0_ORYSA	Q948d0 oryza sativ
92	36	73.5	438	2	Q4RUC5_TETNG	Q4ruc5 tetraodon n
93	36	73.5	441	2	Q7U4Q4_SYNPX	Q7u4q4 synechococc
94	36	73.5	450	2	O73786_XENLA	O73786 xenopus lae
95	36	73.5	454	2	Q4JU12_CORJK	Q4ju12 corynebacte
96	36	73.5	465	2	P70223_MOUSE	P70223 mus musculu
97	36	73.5	465	2	Q9D6H7_MOUSE	Q9d6h7 mus musculu
98	36	73.5	467	1	MATK_RAT	P41243 rattus norv
99	36	73.5	485	2	O65475_ARATH	O65475 arabidopsis
100	36	73.5	488	1	SRMS_HUMAN	Q9h3y6 homo sapien

ALIGNMENTS

```
RESULT 1
LCK_AOTNA
ID   LCK_AOTNA      STANDARD;      PRT;   508 AA.
AC   Q5PXS1;
DT   08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT   08-NOV-2005, sequence version 3.
DT   07-MAR-2006, entry version 13.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Aotus nancymaae (Ma's night monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=37293;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Perez-Quintero L.A., Vernot J.P.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways. Association of the TCR with a peptide
CC       antigen-bound MHC complex facilitates the interaction of CD4 and
CC       CD8 with MHC class II and class I molecules, respectively, and
CC       thereby recruits the associated LCK to the vicinity of the TCR/CD3
CC       complex. LCK then phosphorylates tyrosines residues within the
CC       immunoreceptor tyrosines-based activation motifs (ITAMs) in the
CC       cytoplasmic tails of the TCRgamma chains and CD3 subunits,
CC       initiating the TCR/CD3 signaling pathway. In addition, contributes
CC       to signaling by other receptor molecules. Associates directly with
CC       the cytoplasmic tail of CD2, and upon engagement of the CD2
CC       molecule, LCK undergoes hyperphosphorylation and activation. Also
CC       plays a role in the IL2 receptor-linked signaling pathway that
CC       controls T-cell proliferative response. Binding of IL2 to its
CC       receptor results in increased activity of LCK. Is expressed at all
CC       stages of thymocyte development and is required for the regulation
CC       of maturation events that are governed by both pre-TCR and mature
CC       alpha beta TCR (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also
CC       binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to
CC       other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds
CC       to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes
CC       through its SH3 domain and to the tyrosine phosphorylated form of
CC       KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.
CC       Interacts with phosphorylated LIME1. Interacts with CBLB (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.
CC       Present in lipid rafts in an unactive form (By similarity).
CC   -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.
CC       Interaction is regulated by Ser-58 phosphorylation (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ----------------------------------------------------------------------
DR   EMBL; AY821852; AAV70114.2; -; mRNA.
DR   SMR; Q5PXS1; 64-508.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    508       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088123.
FT   DOMAIN       60    120       SH3.
FT   DOMAIN      126    223       SH2.
FT   DOMAIN      244    497       Protein kinase.
FT   NP_BIND     250    258       ATP (By similarity).
FT   REGION        1     71       Interactions with CD4 and CD8 (By
FT                                similarity).
FT   ACT_SITE    363    363       Proton acceptor (By similarity).
FT   BINDING     272    272       ATP (By similarity).
FT   MOD_RES     393    393       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     504    504       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   508 AA;  58041 MW;  8B61951BC192A3A4 CRC64;

  Query Match             100.0%;  Score 49;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
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Db        293 QLQHQRLVRL 302


RESULT 2
LCK_HUMAN
ID   LCK_HUMAN      STANDARD;      PRT;   508 AA.
AC   P06239; P07100; Q12850; Q13152; Q5TDH8; Q5TDH9; Q96DW4; Q9NYT8;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1994, sequence version 5.
DT   07-MAR-2006, entry version 87.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase) (LSK) (T cell-
DE   specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=87133831; PubMed=3493153;
RA   Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
RA   Mak T.W.;
RT   "A human T cell-specific cDNA clone (YT16) encodes a protein with
```

RT extensive homology to a family of protein-tyrosine kinases.";
RL Eur. J. Immunol. 16:1643-1646(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=89123626; PubMed=3265417;
RA Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F.,
RA Wilson C.B.;
RT "Structure and expression of lck transcripts in human lymphoid
RT cells.";
RL J. Cell. Biochem. 38:117-126(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=90108697; PubMed=2558056; DOI=10.1016/0378-1119(89)90144-3;
RA Rouer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
RA Benarous R.;
RT "Structure of the human lck gene: differences in genomic organisation
RT within src-related genes affect only N-terminal exons.";
RL Gene 84:105-113(1989).
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA], VARIANTS LEU-27; GLN-LYS-PRO-231 INS;
RP VAL-352 AND LEU-446, AND PHOSPHORYLATION SITES TYR-393 AND TYR-504.
RC TISSUE=Leukemia;
RX MEDLINE=94187714; PubMed=8139546;
RA Wright D.D., Sefton B.M., Kamps M.P.;
RT "Oncogenic activation of the Lck protein accompanies translocation of
RT the LCK gene in the human HSB2 T-cell leukemia.";
RL Mol. Cell. Biol. 14:2429-2437(1994).
RN [5]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM SHORT), AND ALTERNATIVE SPLICING.
RC TISSUE=Leukemic T-cell;
RX MEDLINE=96085119; PubMed=7495859; DOI=10.1016/0167-4781(95)00162-A;
RA Vogel L.B., Arthur R., Fujita D.J.;
RT "An aberrant lck mRNA in two human T-cell lines.";
RL Biochim. Biophys. Acta 1264:168-172(1995).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG Human chromosome 1 international sequencing consortium;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX MEDLINE=89096891; PubMed=2850479;
RA Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT "Structure of the murine lck gene and its rearrangement in a murine
RT lymphoma cell line.";
RL Mol. Cell. Biol. 8:3058-3064(1988).
RN [9]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX MEDLINE=89313764; PubMed=2787474;
RA Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
RA Miyamoto N.G., Mak T.W.;
RT "Structure of the two promoters of the human lck gene: differential
RT accumulation of two classes of lck transcripts in T cells.";
RL Mol. Cell. Biol. 9:2173-2180(1989).
RN [10]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 13-508.
RC TISSUE=Peripheral blood lymphocyte;
RX MEDLINE=20462621; PubMed=11009097;
RX DOI=10.1002/1521-4141(200009)30:9<2632::AID-IMMU2632>3.0.CO;2-C;
RA Boncristiano M., Majolini M.B., D'Elios M.M., Pacini S., Valensin S.,
RA Ulivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,
RA Baldari C.T.;
RT "Defective recruitment and activation of ZAP-70 in common variable
RT immunodeficiency patients with T cell defects.";
RL Eur. J. Immunol. 30:2632-2638(2000).
RN [11]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 367-508.
RX MEDLINE=88217332; PubMed=2835736;
RA Veillette A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.;
RT "Expression of the lck tyrosine kinase gene in human colon carcinoma
RT and other non-lymphoid human tumor cell lines.";
RL Oncogene Res. 1:357-374(1987).
RN [12]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 374-508.
RX MEDLINE=87000726; PubMed=3489486; DOI=10.1016/0167-4889(86)90228-4;
RA Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
RA Linna T.J.;
RT "Human T lymphocytes express a protein-tyrosine kinase homologous to
RT p56LSTRA.";
RL Biochim. Biophys. Acta 888:286-295(1986).
RN [13]
RP PHOSPHORYLATION SITE TYR-504.
RX MEDLINE=92347326; PubMed=1639064;
RA Bergman M., Mustelin T., Oetken C., Partanen J., Flint N.A.,
RA Amrein K.E., Autero M., Burn P., Alitalo K.;
RT "The human p50csk tyrosine kinase phosphorylates p56lck at Tyr-505 and
RT down regulates its catalytic activity.";
RL EMBO J. 11:2919-2924(1992).
RN [14]
RP INTERACTION WITH PI3K.
RX MEDLINE=94067101; PubMed=7504174;
RA Vogel L.B., Fujita D.J.;
RT "The SH3 domain of p56lck is involved in binding to
RT phosphatidylinositol 3'-kinase from T lymphocytes.";
RL Mol. Cell. Biol. 13:7408-7417(1993).
RN [15]
RP INTERACTION WITH KHDRBS1.
RX MEDLINE=95155308; PubMed=7852312; DOI=10.1074/jbc.270.6.2506;
RA Vogel L.B., Fujita D.J.;
RT "p70 phosphorylation and binding to p56lck is an early event in
RT interleukin-2-induced onset of cell cycle progression in T-
RT lymphocytes.";
RL J. Biol. Chem. 270:2506-2511(1995).
RN [16]
RP INTERACTION WITH SQSTM1, AND MUTAGENESIS OF SER-58 AND ARG-153.
RX PubMed=8618896;
RA Park I., Chung J., Walsh C.T., Yun Y., Strominger J.L., Shin J.;
RT "Phosphotyrosine-independent binding of a 62-kDa protein to the src
RT homology 2 (SH2) domain of p56lck and its regulation by
RT phosphorylation of Ser-59 in the lck unique N-terminal region.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:12338-12342(1995).
RN [17]
RP INTERACTION WITH HIV-1 NEF.
RX MEDLINE=96386556; PubMed=8794306;
RA Greenway A.L., Azad A., Mills J., McPhee D.A.;
RT "Human immunodeficiency virus type 1 Nef binds directly to LCK and
RT mitogen-activated protein kinase, inhibiting kinase activity.";
RL J. Virol. 70:6701-6708(1996).
RN [18]
RP REVIEW.
RX PubMed=10848956;
RA Isakov N., Biesinger B.;
RT "Lck protein tyrosine kinase is a key regulator of T-cell activation

```
RT   and a target for signal intervention by Herpesvirus saimiri and other
RT   viral gene products.";
RL   Eur. J. Biochem. 267:3413-3421(2000).
RN   [19]
RP   SUBCELLULAR LOCATION.
RX   PubMed=12218089;
RA   Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA   Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT   "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT   protein/phosphoprotein associated with glycolipid-enriched
RT   microdomains in lipid rafts in resting T cells.";
RL   J. Immunol. 169:2813-2817(2002).
RN   [20]
RP   MASS SPECTROMETRY.
RC   TISSUE=Mammary cancer;
RX   MEDLINE=21829512; PubMed=11840567;
RX   DOI=10.1002/1615-9861(200202)2:2<212::AID-PROT212>3.0.CO;2-H;
RA   Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
RA   Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
RA   Zvelebil M.J.;
RT   "Cluster analysis of an extensive human breast cancer cell line
RT   protein expression map database.";
RL   Proteomics 2:212-223(2002).
RN   [21]
RP   INTERACTION WITH LIME1.
RX   PubMed=14610046; DOI=10.1084/jem.20031484;
RA   Brdickova N., Brdicka T., Angelisova P., Horvath O., Spicka J.,
RA   Hilgert I., Paces J., Simeoni L., Kliche S., Merten C., Schraven B.,
RA   Horejsi V.;
RT   "LIME: a new membrane raft-associated adaptor protein involved in CD4
RT   and CD8 coreceptor signaling.";
RL   J. Exp. Med. 198:1453-1462(2003).
RN   [22]
RP   INTERACTION WITH LIME1.
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Qy          1 QLQHQRLVRL 10
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Db        293 QLQHQRLVRL 302
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AC   Q7RTZ3;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Protein tyrosine kinase.
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22289034; PubMed=12401726;
RA   Nervi S., Nicodeme S., Gartioux C., Atlan C., Lathrop M., Reviron D.,
RA   Naquet P., Matsuda F., Imbert J., Vialettes B.;
RT   "No association between lck gene polymorphisms and protein level in
RT   type 1 diabetes.";
RL   Diabetes 51:3326-3330(2002).
CC   -!- MISCELLANEOUS: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ third party annotation (TPA) entry.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BN000073; CAD55807.1; -; Genomic_DNA.
DR   HSSP; P06239; 1BHF.
DR   SMR; Q7RTZ3; 65-509.
DR   Ensembl; ENSG00000182866; Homo sapiens.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   509 AA;  58001 MW;  44BFF0D43FFB420D CRC64;
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  Query Match             100.0%;  Score 49;  DB 2;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
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Db        294 QLQHQRLVRL 303
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AC   Q95M32;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Lck protein.
GN   Name=lck;
OS   Hylobates sp. (gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Hylobatidae; Hylobates.
OX   NCBI_TaxID=9581;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22031236; PubMed=12033791; DOI=10.1006/viro.2002.1381;
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RA   Picard C., Greenway A., Holloway G., Olive D., Collette Y.;
RT   "Interaction with simian Hck tyrosine kinase reveals convergent
RT   evolution of the Nef protein from simian and human immunodeficiency
RT   viruses despite differential molecular surface usage.";
RL   Virology 295:320-327(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Picard C.;
RL   Thesis (2001), Department of Experimental Oncology laboratory, U.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ320182; CAC44027.1; -; mRNA.
DR   HSSP; P06239; 1LCK.
DR   SMR; Q95M32; 65-509.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   509 AA;  57947 MW;  F1BFE5C237C8DB7E CRC64;

  Query Match            100.0%;  Score 49;  DB 2;  Length 509;
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Qy          1 QLQHQRLVRL 10
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Db        294 QLQHQRLVRL 303


RESULT 5
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ID   Q3ZCM0_BOVIN   PRELIMINARY;   PRT;   509 AA.
AC   Q3ZCM0;
DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
DT   07-MAR-2006, entry version 6.
DE   Hypothetical protein MGC126900.
GN   Name=MGC126900;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Crossbred x Angus; TISSUE=Ileum;
RA   Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA   Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA   Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA   Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA   Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA   Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC102046; AAI02047.1; -; mRNA.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   509 AA;  58116 MW;  CE0E80DCD6D0F2F8 CRC64;

  Query Match            100.0%;  Score 49;  DB 2;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
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              ||||||||||
Db        294 QLQHQRLVRL 303


RESULT 6
Q573B4_HUMAN
ID   Q573B4_HUMAN   PRELIMINARY;   PRT;   516 AA.
AC   Q573B4;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Proto-oncogene tyrosine-protein kinase LCK.
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Blood;
RX   PubMed=16107303; DOI=10.1016/j.gene.2005.06.018;
RA   Nervi S., Guinamard R., Delaval B., Lecine P., Vialettes B.,
RA   Naquet P., Imbert J.;
RT   "A rare mRNA variant of the human lymphocyte-specific protein tyrosine
RT   kinaseLCK gene with intron B retention and exon 7 skipping encodes a
RT   putativeprotein with altered SH3-dependent molecular interactions.";
RL   Gene 359:18-25(2005).
CC   -----------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AJ865079; CAI23831.1; -; mRNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   516 AA;  58333 MW;  EB9A52D4EBDF14D2 CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 516;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
              ||||||||||
Db        301 QLQHQRLVRL 310


RESULT 7
Q4RR72_TETNG
ID   Q4RR72_TETNG   PRELIMINARY;   PRT;   322 AA.
AC   Q4RR72;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   Chromosome 14 SCAF15003, whole genome shotgun sequence. (Fragment).
GN   ORFNames=GSTENG00030294001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC       cycle. It is required in higher cells for entry into S-phase and
CC       mitosis. Component of the kinase complex that phosphorylates the
CC       repetitive C-terminus of RNA polymerase II. Catalytic component of
CC       MPF (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC       mature oocytes (By similarity).
CC   -----------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; CAAE01015003; CAG09110.1; -; Genomic_DNA.
DR   SMR; Q4RR72; 2-322.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   322 AA;  36768 MW;  EC0ED0B6DB1CBB2F CRC64;

  Query Match             93.9%;  Score 46;  DB 2;  Length 322;
  Best Local Similarity   90.0%;  Pred. No. 2.5;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 QLQHQRLVRL 10
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Db         82 QLQHERLVRL 91


RESULT 8
LCK_SAISC
ID   LCK_SAISC      STANDARD;      PRT;   508 AA.
AC   Q95KR7;
DT   08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT   08-NOV-2005, sequence version 2.
DT   07-MAR-2006, entry version 26.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], ENZYME REGULATION, AND INTERACTION WITH
RP   SAIMIRINE HERPESVIRUS 2 TIP.
RC   TISSUE=T-cell;
RX   MEDLINE=21424508; PubMed=11533187;
RX   DOI=10.1128/JVI.75.19.9252-9261.2001;
RA   Greve T., Tamgueney G., Fleischer B., Fickenscher H., Broeker B.M.;
RT   "Downregulation of p56Lck tyrosine kinase activity in T cells of
RT   squirrel monkeys (Saimiri sciureus) correlates with the non-
RT   transforming and apathogenic properties of herpesvirus saimiri in its
RT   natural host.";
RL   J. Virol. 75:9252-9261(2001).
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways. Association of the TCR with a peptide
CC       antigen-bound MHC complex facilitates the interaction of CD4 and
CC       CD8 with MHC class II and class I molecules, respectively, and
CC       thereby recruits the associated LCK to the vicinity of the TCR/CD3
CC       complex. LCK then phosphorylates tyrosines residues within the
CC       immunoreceptor tyrosines-based activation motifs (ITAMs) in the
CC       cytoplasmic tails of the TCRgamma chains and CD3 subunits,
CC       initiating the TCR/CD3 signaling pathway. In addition, contributes
CC       to signaling by other receptor molecules. Associates directly with
CC       the cytoplasmic tail of CD2, and upon engagement of the CD2
CC       molecule, LCK undergoes hyperphosphorylation and activation. Also
CC       plays a role in the IL2 receptor-linked signaling pathway that
CC       controls T-cell proliferative response. Binding of IL2 to its
CC       receptor results in increased activity of LCK. Is expressed at all
CC       stages of thymocyte development and is required for the regulation
CC       of maturation events that are governed by both pre-TCR and mature
CC       alpha beta TCR (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- ENZYME REGULATION: Regulated by phosphatases.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also
CC       binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to
CC       other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds
CC       to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes
CC       through its SH3 domain and to the tyrosine phosphorylated form of
CC       KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.
CC       Interacts with phosphorylated LIME1. Interacts with CBLB (By
CC       similarity). Interacts with saimirine herpesvirus 2 TIP.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.
CC       Present in lipid rafts in an unactive form (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed specificaly in lymphoid cells.
CC   -!- DEVELOPMENTAL STAGE: Levels remain relatively constant throughout
CC       T-cell ontogeny.
CC   -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.
CC       Interaction is regulated by Ser-58 phosphorylation (By
CC       similarity).
CC   -!- PTM: Phosphorylated on Tyr-504 presumably by CSK. This
CC       phosphorylation downregulates catalytic activity. Phosphorylated
CC       on Tyr-393 either by itself or another kinase, leading to
CC       increased enzymatic activity.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   -!- CAUTION: LCK seems to be active in all vertebrates, except in
CC       squirrel monkey T-cells, in which it is inactivated. The reason
CC       seems to be that squirrel monkey are the natural host for
CC       Saimiriine herpesvirus 2, which is able to efficiently transform
CC       T-cells through a mecanism involving viral Tip/ host LCK
CC       interaction. Its inactivation may a mecanism that specificaly
CC       counteracts the transformation effects of viral Tip.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ277921; CAC38871.1; -; mRNA.
DR   HSSP; P06239; 1LKK.
DR   SMR; Q95KR7; 64-508.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    508       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088127.
FT   DOMAIN       60    120       SH3.
FT   DOMAIN      126    223       SH2.
FT   DOMAIN      244    497       Protein kinase.
FT   NP_BIND     250    258       ATP (By similarity).
FT   REGION        1     71       Interactions with CD4 and CD8 (By
FT                                similarity).
FT   ACT_SITE    363    363       Proton acceptor (By similarity).
FT   BINDING     272    272       ATP (By similarity).
FT   MOD_RES     393    393       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     504    504       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   508 AA;  58122 MW;  5088C64061853819 CRC64;

  Query Match             91.8%;  Score 45;  DB 1;  Length 508;
  Best Local Similarity   90.0%;  Pred. No. 6.5;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 QLQHQRLVRL 10
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Db        293 QLQHKRLVRL 302


RESULT 9
Q3TLX4_MOUSE
ID   Q3TLX4_MOUSE   PRELIMINARY;   PRT;   368 AA.
AC   Q3TLX4;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched
DE   library, clone:G830026O06 product:lymphocyte protein tyrosine kinase,
DE   full insert sequence. (Fragment).
GN   Name=Lck;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
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RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK166263; BAE38668.1; -; mRNA.
DR   MGI; MGI:96756; Lck.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   368 AA;  42018 MW;  7AB6AE53AF1A5059 CRC64;

  Query Match           87.8%;  Score 43;  DB 2;  Length 368;
  Best Local Similarity   90.0%;  Pred. No. 11;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
              |||| |||||
Db        153 QLQHPRLVRL 162


RESULT 10
Q4FZR6_RAT
ID   Q4FZR6_RAT     PRELIMINARY;   PRT;   379 AA.
AC   Q4FZR6;
DT   30-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   30-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Lck_mapped protein (Fragment).
GN   Name=Lck_mapped;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC099218; AAH99218.1; -; mRNA.
DR   SMR; Q4FZR6; 2-379.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   379 AA;  43336 MW;  7CDEB573BAFB53AB CRC64;

  Query Match           87.8%;  Score 43;  DB 2;  Length 379;
  Best Local Similarity   90.0%;  Pred. No. 11;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 QLQHQRLVRL 10
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Db        164 QLQHPRLVRL 173


RESULT 11
Q5TYU7_BRARE
ID   Q5TYU7_BRARE   PRELIMINARY;   PRT;   485 AA.
AC   Q5TYU7;
DT   07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   07-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   Novel protein tyrosine kinase.
GN   Name=si:dkey-33i22.2; Synonyms=OTTDARP00000004623;
GN   ORFNames=DKEY-33I22.2-001;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Dunn M.;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BX842684; CAH69080.1; -; Genomic_DNA.
DR   SMR; Q5TYU7; 42-485.
DR   Ensembl; ENSDARG00000007783; Danio rerio.
DR   ZFIN; ZDB-GENE-040724-106; si:dkey-33i22.2.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   485 AA;  55644 MW;  3ED1878453666747 CRC64;

  Query Match             87.8%;  Score 43;  DB 2;  Length 485;
  Best Local Similarity   80.0%;  Pred. No. 15;
  Matches    8;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
              ||||:|||:|
Db        271 QLQHERLVKL 280


RESULT 12
LCK_MOUSE
ID   LCK_MOUSE       STANDARD;       PRT;   508 AA.
AC   P06240; Q61794; Q61795; Q62320; Q91X65;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   25-OCT-2005, sequence version 3.
DT   07-MAR-2006, entry version 74.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase) (LSK).
GN   Name=Lck; Synonyms=Lsk-t;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86079521; PubMed=2416464; DOI=10.1016/0092-8674(85)90169-2;
RA   Marth J.D., Peet R., Krebs E.G., Perlmutter R.M.;
RT   "A lymphocyte-specific protein-tyrosine kinase gene is rearranged and
RT   overexpressed in the murine T cell lymphoma LSTRA.";
RL   Cell 43:393-404(1985).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86146842; PubMed=3081813;
RA   Voronova A.F., Sefton B.M.;
RT   "Expression of a new tyrosine protein kinase is stimulated by
RT   retrovirus promoter insertion.";
RL   Nature 319:682-685(1986).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=NOD; TISSUE=Thymus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX MEDLINE=89096891; PubMed=2850479;
RA Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT "Structure of the murine lck gene and its rearrangement in a murine
RT lymphoma cell line.";
RL Mol. Cell. Biol. 8:3058-3064(1988).
RN [6]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-10.
RX MEDLINE=88142832; PubMed=3501824;
RA Voronova A.F., Adler H.T., Sefton B.M.;
RT "Two lck transcripts containing different 5' untranslated regions are
RT present in T cells.";
RL Mol. Cell. Biol. 7:4407-4413(1987).
RN [7]
RP MUTAGENESIS OF TYR-504.
RX MEDLINE=88248001; PubMed=3380790;
RA Amrein K.E., Sefton B.M.;
RT "Avian reovirus mRNAs are nonfunctional in infected mouse cells:
RT translational basis for virus host-range restriction.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:4257-4261(1988).
RN [8]
RP INTERACTIONS WITH CD4 AND CD8, AND MUTAGENESIS OF 2-CYS--CYS-4; CYS-19
RP AND CYS-22.
RX MEDLINE=90182665; PubMed=2107025; DOI=10.1016/0092-8674(90)90090-2;
RA Turner J.M., Brodsky M.H., Irving B.A., Levin S.D., Perlmutter R.M.,
RA Littman D.R.;
RT "Interaction of the unique N-terminal region of tyrosine kinase p56lck
RT with cytoplasmic domains of CD4 and CD8 is mediated by cysteine
RT motifs.";
RL Cell 60:755-765(1990).
RN [9]
RP MUTAGENESIS.
RX MEDLINE=93059694; PubMed=1279202;
RA Hurley T.R., Amrein K.E., Sefton B.M.;
RT "Creation and characterization of temperature-sensitive mutants of the
RT lck tyrosine protein kinase.";
RL J. Virol. 66:7406-7413(1992).
RN [10]
RP MUTAGENESIS OF LYS-272.
RX MEDLINE=91163633; PubMed=1706070; DOI=10.1038/350062a0;
RA Abraham N., Miceli M.C., Parnes J.C., Veillette A.;
RT "Enhancement of T-cell responsiveness by the lymphocyte-specific
RT tyrosine protein kinase p56lck.";
RL Nature 350:62-66(1991).
RN [11]
RP MUTAGENESIS OF TYR-504.
RX MEDLINE=91219495; PubMed=1708890;
RA Abraham K.M., Levin S.D., Marth J.D., Forbush K.A., Perlmutter R.M.;
RT "Thymic tumorigenesis induced by overexpression of p56lck.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981(1991).
RN [12]
RP PHOSPHORYLATION BY CSK.
RX PubMed=8371758; DOI=10.1038/365156a0;
RA Chow L.M., Fournel M., Davidson D., Veillette A.;
RT "Negative regulation of T-cell receptor signalling by tyrosine protein
RT kinase p50csk.";
RL Nature 365:156-160(1993).
RN [13]
RP MUTAGENESIS.
RX MEDLINE=93133805; PubMed=8421674;
RA Carrera A.C., Alexandrov K., Roberts T.M.;
RT "The conserved lysine of the catalytic domain of protein kinases is
RT actively involved in the phosphotransfer reaction and not required for
RT anchoring ATP.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:442-446(1993).
RN [14]
RP PALMITOYLATION.
RX MEDLINE=94019312; PubMed=8413237;
RA Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;
RT "Palmitylation of an amino-terminal cysteine motif of protein tyrosine
RT kinases p56lck and p59fyn mediates interaction with glycosyl-
RT phosphatidylinositol-anchored proteins.";
RL Mol. Cell. Biol. 13:6385-6392(1993).
RN [15]
RP PALMITOYLATION.
RX MEDLINE=95071286; PubMed=7980442;
RA Koegl M., Zlatkine P., Ley S.C., Courtneidge S.A., Magee A.I.;
RT "Palmitoylation of multiple Src-family kinases at a homologous N-
RT terminal motif.";
RL Biochem. J. 303:749-753(1994).
RN [16]
RP INTERACTION WITH CBLB.
RX PubMed=10646608; DOI=10.1038/35003228;
RA Bachmaier K., Krawczyk C., Kozieradzki I., Kong Y.-Y., Sasaki T.,
RA Oliveira-dos-Santos A., Mariathasan S., Bouchard D., Wakeham A.,
RA Itie A., Le J., Ohashi P.S., Sarosi I., Nishina H., Lipkowitz S.,
RA Penninger J.M.;
RT "Negative regulation of lymphocyte activation and autoimmunity by the
RT molecular adaptor Cbl-b.";
RL Nature 403:211-216(2000).
RN [17]
RP SUBCELLULAR LOCATION.
RX PubMed=12218089;
RA Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT protein/phosphoprotein associated with glycolipid-enriched
RT microdomains in lipid rafts in resting T cells.";
RL J. Immunol. 169:2813-2817(2002).
RN [18]
RP PHOSPHORYLATION SITE TYR-393, AND MASS SPECTROMETRY.
RX PubMed=15592455; DOI=10.1038/nbt1046;
RA Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
RA Zha X.-M., Polakiewicz R.D., Comb M.J.;
RT "Immunoaffinity profiling of tyrosine phosphorylation in cancer

Query Match 87.8%; Score 43; DB 1; Length 508;
Best Local Similarity 90.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 QLQHQRLVRL 10
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Db        293 QLQHPRLVRL 302
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RESULT 13
Q6KA98_ORYSA
ID Q6KA98_ORYSA PRELIMINARY; PRT; 490 AA.
AC Q6KA98;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Hypothetical protein OJ1063_D06.21.
GN Name=OJ1063_D06.21;

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OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
CC   -----------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AP003989; BAD22873.1; -; Genomic_DNA.
DR   Gramene; Q6KA98; -.
DR   InterPro; IPR001810; F-box.
DR   Pfam; PF00646; F-box; 1.
DR   PROSITE; PS50181; FBOX; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   490 AA;  56815 MW;  2C3B2BDA3745CA28 CRC64;

  Query Match             83.7%;  Score 41;  DB 2;  Length 490;
  Best Local Similarity   80.0%;  Pred. No. 37;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
              ||:||||| |
Db        223 QLEHQRLVEL 232


RESULT 14
BLK_MOUSE
ID   BLK_MOUSE      STANDARD;      PRT;   498 AA.
AC   P16277;
DT   01-AUG-1990, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1995, sequence version 2.
DT   07-MAR-2006, entry version 63.
DE   Tyrosine-protein kinase BLK (EC 2.7.1.112) (B lymphocyte kinase) (p55-
DE   BLK).
GN   Name=Blk;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=B-cell;
RX   MEDLINE=90117147; PubMed=2404338;
RA   Dymecki S.M., Niederhuber J.E., Desiderio S.V.;
RT   "Specific expression of a tyrosine kinase gene, blk, in B lymphoid
RT   cells.";
RL   Science 247:332-336(1990).
RN   [2]
RP   STRUCTURE BY NMR OF SH2 DOMAIN.
RX   MEDLINE=96224819; PubMed=8639560; DOI=10.1021/bi960157x;
RA   Metzler W.J., Leiting B., Pryor K., Mueller L., Farmer B.T. II;
RT   "The three-dimensional solution structure of the SH2 domain from
RT   p55blk kinase.";
RL   Biochemistry 35:6201-6211(1996).
CC   -!- FUNCTION: May function in a signal transduction pathway that is
CC       restricted to B lymphoid cells.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   -----------------------------------------------------------------------
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CC   -----------------------------------------------------------------------
DR   EMBL; M30903; AAA40453.1; -; mRNA.
DR   PIR; A40092; A40092.
DR   PDB; 1BLJ; NMR; @=106-217.
DR   PDB; 1BLK; NMR; @=106-217.
DR   SMR; P16277; 56-498.
DR   Ensembl; ENSMUSG00000014453; Mus musculus.
DR   MGI; MGI:88169; Blk.
DR   LinkHub; P16277; -.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; FALSE_NEG.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   3D-structure; ATP-binding; Kinase; Lipoprotein; Myristate;
KW   Nucleotide-binding; Phosphorylation; SH2 domain; SH3 domain;
KW   Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       By similarity.
FT   CHAIN         1    498       Tyrosine-protein kinase BLK.
FT                                /FTId=PRO_0000088062.
FT   DOMAIN       51    111       SH3.
FT   DOMAIN      117    213       SH2.
FT   DOMAIN      234    487       Protein kinase.
FT   NP_BIND     240    248       ATP (By similarity).
FT   ACT_SITE    353    353       Proton acceptor (By similarity).
FT   BINDING     262    262       ATP (By similarity).
FT   MOD_RES     382    382       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   STRAND      108    109
FT   STRAND      112    112
FT   STRAND      115    118
FT   STRAND      121    121
FT   HELIX       124    131
FT   STRAND      132    133
FT   TURN        134    135
FT   TURN        138    139
FT   STRAND      141    143
FT   STRAND      145    145
FT   TURN        147    148
FT   STRAND      150    151
FT   STRAND      153    157
FT   STRAND      159    159
FT   TURN        162    164
FT   STRAND      166    166
FT   STRAND      170    175
FT   TURN        176    178
FT   STRAND      179    183
FT   TURN        184    185
FT   STRAND      186    190
FT   HELIX       191    200
FT   STRAND      203    207
FT   STRAND      213    213
SQ   SEQUENCE   498 AA;  56513 MW;  BE49D7B079FDD577 CRC64;

  Query Match             83.7%;  Score 41;  DB 1;  Length 498;
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  Best Local Similarity   88.9%;  Pred. No. 38;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LQHQRLVRL 10
              |||:|||||
Db        284 LQHERLVRL 292


RESULT 15
Q5FW27_XENTR
ID   Q5FW27_XENTR   PRELIMINARY;   PRT;   498 AA.
AC   Q5FW27;
DT   01-MAR-2005, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2005, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   MGC107870 protein.
GN   Name=MGC107870;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole body;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole body;
RA   Klein S., Gerhard D.S.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC089654; AAH89654.1; -; mRNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   498 AA;  56437 MW;  3C5B9CEED5A0DF00 CRC64;

  Query Match            83.7%;  Score 41;  DB 2;  Length 498;
  Best Local Similarity   88.9%;  Pred. No. 38;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LQHQRLVRL 10
              |||:|||||
Db        283 LQHERLVRL 291


RESULT 16
Q3TAT8_MOUSE
ID   Q3TAT8_MOUSE   PRELIMINARY;   PRT;   499 AA.
AC   Q3TAT8;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Activated spleen cDNA, RIKEN full-length enriched library,
DE   clone:F830002A02 product:B lymphoid kinase, full insert sequence.
GN   Name=Blk;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
```

RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
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CC ---
DR EMBL; AK171640; BAE42580.1; -; mRNA.
DR MGI; MGI:88169; Blk.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF07714; Pkinase_Tyr; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3_1; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KW Kinase.
SQ SEQUENCE 499 AA; 56614 MW; E1C607564BB4FD6C CRC64;

Query Match 83.7%; Score 41; DB 2; Length 499;
Best Local Similarity 88.9%; Pred. No. 38;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 LQHQRLVRL 10
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Db        285 LQHERLVRL 293


RESULT 17
Q4KM97_RAT
ID   Q4KM97_RAT     PRELIMINARY;   PRT;   499 AA.
AC   Q4KM97;
DT   02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   02-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   B lymphoid kinase.
GN   Name=Blk;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC098683; AAH98683.1; -; mRNA.
DR   SMR; Q4KM97; 57-499.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   499 AA;  56648 MW;  BABC593E15CAAFD7 CRC64;

  Query Match           83.7%;  Score 41;  DB 2;  Length 499;
  Best Local Similarity   88.9%;  Pred. No. 38;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LQHQRLVRL 10
              |||:|||||
Db        285 LQHERLVRL 293


RESULT 18
Q8K2M8_MOUSE
ID   Q8K2M8_MOUSE   PRELIMINARY;   PRT;   499 AA.
AC   Q8K2M8;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 27.
DE   B lymphoid kinase (Blk protein) (Activated spleen cDNA, RIKEN full-
DE   length enriched library, clone:F830045C23 product:B lymphoid kinase,
DE   full insert sequence).
GN   Name=Blk;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RG   NIH MGC Project;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E.,
RA   Mollenhauer J., Wiemann S., Schick M., Korn B.;
RT   "Cloning of mouse full open reading frames in Gateway(R) system entry
RT   vector (pDONR201).";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
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RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [10]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [11]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

```
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

  Query Match             83.7%;  Score 41;  DB 2;  Length 499;
  Best Local Similarity   88.9%;  Pred. No. 38;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LQHQRLVRL 10
              |||:|||||
Db        285 LQHERLVRL 293


RESULT 19
BLK_HUMAN
ID   BLK_HUMAN      STANDARD;      PRT;   504 AA.
AC   P51451; Q16291;
DT   01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-1996, sequence version 1.
DT   07-MAR-2006, entry version 48.
DE   Tyrosine-protein kinase BLK (EC 2.7.1.112) (B lymphocyte kinase) (p55-
DE   BLK).
GN   Name=BLK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=95123078; PubMed=7822795;
RA   Islam K.B., Rabbani H., Larsson C., Sanders R., Smith C.I.;
RT   "Molecular cloning, characterization, and chromosomal localization of
RT   a human lymphoid tyrosine kinase related to murine Blk.";
RL   J. Immunol. 154:1265-1272(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=95148218; PubMed=7845672;
RA   Drebin J.A., Hartzell S.W., Griffin C., Campbell M.J.,
RA   Niederhuber J.E.;
RT   "Molecular cloning and chromosomal localization of the human homologue
RT   of a B-lymphocyte specific protein tyrosine kinase (blk).";
RL   Oncogene 10:477-486(1995).
CC   -!- FUNCTION: May function in a signal transduction pathway that is
CC       restricted to B lymphoid cells.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; Z33998; CAA83965.1; -; mRNA.
DR   EMBL; S76617; AAB33265.1; -; mRNA.
DR   PIR; I37206; I37206.
DR   HSSP; P16277; 1BLK.
DR   SMR; P51451; 62-504.
DR   Ensembl; ENSG00000136573; Homo sapiens.
DR   H-InvDB; HIX0007315; -.
DR   HGNC; HGNC:1057; BLK.
DR   MIM; 191305; gene.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; TAS.
DR   GO; GO:0007243; P:protein kinase cascade; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; FALSE_NEG.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;
KW   Phosphorylation; SH2 domain; SH3 domain; Transferase;
KW   Tyrosine-protein kinase.
FT   INIT_MET      0      0       By similarity.
FT   CHAIN         1    504       Tyrosine-protein kinase BLK.
FT                                /FTId=PRO_0000088061.
FT   DOMAIN       57    117       SH3.
FT   DOMAIN      123    219       SH2.
FT   DOMAIN      240    493       Protein kinase.
FT   NP_BIND     246    254       ATP (By similarity).
FT   ACT_SITE    359    359       Proton acceptor (By similarity).
FT   BINDING     268    268       ATP (By similarity).
FT   MOD_RES     388    388       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   CONFLICT    286    286       M -> V (in Ref. 2).
FT   CONFLICT    406    406       I -> Y (in Ref. 2).
SQ   SEQUENCE   504 AA;  57607 MW;  BDB1DF50EC7370C8 CRC64;

  Query Match             83.7%;  Score 41;  DB 1;  Length 504;
  Best Local Similarity   88.9%;  Pred. No. 38;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LQHQRLVRL 10
              |||:|||||
Db        290 LQHERLVRL 298


RESULT 20
Q96IN1_HUMAN
ID   Q96IN1_HUMAN   PRELIMINARY;   PRT;   505 AA.
AC   Q96IN1;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 24.
DE   B lymphoid tyrosine kinase.
GN   Name=BLK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Blood, and Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Blood;
RA   Director MGC Project;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC007371; AAH07371.1; -; mRNA.
DR   EMBL; BC032413; AAH32413.1; -; mRNA.
DR   HSSP; P16277; 1BLK.
DR   SMR; Q96IN1; 63-505.
DR   Ensembl; ENSG00000136573; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   505 AA;  57706 MW;  B5F739BEF8389176 CRC64;

  Query Match             83.7%;  Score 41;  DB 2;  Length 505;
  Best Local Similarity   88.9%;  Pred. No. 38;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LQHQRLVRL 10
              |||:|||||
Db        291 LQHERLVRL 299


RESULT 21
Q3XC39_METFL
ID   Q3XC39_METFL   PRELIMINARY;   PRT;   320 AA.
AC   Q3XC39;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   FecR protein.
GN   ORFNames=MflaDRAFT_2314;
OS   Methylobacillus flagellatus KT.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Methylophilales;
OC   Methylophilaceae; Methylobacillus.
OX   NCBI_TaxID=265072;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=KT;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome and assembly of Methylobacillus
RT   flagellatus KT.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=KT;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Methylobacillus
RT   flagellatus KT.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=KT;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AADX02000002; EAN03635.1; -; Genomic_DNA.
DR   InterPro; IPR006860; FecR.
DR   InterPro; IPR012373; Ferrdict_sens_TM.
DR   Pfam; PF04773; FecR; 1.
DR   PIRSF; PIRSF018266; FecR; 1.
SQ   SEQUENCE   320 AA;  35823 MW;  24B1EF921196EFE0 CRC64;

  Query Match             81.6%;  Score 40;  DB 2;  Length 320;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 QHQRLVRL 10
              ||||||||
Db        143 QHQRLVRL 150


RESULT 22
Q4RL31_TETNG
ID   Q4RL31_TETNG   PRELIMINARY;   PRT;   511 AA.
AC   Q4RL31;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   Chromosome undetermined SCAF15024, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00032670001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
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RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC       cycle. It is required in higher cells for entry into S-phase and
CC       mitosis. Component of the kinase complex that phosphorylates the
CC       repetitive C-terminus of RNA polymerase II. Catalytic component of
CC       MPF (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC       mature oocytes (By similarity).
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CAAE01015024; CAG10901.1; -; Genomic_DNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   511 AA;  58279 MW;  9B7977111E4685AC CRC64;

  Query Match             81.6%;  Score 40;  DB 2;  Length 511;
  Best Local Similarity   80.0%;  Pred. No. 60;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
              :||| |||||
Db        258 KLQHDRLVRL 267
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RESULT 23
Q9U8V6_EPTBU
ID   Q9U8V6_EPTBU   PRELIMINARY;   PRT;   249 AA.
AC   Q9U8V6;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 28.
DE   Src-like A (Fragment).
OS   Eptatretus burgeri (Inshore hagfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
OC   Myxinidae; Eptatretinae; Eptatretus.
OX   NCBI_TaxID=7764;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20020330; PubMed=10552041;
RA   Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
RT   "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey:
RT   isoform duplications around the divergence of cyclostomes and
RT   gnathostomes.";
RL   J. Mol. Evol. 49:601-608(1999).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB025546; BAA84736.1; -; mRNA.
DR   HSSP; P06239; 1QPC.
DR   SMR; Q9U8V6; 1-249.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   249 AA;  28636 MW;  D7F37EE197EA580C CRC64;

  Query Match             79.6%;  Score 39;  DB 2;  Length 249;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LQHQRLVRL 10
              ||| |||||
Db         35 LQHDRLVRL 43


RESULT 24
Q6L576_ORYSA
ID   Q6L576_ORYSA   PRELIMINARY;   PRT;   371 AA.
AC   Q6L576;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   Hypothetical protein OJ1008_D08.5.
GN   Name=OJ1008_D08.5;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
```

```
RA   Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA   Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA   Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA   Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA   Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA   Wu H.-P., Shaw J.-F.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AC104705; AAT44173.1; -; Genomic_DNA.
DR   Gramene; Q6L576; -.
DR   GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
DR   GO; GO:0006629; P:lipid metabolism; IEA.
DR   InterPro; IPR001087; Lipase_GDSL.
DR   Pfam; PF00657; Lipase_GDSL; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   371 AA;  42000 MW;  01AA0FD3200A8D28 CRC64;

  Query Match             79.6%;  Score 39;  DB 2;  Length 371;
  Best Local Similarity   77.8%;  Pred. No. 66;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVR 9
              ||||:|:||
Db        306 QLQHERVVR 314


RESULT 25
O93411_XENLA
ID   O93411_XENLA   PRELIMINARY;   PRT;   496 AA.
AC   O93411;
DT   01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1998, sequence version 1.
DT   07-FEB-2006, entry version 25.
DE   Non-receptor protein tyrosine kinase laloo.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Weinstein D.C., Marden J., Carnevali F., Hemmati-Brivanlou A.;
RT   "FGF-mediated mesoderm induction involves the Src-family kinase
RT   laloo.";
RL   Nature 0:0-0(1998).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF081803; AAC31209.1; -; mRNA.
DR   HSSP; P06239; 1QPC.
DR   SMR; O93411; 54-496.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase; Receptor.
SQ   SEQUENCE   496 AA;  56275 MW;  96223A6F99689965 CRC64;

  Query Match             79.6%;  Score 39;  DB 2;  Length 496;
  Best Local Similarity   88.9%;  Pred. No. 91;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LQHQRLVRL 10
              ||| |||||
Db        281 LQHDRLVRL 289


RESULT 26
Q66I04_BRARE
ID   Q66I04_BRARE   PRELIMINARY;   PRT;   510 AA.
AC   Q66I04;
DT   11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2004, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Zgc:92124.
GN   ORFNames=zgc:92124;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RA   Director MGC Project;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC081601; AAH81601.1; -; mRNA.
DR   SMR; Q66I04; 65-510.
DR   Ensembl; ENSDARG00000031715; Danio rerio.
DR   ZFIN; ZDB-GENE-040912-7; zgc:92124.
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DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   510 AA;  58258 MW;  5EE8F68226569BA2 CRC64;

  Query Match             79.6%;  Score 39;  DB 2;  Length 510;
  Best Local Similarity   88.9%;  Pred. No. 94;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LQHQRLVRL 10
              ||| |||||
Db        295 LQHDRLVRL 303


RESULT 27
Q7QS13_GIALA
ID   Q7QS13_GIALA   PRELIMINARY;   PRT;   646 AA.
AC   Q7QS13;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   GLP_228_4192_2252.
OS   Giardia lamblia ATCC 50803.
OC   Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX   NCBI_TaxID=184922;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=WB C6;
RA   Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA   Olsen G.J., Sogin M.L.;
RT   "Draft sequence of the Giardia lamblia genome.";
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AACB01000126; EAA37797.1; -; Genomic_DNA.
DR   InterPro; IPR002110; ANK.
DR   PRINTS; PR01415; ANKYRIN.
DR   SMART; SM00248; ANK; 1.
SQ   SEQUENCE   646 AA;  71121 MW;  00AB6794E2516E55 CRC64;

  Query Match             79.6%;  Score 39;  DB 2;  Length 646;
  Best Local Similarity   70.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
              ::|||| ||
Db        382 EVQHQRLARL 391


RESULT 28
Q2IJL1_9DELT
ID   Q2IJL1_9DELT   PRELIMINARY;   PRT;   175 AA.
AC   Q2IJL1;
DT   07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT   07-MAR-2006, sequence version 1.
DT   07-MAR-2006, entry version 1.
DE   Rubrerythrin.
GN   ORFNames=Adeh_2075;
OS   Anaeromyxobacter dehalogenans 2CP-C.
OC   Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC   Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX   NCBI_TaxID=290397;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=2CP-C;
RG   US DOE Joint Genome Institute;
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Brettin T., Bruce D., Han C.,
RA   Tapia R., Gilna P., Kiss H., Schmutz J., Larimer F., Land M.,
RA   Kyrpides N., Anderson I., Sanford R.A., Ritalahti K.M., Thomas H.S.,
RA   Kirby J.R., Zhulin I.B., Loeffler F.E., Richardson P.;
RT   "Complete sequence of Anaeromyxobacter dehalogenans 2CP-C.";
RL   Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; CP000251; ABC81845.1; -; Genomic_DNA.
SQ   SEQUENCE   175 AA;  19497 MW;  3CDB642B8F604347 CRC64;

  Query Match             77.6%;  Score 38;  DB 2;  Length 175;
  Best Local Similarity   77.8%;  Pred. No. 46;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVR 9
              :|:||||||
Db        142 ELKHQRLVR 150


RESULT 29
Q6KAA1_ORYSA
ID   Q6KAA1_ORYSA   PRELIMINARY;   PRT;   327 AA.
AC   Q6KAA1;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Hypothetical protein OJ1063_D06.18.
GN   Name=OJ1063_D06.18;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AP003989; BAD22870.1; -; Genomic_DNA.
DR   Gramene; Q6KAA1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   327 AA;  38081 MW;  90DCDF0AEBA8AF50 CRC64;

  Query Match             77.6%;  Score 38;  DB 2;  Length 327;
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  Best Local Similarity   70.0%;  Pred. No. 90;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
              |::|||||  |
Db         91 QVEHQRLVEL 100


RESULT 30
Q514Y0_ENTHI
ID   Q514Y0_ENTHI   PRELIMINARY;   PRT;   335 AA.
AC   Q514Y0;
DT   07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT   07-JUN-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Protein kinase, putative.
GN   ORFNames=72.t00027;
OS   Entamoeba histolytica HM-1:IMSS.
OC   Eukaryota; Entamoebidae; Entamoeba.
OX   NCBI_TaxID=294381;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=HM-1:IMSS;
RX   PubMed=15729342; DOI=10.1038/nature03291;
RA   Loftus B.J., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA   Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA   Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA   Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA   Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
RA   Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,
RA   Whitehead S., Quail M.A., Rabbinowitsch E., Norbertczak H., Price C.,
RA   Wang Z., Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S.,
RA   Lohia A., Foster P.G., Sicheritz-Ponten T., Weber C., Singh U.,
RA   Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
RA   Barrell B.G., Fraser C.M., Hall N.;
RT   "The genome of the protist parasite Entamoeba histolytica.";
RL   Nature 433:865-868(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AAFB01000275; EAL48399.1; -; Genomic_DNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   335 AA;  38352 MW;  765FABA2D3D27D5F CRC64;

  Query Match             77.6%;  Score 38;  DB 2;  Length 335;
  Best Local Similarity   70.0%;  Pred. No. 93;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QLQHQRLVRL 10
              ||:|| :|||
Db         60 QLKHQNIVRL 69


Search completed: June 29, 2006, 09:29:26
Job time : 120.701 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:14 ; Search time 87.8313 Seconds
(without alignments)
46.851 Million cell updates/sec

Title: US-10-062-257A-14
Perfect score: 41
Sequence: 1 KLLDMAAQI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	100.0	9	4	AAB73130	Aab73130 Tumour an
2	41	100.0	259	2	AAY43956	Aay43956 Mouse pro
3	41	100.0	259	2	AAY43955	Aay43955 Human pro
4	41	100.0	263	8	ADR88385	Adr88385 LCK tyros
5	41	100.0	265	7	ABR56203	Abr56203 Mutant Ly
6	41	100.0	271	7	ABR56204	Abr56204 Mutant Ly
7	41	100.0	279	9	ADY85449	Ady85449 Catalytic
8	41	100.0	346	3	AAY76750	Aay76750 Human pro
9	41	100.0	346	4	AAE06208	Aae06208 Human pro
10	41	100.0	346	5	ABB84435	Abb84435 Human pro
11	41	100.0	355	8	ABM82980	Abm82980 Human dia
12	41	100.0	417	2	AAR14201	Aar14201 (Beta-gal
13	41	100.0	437	5	ABG79672	Abg79672 Tumour in
14	41	100.0	458	7	ADC99048	Adc99048 Human KPP
15	41	100.0	508	3	AAB37700	Aab37700 Human lym
16	41	100.0	508	7	ADE58802	Ade58802 Human Pro
17	41	100.0	508	7	ADE58799	Ade58799 Human Pro
18	41	100.0	508	7	ADF45072	Adf45072 Human kin
19	41	100.0	508	7	ADL34479	Adl34479 Human lym
20	41	100.0	508	8	ADS88148	Ads88148 Human pro
21	41	100.0	509	3	AAY49420	Aay49420 PKA subst
22	41	100.0	509	6	ABR58699	Abr58699 Human can
23	41	100.0	509	7	ABR56202	Abr56202 Human Lym
24	41	100.0	509	7	ADE40449	Ade40449 Human pro
25	41	100.0	509	8	ADL22907	Adl22907 Human MP2
26	41	100.0	509	8	ADP12458	Adp12458 Protein e
27	41	100.0	509	8	ADP48374	Adp48374 Human lym
28	41	100.0	509	9	ADZ51107	Adz51107 Amino aci
29	41	100.0	509	9	AEA35921	Aea35921 Human Lck
30	41	100.0	539	8	ABM82981	Abm82981 Human dia
31	41	100.0	539	8	ABM82982	Abm82982 Human dia
32	41	100.0	551	4	ABG22264	Abg22264 Novel hum
33	41	100.0	567	5	ABG79673	Abg79673 Tumour in
34	40	97.6	363	6	ABR59690	Abr59690 Human p56
35	40	97.6	363	8	ADP48375	Adp48375 Human lym
36	37	90.2	269	6	ABU23401	Abu23401 Protein e
37	36	87.8	212	6	ABU40371	Abu40371 Protein e
38	36	87.8	268	8	ADS24626	Ads24626 Bacterial
39	35	85.4	434	6	ABU20957	Abu20957 Protein e
40	35	85.4	435	8	ADS21257	Ads21257 Bacterial
41	34	82.9	22	4	AAU07595	Aau07595 Human try
42	34	82.9	150	7	ADE31093	Ade31093 Human dia
43	34	82.9	251	4	AAB95778	Aab95778 Human pro
44	34	82.9	254	1	AAP60009	Aap60009 Sequence
45	34	82.9	259	2	AAY43950	Aay43950 Human pro
46	34	82.9	259	2	AAY43951	Aay43951 Human pro
47	34	82.9	263	5	ABP52384	Abp52384 Human JAK
48	34	82.9	273	8	ADR88383	Adr88383 SAC tyros
49	34	82.9	302	9	ADY85467	Ady85467 Catalytic
50	34	82.9	319	9	ADY85450	Ady85450 Catalytic
51	34	82.9	351	4	ABG23777	Abg23777 Novel hum
52	34	82.9	393	5	ABP53494	Abp53494 Human c-S
53	34	82.9	499	8	ABM84206	Abm84206 Human dia
54	34	82.9	517	4	ABB57957	Abb57957 Drosophil
55	34	82.9	523	9	AEB07190	Aeb07190 Rous sarc
56	34	82.9	530	8	ADQ88402	Adq88402 Human mut
57	34	82.9	530	9	ADV94836	Adv94836 Human mut
58	34	82.9	533	2	AAR39705	Aar39705 Chicken p
59	34	82.9	533	3	AAY44449	Aay44449 Mutant ch
60	34	82.9	533	3	AAY44447	Aay44447 Wild-type
61	34	82.9	533	3	AAY44451	Aay44451 Mutant ch
62	34	82.9	533	4	AAB84661	Aab84661 Amino aci
63	34	82.9	533	9	AEB07192	Aeb07192 Chicken c
64	34	82.9	535	7	ADF45087	Adf45087 Human kin
65	34	82.9	535	9	AED21154	Aed21154 Human non
66	34	82.9	536	2	AAR39706	Aar39706 Human pp6
67	34	82.9	536	5	ABG95123	Abg95123 Human v-s
68	34	82.9	536	5	AAU78678	Aau78678 Human SH2
69	34	82.9	536	6	ABP57260	Abp57260 Human src
70	34	82.9	536	7	ADI20072	Adi20072 Human c-S
71	34	82.9	536	8	ADL22904	Adl22904 Human MP2
72	34	82.9	536	8	ADQ88400	Adq88400 Human wil
73	34	82.9	536	8	ADQ97772	Adq97772 Human can
74	34	82.9	536	8	ADU04517	Adu04517 Protein t
75	34	82.9	536	8	ADY84076	Ady84076 Human Src
76	34	82.9	536	9	ADV94834	Adv94834 Human wil
77	34	82.9	536	9	AEA35917	Aea35917 Chicken Y
78	34	82.9	536	9	AEA35914	Aea35914 Human Src
79	34	82.9	541	5	AAU74614	Aau74614 Perinucle
80	34	82.9	542	5	ABB97339	Abb97339 Novel hum
81	34	82.9	542	8	ADY84075	Ady84075 Human Src
82	34	82.9	543	2	AAY24421	Aay24421 Human yes
83	34	82.9	543	4	AAB84663	Aab84663 Amino aci
84	34	82.9	543	4	ABG10302	Abg10302 Novel hum
85	34	82.9	543	6	ADA00843	Ada00843 Human Src
86	34	82.9	543	7	ADF45099	Adf45099 Human kin
87	34	82.9	543	8	ADL22913	Adl22913 Human MP2
88	34	82.9	543	8	ADO19329	Ado19329 Human PRO
89	34	82.9	543	8	ADO19331	Ado19331 Human PRO
90	34	82.9	543	8	ADQ26047	Adq26047 v-yes-1 Y
91	34	82.9	543	8	ADU06318	Adu06318 Novel bro
92	34	82.9	543	9	ADW78761	Adw78761 Human Yam
93	34	82.9	543	9	ADY19868	Ady19868 PRO polyp
94	34	82.9	543	9	AEA23955	Aea23955 Human PRO
95	34	82.9	543	9	AEA35915	Aea35915 Human Yes
96	34	82.9	543	9	AED01122	Aed01122 Human c-Y

97	34	82.9	549	8	ADY84080	Ady84080 Human Src
98	34	82.9	565	4	ABG23778	Abg23778 Novel hum
99	33	80.5	106	7	ABM88001	Abm88001 Rice abio
100	33	80.5	134	7	ABM87949	Abm87949 Rice abio

ALIGNMENTS

RESULT 1
AAB73130
ID AAB73130 standard; peptide; 9 AA.
XX
AC AAB73130;
XX
DT 09-MAY-2001 (first entry)
XX
DE Tumour antigen peptide #14.
XX
KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS Homo sapiens.
XX
PN WO200111044-A1.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-JP005220.
XX
PR 05-AUG-1999; 99JP-00222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT polynucleotides encoding them for treatment of cancer.
XX
PS Claim 1; Page 70; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 1 KLLDMAAQI 9

RESULT 2
AAY43956
ID AAY43956 standard; protein; 259 AA.
XX
AC AAY43956;
XX
DT 21-DEC-1999 (first entry)
XX
DE Mouse protein kinase #6.
XX
KW Prediction; secondary structure; alignment; evolutionary conservation;
KW homology; periodicity; co-variation analysis; antigenic site;
KW site directed mutagenesis; interaction.
XX
OS Mus sp.
XX
PN US5958784-A.
XX
PD 28-SEP-1999.
XX
PF 25-MAR-1992; 92US-00857224.
XX
PR 25-MAR-1992; 92US-00857224.
XX
PA (BENN/) BENNER S A.
XX
PI Benner SA;
XX
DR WPI; 1999-570766/48.
XX
PT Predicting the folded structure of proteins.
XX
PS Disclosure; Col 255-258; 113pp; English.
XX
CC Sequences AAY43902-Y44015 represent proteins used in a novel method of
CC predicting the folded structure of proteins, by aligning sequences of
CC homologous proteins and using patterns of evolutionarily conserved and
CC varied sequences to assign positions. Positions in the alignment are
CC assigned to the surface or inside of the folded structure, active sites,
CC and parsing segments. Secondary structural units are assigned by
CC identifying periodicity in the assignments, and assembled into globular
CC form using distance constraints imposed by disulfide bridges, active site
CC assignments and co-variation analysis. The predicted secondary structures
CC are useful for identifying antigenic sites on a protein molecule, as
CC guides for site directed mutagenesis studies, and for understanding the
CC interaction of a protein with other molecules
XX
SQ Sequence 259 AA;

Query Match 100.0%; Score 41; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 98 KLLDMAAQI 106

RESULT 3
AAY43955
ID AAY43955 standard; protein; 259 AA.
XX
AC AAY43955;
XX
DT 21-DEC-1999 (first entry)
XX
DE Human protein kinase #15.
XX
KW Prediction; secondary structure; alignment; evolutionary conservation;
KW homology; periodicity; co-variation analysis; antigenic site;
KW site directed mutagenesis; interaction.
XX
OS Homo sapiens.
XX
PN US5958784-A.
XX
PD 28-SEP-1999.
XX
PF 25-MAR-1992; 92US-00857224.
XX
PR 25-MAR-1992; 92US-00857224.
XX
PA (BENN/) BENNER S A.
XX
PI Benner SA;
XX
DR WPI; 1999-570766/48.
XX

PT Predicting the folded structure of proteins.
XX
PS Disclosure; Col 253-256; 113pp; English.
XX
CC Sequences AAY43902-Y44015 represent proteins used in a novel method of
CC predicting the folded structure of proteins, by aligning sequences of
CC homologous proteins and using patterns of evolutionarily conserved and
CC varied sequences to assign positions. Positions in the alignment are
CC assigned to the surface or inside of the folded structure, active sites,
CC and parsing segments. Secondary structural units are assigned by
CC identifying periodicity in the assignments, and assembled into globular
CC form using distance constraints imposed by disulfide bridges, active site
CC assignments and co-variation analysis. The predicted secondary structures
CC are useful for identifying antigenic sites on a protein molecule, as
CC guides for site directed mutagenesis studies, and for understanding the
CC interaction of a protein with other molecules
XX
SQ Sequence 259 AA;

Query Match 100.0%; Score 41; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 98 KLLDMAAQI 106

RESULT 4
ADR88385
ID ADR88385 standard; protein; 263 AA.
XX
AC ADR88385;
XX
DT 18-NOV-2004 (first entry)
XX
DE LCK tyrosine kinase protein.
XX
KW Molecular scaffold; nuclear hormone receptor; TNF receptor;
KW G-protein coupled receptor; methyl transferase; ligase;
KW LCK tyrosine kinase; enzyme.
XX
OS Unidentified.
XX
PN US2004171062-A1.
XX
PD 02-SEP-2004.
XX
PF 28-FEB-2003; 2003US-00377268.
XX
PR 28-FEB-2002; 2002US-0360651P.
PR 16-SEP-2002; 2002US-0411398P.
PR 20-SEP-2002; 2002US-0412341P.
PR 02-JAN-2003; 2003US-0437929P.
XX
PA (PLEX-) PLEXXIKON INC.
XX
PI Hirth K, Milburn MV;
XX
DR WPI; 2004-642017/62.
XX
PT Designing a ligand binding to a target molecule, comprises identifying as
PT molecular scaffolds compounds binding to members of a molecular family,
PT detecting orientation of scaffolds at a binding site of target, and
PT synthesizing ligand.
XX
PS Disclosure; SEQ ID NO 24; 186pp; English.
XX
CC The present invention relates to a method of designing a ligand binding
CC to a target molecule. The method involves identifying as molecular
CC scaffolds compounds binding to members of a molecular family, detecting
CC orientation of scaffolds at a binding site of target, and synthesising
CC ligand. The invention is useful for designing drug products and for
CC designing ligand binding to target molecules such as nuclear hormone
CC receptors, TNF receptors, G-protein coupled receptors, methyl
CC transferases, ligases, etc. The present sequence is the LCK tyrosine
CC kinase protein. This sequence is used to illustrate the method of
CC invention.
XX
SQ Sequence 263 AA;

Query Match 100.0%; Score 41; DB 8; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 102 KLLDMAAQI 110

RESULT 5
ABR56203
ID ABR56203 standard; protein; 265 AA.
XX
AC ABR56203;
XX
DT 18-DEC-2003 (first entry)
XX
DE Mutant Lymphocyte Cell Kinase, Lck, fragment (237-501, D364N).
XX
KW Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW Src-family protein tyrosine kinase; T-cell; immune response; mutein;
KW mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 128
FT /note= "Wild-type D substituted with N. This position is
FT 364 in the full-length sequence (see ABR56202 for the
FT wild-type full length sequence"
FT Modified-site 158
FT /note= "Phosphorylation site"
XX
PN WO2003020880-A2.
XX
PD 13-MAR-2003.
XX
PF 02-AUG-2002; 2002WO-US024546.
XX
PR 03-AUG-2001; 2001US-0310051P.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Borhani DW, Calderwood D, Dixon RW, Hirst GC, Hrnciar P, Loew A;
PI Leung A, Ritter K;
XX
DR WPI; 2003-300872/29.
XX
PT New crystalline polypeptide comprising ligand binding domain or catalytic
PT domain of Lck protein, for determining three-dimensional structure of
PT catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS Claim 12; Fig 2; 994pp; English.
XX
CC The present invention relates to a crystalline polypeptide (I),
CC comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC in T-cells and plays an essential role in immune response. (I) is useful
CC for identifying a compound which is an inhibitor of human Lck protein.
CC The present sequence is a mutated fragment of the human Lck sequence,
CC which approximately comprises the catalytic domain
XX
SQ Sequence 265 AA;

```
  Query Match             100.0%;  Score 41;  DB 7;  Length 265;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||||
Db        104 KLLDMAAQI 112


RESULT 6
ABR56204
ID   ABR56204 standard; protein; 271 AA.
XX
AC   ABR56204;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Mutant Lymphocyte Cell Kinase, Lck, fragment (231-501, D364N).
XX
KW   Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW   Src-family protein tyrosine kinase; T-cell; immune response; mutein;
KW   mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 134
FT                   /note= "Wild-type D substituted with N. This position is
FT                   364 in the full-length sequence (see ABR56202 for the
FT                   wild-type full length sequence"
FT   Modified-site   164
FT                   /note= "Phosphorylation site"
XX
PN   WO2003020880-A2.
XX
PD   13-MAR-2003.
XX
PF   02-AUG-2002; 2002WO-US024546.
XX
PR   03-AUG-2001; 2001US-0310051P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Borhani DW,  Calderwood D,  Dixon RW,  Hirst GC,  Hrnciar P,  Loew A;
PI   Leung A,  Ritter K;
XX
DR   WPI; 2003-300872/29.
XX
PT   New crystalline polypeptide comprising ligand binding domain or catalytic
PT   domain of Lck protein, for determining three-dimensional structure of
PT   catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS   Example 1; Fig 3; 994pp; English.
XX
CC   The present invention relates to a crystalline polypeptide (I),
CC   comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC   protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC   in T-cells and plays an essential role in immune response. (I) is useful
CC   for identifying a compound which is an inhibitor of human Lck protein.
CC   The present sequence is a mutated fragment of the human Lck sequence,
CC   which approximately comprises the catalytic domain
XX
SQ   Sequence 271 AA;

  Query Match             100.0%;  Score 41;  DB 7;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 2.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||||
Db        110 KLLDMAAQI 118


RESULT 7
ADY85449
ID   ADY85449 standard; protein; 279 AA.
XX
AC   ADY85449;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Catalytic domain of PIM kinase-like protein LCK.
XX
KW   Kinase; protein co-ordinate data; protein structure; cancer; cytostatic;
KW   neoplasm; inflammation; antiinflammatory.
XX
OS   Unidentified.
XX
PN   WO2005028624-A2.
XX
PD   31-MAR-2005.
XX
PF   15-SEP-2004; 2004WO-US030360.
XX
PR   15-SEP-2003; 2003US-0503277P.
XX
PA   (PLEX-) PLEXXIKON INC.
XX
PI   Artis DR,  Bremer RE,  Gillette SJ,  Hurt CR,  Ibrahim PL;
PI   Zuckerman RL;
XX
DR   WPI; 2005-273155/28.
XX
PT   New scaffold library used for identifying and developing ligands for
PT   protein kinases and treating kinase associated disorders e.g. cancer,
PT   comprises set of compounds comprising N-heterocyclic compounds.
XX
PS   Disclosure; Page 170-174; 236pp; English.
XX
CC   The invention relates to a new kinase scaffold library comprises at least
CC   1 set of compounds, each set comprising at least 1 N-heterocyclic
CC   compound of formulae (I)-(VII) given in the specification. Also included
CC   are a system for fitting compounds in binding sites of protein kinases
CC   (comprising an electronic kinase scaffold, and a scaffold library
CC   comprising at least 1 collection of electronic representations of (I)-
CC   (VII), where the scaffold library is embedded in a computer device and
CC   the electronic representations of the compounds can be selectively
CC   retrieved and functionally connected with computer software adapted to
CC   fit electronic representations of compounds in an electronic
CC   representation of a binding site of a kinase), obtaining improved ligands
CC   binding to a protein kinase (which comprises determining if a derivative
CC   of (I)-(VII) binds to the kinase with greater affinity and/or specificity
CC   than (I)-(VII)), developing ligands specific for a particular kinase
CC   (which comprises determining if a derivative of (I)-(VII) that binds to
CC   kinases has greater for specificity for the particular kinase than (I)-
CC   (VII), developing ligands binding to a kinase (which comprises
CC   determining the orientation of at least 1 molecular scaffold of (I)-(VII)
CC   in co-crystals with the kinase, identifying chemical structures of the
CC   scaffolds, that, when modified, change the binding affinity and/or
CC   specificity between the scaffold and kinase and synthesizing a ligand in
CC   which at least 1 chemical structure of the scaffold is modified),
CC   developing ligands with increased specificity on a kinase (which
CC   comprises testing a derivative of a kinase binding compound (I)-(VII) for
CC   increased specificity on the kinase), identifying a ligand binding to a
CC   kinase (which comprises determining if a derivative compound including a
CC   core structure (I)-(VII) binds to the kinase with changed binding
CC   affinity and/or specificity), a co-crystal of a kinase and a binding
CC   compound (I)-(VII), preparation of co-crystals of Pim-1 with (I)-(VII),
CC   identifying potential kinase binding compounds (which comprises fitting
CC   electronic representations of (I)-(VII) in an electronic representation
CC   of a kinase binding site), attaching a kinase binding compound to an
CC   attachment component (which comprises identifying energetically allowed
CC   sites for attachment of the component on a kinase binding compound (I)-
CC   (VII) and attaching the compound or derivative to the attachment
CC   component at the allowed site), modified compounds (comprising (I)-(VIII)
```

CC with an attached linker group, and developing a ligand for a kinase
CC comprising conserved residues matching at least on of Pim-1 residues 49,
CC 52, 67, 121, 128 and 186 which comprises determining if (I)-(VII) binds
CC to the kinase. The kinases comprise Pim-1, Pyk2, c-Abl, Her2, cMet,
CC vascular endothelial growth factor receptor, endothelial growth factor
CC receptor, cKit, Pkcbeta, p38, Cdk2, Akt or Gsk3beta. The kinase scaffold
CC library is used for identifying and developing ligands binding to
CC kinases, for modulating kinase activity and for treating disease
CC condition associated with abnormal kinase activity e.g. cancer,
CC inflammatory disease. The method identifies improved ligands binding to a
CC kinase resulting in ligands having high affinity and specificity towards
CC kinase. The co-crystals of kinase and the binding compound are of
CC sufficient size and quality to allow structural determination of at least
CC 2 Angstroms. The present sequence is a catalytic domain from a PIM-like
CC kinase. NOTE: It is not clear whether the sequence as presented
CC represents a continuous amino acid sequence.
XX
SQ Sequence 279 AA;

Query Match 100.0%; Score 41; DB 9; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 110 KLLDMAAQI 118

RESULT 8
AAY76750
ID AAY76750 standard; protein; 346 AA.
XX
AC AAY76750;
XX
DT 17-APR-2000 (first entry)
XX
DE Human protein kinase homologue, PKH-3.
XX
KW Protein kinase homologue; human; PKH; diagnosis; therapy; cancer; AIDS;
KW autoimmune disorder; inflammatory disorder; reproductive defect; asthma;
KW diabetes mellitus; infertility; ovulatory defect; endometriosis;
KW polycystic ovary syndrome.
XX
OS Homo sapiens.
XX
PN US6013455-A.
XX
PD 11-JAN-2000.
XX
PF 15-OCT-1998; 98US-00173581.
XX
PR 15-OCT-1998; 98US-00173581.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Hillman JL, Yue H, Yang YT, Corley NC, Gorgone GA, Azimzai Y;
PI Lu DAM, Bandman O, Guegler KJ;
XX
DR WPI; 2000-136321/12.
DR N-PSDB; AAZ86794.
XX
PT Nucleic acids encoding a human protein kinase homolog useful for
PT preventing, diagnosing and treating cancer, autoimmune/inflammatory
PT disorders and reproductive defects.
XX
PS Claim 1; Col 47-50; 38pp; English.
XX
CC This sequence represents a human protein kinase homolog (PKH) of the
CC invention. The PKH sequences may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate PKH expression such
CC as cancers, autoimmune/inflammatory disorders and reproductive defects.
CC They may be used to treat disorders associated with decreased PKH
CC expression such as cancers (e.g. lymphoma, melanoma and cancers of the
CC breast lung and prostate), autoimmune/inflammatory disorders (e.g. AIDS,
CC asthma and diabetes mellitus), and reproductive defects (e.g.
CC infertility, ovulatory defects, endometriosis and polycystic ovary
CC syndrome). The DNA may be administered to treat diseases by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC PKH by expressing inactive proteins or to supplement the patients own
CC production of PKH polypeptides. Additionally, the DNA may be used to
CC produce PKH, according to standard recombinant DNA methodology, by
CC inserting the nucleic acids into a host cell and culturing the cell to
CC express the protein. Conversely, antisense nucleic acid molecules may be
CC administered to down regulate PKH expression by binding with the cells
CC own PKH genes and preventing their expression. The DNA, and antisense
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acid sequences in samples,
CC and hence which patients may be in need of restorative therapy. They may
CC also be used to study the expression and function of PKH polypeptides and
CC their role in metabolism. The PKH polypeptides may be used as antigens in
CC the production of antibodies against PKH and in assays to identify
CC modulators (agonists and antagonists) of PKH expression and activity. The
CC anti-PKH antibodies and PKH antagonists may also be used to down regulate
CC PKH expression and activity. The anti-PKH antibodies may also be used as
CC diagnostic agents for detecting the presence of PKH polypeptides in
CC samples
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 41; DB 3; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 177 KLLDMAAQI 185

RESULT 9
AAE06208
ID AAE06208 standard; protein; 346 AA.
XX
AC AAE06208;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human protein kinase homolog-3 (PKH-3).
XX
KW Human; protein kinase homolog-3; PKH-3; cytostatic; protein therapy;
KW vaccine; immunosuppressive; antisclerotic; antiabortive; adenocarcinoma;
KW Acquired Immune deficiency Syndrome; AIDS; melanoma; cancer; bone; liver;
KW breast; autoimmune disorder; multiple sclerosis; drug screening; anaemia;
KW Crohn's disease; ectopic pregnancy; tubal disease; inflammatory disorder;
KW reproductive disorder; polycystic ovary syndrome; asthma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 125. .333
FT /note= "Signature sequence"
XX
PN US6264947-B1.
XX
PD 24-JUL-2001.
XX
PF 20-OCT-1999; 99US-00420915.
XX
PR 15-OCT-1998; 98US-00173581.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Bandman O, Tang YT, Hillman JL, Yue H, Guegler KJ, Corley NC;
PI Gorgone GA, Azimzai Y, Lu DAM;
XX
DR WPI; 2001-450728/48.
DR N-PSDB; AAD11845.

XX
PT Human protein kinase proteins and homologs, useful for preventing,
PT diagnosing and treating cancers, autoimmune/inflammatory disorders and
PT reproductive disorders.
XX
PS Claim 1; Col 47-50; 38pp; English.
XX
CC The present sequence is human protein kinase homolog-3 (PKH-3). Human
CC protein kinase homologs (PKH) and their cDNA molecules are used in the
CC prevention, diagnosis and treatment of diseases associated with increased
CC or decreased expression of PKH. Examples of such disorders include,
CC cancer (e.g. adenocarcinoma, melanoma and bone, breast and liver cancer),
CC autoimmune/inflammatory disorders (e.g. Acquired Immune deficiency
CC Syndrome (AIDS), anaemia, asthma, Crohn's disease and multiple sclerosis)
CC and reproductive disorders (e.g. tubal disease, ectopic pregnancy and
CC polycystic ovary syndrome). PKH, its catalytic or immunogenic fragment
CC are used for screening libraries of compounds in any of the drug
CC screening techniques. PKH nucleic acids are used to generate
CC hybridisation probes useful in mapping the naturally occurring genomic
CC sequences. PKH are also used as antigens in the production of antibodies
CC against protein kinases (PK) and in assays to identify modulators of PK
CC expression and activity. PKH is also used in protein therapy
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 41; DB 4; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 177 KLLDMAAQI 185

RESULT 10
ABB84435
ID ABB84435 standard; protein; 346 AA.
XX
AC ABB84435;
XX
DT 08-NOV-2002 (first entry)
XX
DE Human protein kinase homologue from clone 507669.
XX
KW Protein kinase homologue; PKH; cytostatic; immunosuppressive; antifungal;
KW antiinflammatory; antiallergic; antiasthmatic; antianaemic; antidiabetic;
KW antiarteriosclerotic; antithyroid; dermatological; nephrotropic; human;
KW antigout; thyromimetic; nootropic; osteopathic; antiarthritic; allergy;
KW antirheumatic; ophthalmological; antiulcer; antiviral; antibacterial;
KW antiprotozoal; antiparasitic; antihelmintic; ankylosing spondylitis;
KW acquired immunodeficiency syndrome; AIDS; Addison's disease; amyloidosis;
KW adult respiratory distress syndrome; anaemia; asthma; atherosclerosis;
KW autoimmune haemolytic anaemia; autoimmune thyroiditis; bronchitis;
KW cholecystitis; contact dermatitis; Crohn's disease; atopic dermatitis;
KW dermatomyositis; diabetes mellitus; emphysema; atrophic gastritis; gout;
KW glomerulonephritis; Goodpasture's syndrome; Graves' disease; psoriasis;
KW Hashimoto's thyroiditis; hypereosinophilia; irritable bowel syndrome;
KW multiple sclerosis; myasthenia gravis; myocardial inflammation; uveitis;
KW pericardial inflammation; osteoarthritis; osteoporosis; pancreatitis;
KW polymyositis; Reiter's syndrome; rheumatoid arthritis; scleroderma; SLE;
KW Sjogren's syndrome; systemic lupus erythematosus; systemic sclerosis;
KW thrombocytopenic purpura; ulcerative colitis; Werner syndrome; infection;
KW haemodialysis; extracorporeal circulation; infertility; tubal disease;
KW ovulatory defect; endometriosis; oestrous; menstrual cycle; gene therapy;
KW uterine fibroid; autoimmune disorder; polycystic ovary syndrome; enzyme;
KW ovarian hyperstimulation syndrome; ectopic pregnancy; teratogenesis;
KW cancer.
XX
OS Homo sapiens.
XX
PN US2002081290-A1.
XX
PD 27-JUN-2002.
XX
PF 30-MAY-2001; 2001US-00870962.
XX
PR 15-OCT-1998; 98US-00173581.
PR 20-OCT-1999; 99US-00420915.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Tang YT, Hillman JL, Yue H, Guegler KJ, Corley NC;
PI Gorgone GA, Azimzai Y, Lu DAM;
XX
DR WPI; 2002-655433/70.
DR N-PSDB; ABQ76288.
XX
PT Nucleic acids encoding a human protein kinase homolog useful for
PT preventing, diagnosing and treating cancer, autoimmune/inflammatory
PT disorders and reproductive defects.
XX
PS Claim 47; Page 27; 43pp; English.
XX
CC This invention describes a novel protein kinase homologue (PKH)
CC polypeptides which have cytostatic, immunosuppressive, antiinflammatory,
CC antiallergic, antiasthmatic, antianaemic, antiarteriosclerotic,
CC antithyroid, dermatological, antidiabetic, nephrotropic, antigout,
CC thyromimetic, nootropic, osteopathic, antiarthritic, antirheumatic,
CC ophthalmological, antiulcer, antiviral, antibacterial, antifungal,
CC antiprotozoal, antiparasitic and antihelmintic activity. The polypeptide
CC is used for treating a disease or condition associated with decreased
CC expression of functional PKH. The polypeptide is used to screen for
CC agonists and antagonists of PKH which can also be used in disease
CC treatment. The polypeptide and polynucleotide are used for treating
CC acquired immunodeficiency syndrome (AIDS), Addison's disease, adult
CC respiratory distress syndrome, allergies, ankylosing spondylitis,
CC amyloidosis, anaemia, asthma, atherosclerosis, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, bronchitis, cholecystitis, cancer,
CC contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis,
CC diabetes mellitus, emphysema, atrophic gastritis, glomerulonephritis,
CC Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis,
CC hypereosinophilia, irritable bowel syndrome, multiple sclerosis,
CC myasthenia gravis, myocardial or pericardial inflammation,
CC osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis,
CC Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's syndrome,
CC systemic lupus erythematosus (SLE), systemic sclerosis, thrombocytopenic
CC purpura, ulcerative colitis, uveitis, Werner syndrome, complications of
CC cancer, haemodialysis, and extracorporeal circulation, viral, bacterial,
CC fungal, parasitic, protozoal, and helminthic infections, infertility,
CC including tubal disease, ovulatory defects, and endometriosis,
CC disruptions of the oestrous cycle, disruptions of the menstrual cycle,
CC polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial
CC and ovarian tumours, uterine fibroids, autoimmune disorders, ectopic
CC pregnancies, and teratogenesis. The polypeptides of the invention can be
CC used for gene therapy. This sequence represents a PKH from clone ID
CC 507669 isolated from TMLR3DT02, a library constructed using RNA isolated
CC from non-adherent peripheral blood mononuclear cells collected from a
CC pool of male and female donors
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 41; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 177 KLLDMAAQI 185

RESULT 11
ABM82980
ID ABM82980 standard; protein; 355 AA.
XX
AC ABM82980;
XX

DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3229.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN41632.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 355 AA;

Query Match 100.0%; Score 41; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 186 KLLDMAAQI 194

RESULT 12
AAR14201
ID AAR14201 standard; protein; 417 AA.
XX
AC AAR14201;
XX
DT 13-DEC-1991 (first entry)
XX
DE (Beta-galactosidase N-terminal)-(lck gene prod.) fusion protein.
XX
KW Multi-cloning site.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .26
FT /note= "beta-galactosidase fragment"
FT Region 27. .417
FT /note= "lck gene polypeptide"
XX
PN JP03201994-A.
XX
PD 03-SEP-1991.
XX
PF 28-DEC-1989; 89JP-00338268.
XX
PR 28-DEC-1989; 89JP-00338268.
XX
PA (TOKU) TOKUYAMA SODA KK.
XX
DR WPI; 1991-300980/41.
DR N-PSDB; AAQ14201.
XX
PT Fused polypeptide - has amino acid sequence of beta-galactosidase with a
PT LCK gene conjugated to the N-terminal via DNA having multi-cloning site.
XX
PS Claim 1; Fig 4,2; 15pp; Japanese.
XX
CC The sequence consists of the N-terminal amino acids of the beta-
CC galactosidase gene fused with the lck gene. It is produced by E.coli
CC transformed with a recombinant vector (see AAQ13983). It is useful for
CC producing an antibody specifically immunoreactive with only a lck gene-
CC derived polypeptide in T cells. The antibody may recognise lck gene-
CC derived polypeptides in human cells
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 41; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 248 KLLDMAAQI 256

RESULT 13
ABG79672
ID ABG79672 standard; protein; 437 AA.
XX
AC ABG79672;
XX
DT 15-NOV-2002 (first entry)
XX
DE Tumour involved gene (TIG) splice variant protein, NV-3.
XX
KW Human; splice variant; tumour-involved gene; TIG;
KW pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;
KW endothelial cell; cell differentiation; cell proliferation; apoptosis;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US2002086384-A1.
XX
PD 04-JUL-2002.
XX
PF 13-MAR-2001; 2001US-00805020.
XX
PR 14-MAR-2000; 2000IL-00135402.

PR 16-MAY-2000; 2000IL-00136154.
XX
PA (LEVI/) LEVINE Z.
PA (DAVI/) DAVID A.
PA (ROMA/) ROMANO C.
PA (BERN/) BERNSTEIN J.
XX
PI Levine Z, David A, Romano C, Bernstein J;
XX
DR WPI; 2002-635679/68.
DR N-PSDB; ABS65202.
XX
PT Novel nucleic acid sequence, which is an alternative splicing variant of
PT tumor involved genes, useful for detecting cancer, predisposition to
PT cancer, for evaluating cancer state and in gene therapy for treating
PT cancer.
XX
PS Claim 4; Page 68-69; 180pp; English.
XX
CC The invention discloses isolated human nucleic acid alternative splicing
CC variants that are all tumour-involved genes (TIGs). The nucleic acids and
CC polypeptides are useful for determining the level of a nucleic acid or
CC polypeptide in a biological sample, for detecting a variant nucleic acid
CC or polypeptide sequence in a biological sample, for determining the level
CC of variant nucleic acid or polypeptide sequences in a biological sample
CC and for determining the ratio between the level of variant sequence in a
CC first biological sample and the level of the original sequence from which
CC the variant has been varied by alternative splicing in a second
CC biological sample and for raising antibodies. A pharmaceutical
CC composition comprising a carrier and the nucleic acid, is useful for
CC treating diseases (e.g. cancer) that can be ameliorated or cured by
CC increasing or decreasing the level of the encoded protein. The nucleic
CC acids are also useful for diagnostic purposes, especially for detecting
CC cancer or a predisposition to cancer, for evaluating the state or
CC aggressiveness of cancer disease, in basic research, for understanding
CC the physiological function of the original TIG, in targeting or
CC developing pharmaceuticals, for distinguishing various stages in the life
CC cycle of the same type of cells which may be helpful for the development
CC of pharmaceuticals for various cancer stages in which cell cycle is non-
CC normal, for determining mutations in tumour-involved genes and in gene
CC therapy. The polypeptides are useful for identifying compounds capable of
CC binding to the variant product and modulating its activity and for
CC modulating endothelial differentiation and proliferation, as well as to
CC modulate apoptosis either ex vivo or in vivo. The sequences presented in
CC ABG796700-ABG79705 are the new variants (NV) 1-36 proteins of the TIGs
CC disclosed
XX
SQ Sequence 437 AA;

Query Match 100.0%; Score 41; DB 5; Length 437;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 340 KLLDMAAQI 348

RESULT 14
ADC99048
ID ADC99048 standard; protein; 458 AA.
XX
AC ADC99048;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human KPP protein - SEQ ID 1.
XX
KW anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian;
KW nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
KW antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;
KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;
KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;
KW virucide; protozoacide; fungicide; kinase; phosphatase; KPP;
KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;
KW cancer; developmental; mental retardation; neurological;
KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;
KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
KW helminthic infection; transgenic; gene therapy; human; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003033680-A2.
XX
PD 24-APR-2003.
XX
PF 17-OCT-2002; 2002WO-US033723.
XX
PR 19-OCT-2001; 2001US-0345474P.
PR 02-NOV-2001; 2001US-0343910P.
PR 13-NOV-2001; 2001US-0333098P.
PR 16-NOV-2001; 2001US-0332424P.
PR 30-NOV-2001; 2001US-0334288P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;
PI Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;
PI Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;
PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;
PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;
PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;
PI Zebarjadian Y;
XX
DR WPI; 2003-403214/38.
DR N-PSDB; ADC99100.
XX
PT New human kinases and phosphatases and polynucleotides, useful for
PT diagnosing, treating or preventing autoimmune or inflammatory disorders
PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
PT cancer or hepatitis.
XX
PS Claim 1; SEQ ID NO 1; 424pp; English.
XX
CC The invention relates to a novel isolated polypeptide which is a human
CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,
CC agonists and antagonists are useful for diagnosing, treating or
CC preventing cell proliferative disorders such as atherosclerosis,
CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental
CC retardation, neurological disorders including Alzheimer's disease and
CC Parkinson's disease, autoimmune and inflammatory disorders such as
CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,
CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the
CC polynucleotides encoding KPP may be useful for creating transgenic
CC animals to model human disease, as well as during gene therapy
CC procedures. The current sequence is that of the human KPP protein of the
CC invention.
XX
SQ Sequence 458 AA;

Query Match 100.0%; Score 41; DB 7; Length 458;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 289 KLLDMAAQI 297

RESULT 15
AAB37700
ID AAB37700 standard; protein; 508 AA.
XX
AC AAB37700;
XX

DT 02-MAR-2001 (first entry)
XX
DE Human lymphocyte kinase.
XX
KW Human; lymphocyte kinase; protein co-ordinate data; lck; crystal.
XX
OS Homo sapiens.
XX
PN WO200070030-A1.
XX
PD 23-NOV-2000.
XX
PF 19-MAY-2000; 2000WO-US013881.
XX
PR 19-MAY-1999; 99US-0134965P.
XX
PA (KINE-) KINETIX PHARM INC.
XX
PI Zhu X;
XX
DR WPI; 2000-687708/67.
XX
PT Crystal of a protein-ligand complex for identifying kinase inhibitors,
PT comprises a truncated lymphocyte kinase and a ligand, and diffracts X-
PT rays to determine atomic coordinates at a resolution greater than 5
PT angstroms.
XX
PS Claim 1; Page 434-5; 438pp; English.
XX
CC The present invention relates to a crystal of a protein-ligand complex
CC comprising a truncated lymphocyte kinase (lck) and a ligand. The crystal
CC diffracts X-rays so that the atomic coordinates of the protein-ligand
CC complex can be determined to a resolution of greater than 5.0 Angstroms.
CC The truncated lck used in the present invention comprises the globular
CC core of the corresponding full-length lck. The present sequence is the
CC full-length human lck protein. The crystal of the present invention may
CC be used to identify kinase inhibitors in screening assays, in drug
CC screening and drug design processes, to design, select or test inhibitors
CC of kinase enzymes, where the inhibitors are used as therapeutics for the
CC treatment and modulation of diseases, disease symptoms or the effect of
CC other physiological events mediated by kinases, having one or more kinase
CC enzymes involved in their pathology
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 41; DB 3; Length 508;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 339 KLLDMAAQI 347

RESULT 16
ADE58802
ID ADE58802 standard; protein; 508 AA.
XX
AC ADE58802;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P06239, SEQ ID NO 4689.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P06239.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 41; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 339 KLLDMAAQI 347

RESULT 17
ADE58799
ID ADE58799 standard; protein; 508 AA.
XX
AC ADE58799;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P06239, SEQ ID NO 4686.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX

OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P06239.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 41; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 339 KLLDMAAQI 347

RESULT 18
ADF45072
ID ADF45072 standard; protein; 508 AA.
XX
AC ADF45072;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human kinase LCK.
XX
KW Human; protein kinase; enzyme; inhibitor; LCK.
XX
OS Homo sapiens.
XX
PN WO2003081210-A2.
XX
PD 02-OCT-2003.
XX
PF 20-MAR-2003; 2003WO-US008725.
XX
PR 21-MAR-2002; 2002US-0366892P.
XX
PA (SUNE-) SUNESIS PHARM INC.
XX
PI Prescott JC, Braisted A;
XX
DR WPI; 2003-865136/80.
XX
PT Identifying ligand binding to inactive conformation of target protein
PT kinase (T) comprises contacting the conformation modified (T) which
PT contains reactive group at binding site, with ligands and detecting
PT kinase-ligand conjugate formation.
XX
PS Disclosure; SEQ ID NO 41; 260pp; English.
XX
CC The present invention relates to a method for identifying a ligand (L),
CC which binds to an inactive conformation of target protein kinase (T). The
CC method involves contacting inactive conformation of (T), which contains
CC or is modified to contain a reactive group at or near a binding site of
CC interest, with one or more ligand candidates capable of covalently
CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC The method is useful for identifying protein kinase inhibitors that
CC preferentially bind to inactive conformation of a target protein kinase.
CC The present sequence is a protein kinase which may be modified via an
CC amino acid substitution, for use in the method of the invention.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 41; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 339 KLLDMAAQI 347

RESULT 19
ADL34479
ID ADL34479 standard; peptide; 508 AA.
XX
AC ADL34479;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human lymphocyte kinase (Lck) globular core.
XX
KW cytostatic; immunosuppressive; antiinflammatory; antibacterial; virucide;
KW fungicide; nootropic; neuroprotective; kinase inhibitor; crystal;
KW protein-ligand complex; lymphocyte kinase; Lck; Lck ligand;
KW kinase inhibitor; therapeutic; kinase-mediated physiological event;
KW cancer; autoimmunological; metabolic; inflammatory; infection;
KW central nervous system degenerative disease; transplant rejection; human;
KW globular core; protein co-ordinate data.
XX
OS Homo sapiens.
XX
PN US6589758-B1.
XX
PD 08-JUL-2003.
XX
PF 21-MAY-2001; 2001US-00862154.

XX
PR 19-MAY-2000; 2000US-0205510P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zhu X;
XX
DR WPI; 2003-810380/76.
XX
PT Crystal of protein-ligand complex useful for identifying an inhibitor of
PT lymphocyte kinase (Lck), comprises truncated Lck and a ligand.
XX
PS Claim 1; SEQ ID NO 1; 295pp; English.
XX
CC The invention describes a crystal (I) of a protein-ligand complex (C)
CC comprising a truncated lymphocyte kinase (Lck) and a ligand, where (I)
CC effectively diffracts X-rays for determination of atomic coordinates of
CC (C) to a resolution of greater than 5.0 angstroms, and truncated Lck
CC comprises a sequence (S1) of residues 225-508 of a 508 amino acid
CC sequence, given in specification and retains the globular core of full-
CC length Lck. (I) is useful in an inhibitor screening assay and to
CC identify, design, select, and evaluate potential inhibitors of kinases
CC that would be useful as therapeutics for diseases or symptoms of diseases
CC that are associated with kinase-mediated physiological events. The
CC inhibitors identified by the methods may also be useful for inhibition of
CC kinase activity of one or more enzymes. The inhibitors are also useful
CC for inhibiting the biological activity of any enzyme comprising greater
CC than 90%, alternatively greater than 85%, or alternatively greater than
CC 70% sequence homology with a kinase sequence. The inhibitors are useful
CC for inhibiting the biological activity of any enzyme that binds ATP and
CC thus for treating disease or disease symptoms mediated by any enzyme that
CC binds ATP. The inhibitors are useful in inhibiting kinase activity and
CC are useful in treating kinase-mediated disease or disease symptoms in a
CC mammal, particularly a human e.g., cancer, autoimmunological, metabolic,
CC inflammatory, infection, (bacterial, viral, yeast, fungal, etc.), central
CC nervous system degenerative disease etc. The inhibitors are useful in
CC treating or preventing diseases, including, transplant rejection etc.
CC This is the amino acid sequence of a human lymphocyte kinase (Lck)
CC polypeptide comprising the Lck globular core.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 41; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 339 KLLDMAAQI 347

RESULT 20
ADS88148
ID ADS88148 standard; protein; 508 AA.
XX
AC ADS88148;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human protein of a TNF-alpha signalling pathway protein complex SeqID 3.
XX
KW protein complex; tumour necrosis factor-alpha signalling pathway;
KW TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
KW inflammatory bowel disease; infectious disease; septic shock;
KW bacterial infection; neurological disease; stroke-induced inflammation;
KW neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
KW antirheumatic; cytostatic; antibacterial; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004035783-A2.
XX
PD 29-APR-2004.
XX
PF 24-SEP-2003; 2003WO-EP050655.
XX
PR 26-SEP-2002; 2002EP-00021809.
PR 10-FEB-2003; 2003EP-00100274.
XX
PA (CELL-) CELLZOME AG.
XX
PI Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
PI Superti-Furga G, Kruse U;
XX
DR WPI; 2004-348460/32.
XX
PT New protein complex comprising at least one first and second protein of
PT the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
PT diagnosing or treating inflammation, neurological diseases, infectious
PT diseases or cancer.
XX
PS Example; SEQ ID NO 3; 1980pp; English.
XX
CC This invention relates to novel protein complexes of the tumour necrosis
CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
CC methods for preparing these complexes comprising at least two component
CC proteins, as well as screening methods to identify modulators of the
CC pathway, which include antibodies, agonists and antagonists thereof. The
CC present invention describes a protein complex and kit that are useful for
CC diagnosing, prognosing or treating chronic inflammatory diseases such as
CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases
CC such as septic shock and bacterial infections; neurological diseases such
CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
CC cancer. Accordingly, these complexes can be used for the development of
CC pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
CC antirheumatic, cytostatic and antibacterial activities and can be used
CC for gene therapy purposes. In particular, the invention further provides
CC siRNA-oligonucleotides useful for inhibiting protein expression for in
CC vitro or cell culture assays. This polypeptide is a human protein that
CC can be used in combination with other proteins provided in the
CC specification to form novel complexes of the TNF-alpha signalling pathway
CC of the invention.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 41; DB 8; Length 508;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 339 KLLDMAAQI 347

RESULT 21
AAY49420
ID AAY49420 standard; protein; 509 AA.
XX
AC AAY49420;
XX
DT 13-MAR-2000 (first entry)
XX
DE PKA substrate, Src-family protein.
XX
KW Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer;
KW kinase substrate; immunosuppressive disorder; proliferative disease;
KW HIV infection; AIDS; immunodeficiency; autoimmune disease;
KW systemic lupus erythematosus; Src-family.
XX
OS Homo sapiens.
XX
PN WO9962315-A2.
XX
PD 02-DEC-1999.
XX
PF 27-MAY-1999; 99WO-GB001680.

XX
PR 27-MAY-1998; 98NO-00002419.
PR 30-DEC-1998; 98US-0114240P.
XX
PA (LAUR-) LAURAS AS.
PA (JONE/) JONES E L.
XX
PI Hansson V, Levy FO, Mustelin T, Skalhegg BS, Sundvold V;
PI Tasken K, Vang T, Altman A, Munshi A;
XX
DR WPI; 2000-086801/07.
DR N-PSDB; AAZ46491.
XX
PT Altering the activity of protein kinase signaling pathways, used for
PT treating immunosuppressive disorders, e.g. AIDS, proliferative disorders,
PT e.g. cancers or autoimmune diseases.
XX
PS Claim 23; Page 95-96; 111pp; English.
XX
CC The invention provides a novel method of altering the activity of the
CC protein kinase A (PKA) signaling pathway in a cell that comprises
CC altering the extent of phosphorylation of one or more PKA substrates, or
CC kinase substrates downstream in the PKA signaling pathway. Pharmaceutical
CC compositions containing a nucleic acid molecule that encodes a PKA
CC substrate, or fragment, precursor or functionally equivalent variant,
CC where the sequence is modified to alter its susceptibility to
CC phosphorylation by PKA can be used for treating a disorder exhibiting
CC abnormal PKA signaling activity, immunosuppressive disorders or
CC proliferative diseases. They can be used for treating e.g. HIV infection,
CC AIDS, common variable immunodeficiency or cancers. Conditions in which
CC upregulation of the PKA pathway is required, such as autoimmune disease,
CC e.g. systemic lupus erythematosus, may also be treated. The present
CC sequence represents a PKA substrate, wherein the substrate is in the Src-
CC family, preferably Lck, Fyn, Src, Yes, Fgr, Lyn, Hck Blk, Yrk, c-tkl,
CC Fyk, Src-1 or Src-2
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 41; DB 3; Length 509;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 340 KLLDMAAQI 348

RESULT 22
ABR58699
ID ABR58699 standard; protein; 509 AA.
XX
AC ABR58699;
XX
DT 09-JUL-2003 (first entry)
XX
DE Human cancer related protein SEQ ID NO:356.
XX
KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.
XX
OS Homo sapiens.
XX
PN WO2003025138-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-US029560.
XX
PR 17-SEP-2001; 2001US-0323469P.
PR 20-SEP-2001; 2001US-0323887P.
PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI Zlotnik A;
XX
DR WPI; 2003-354600/33.
DR N-PSDB; ACC72850.
XX
PT New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX
PS Claim 12; Page 762; 767pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 41; DB 6; Length 509;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 340 KLLDMAAQI 348

RESULT 23
ABR56202
ID ABR56202 standard; protein; 509 AA.
XX
AC ABR56202;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human Lymphocyte Cell Kinase, Lck.
XX
KW Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW Src-family protein tyrosine kinase; T-cell; immune response.
XX
OS Homo sapiens.
XX
PN WO2003020880-A2.
XX
PD 13-MAR-2003.
XX
PF 02-AUG-2002; 2002WO-US024546.
XX
PR 03-AUG-2001; 2001US-0310051P.
XX
PA (ABBO) ABBOTT LAB.
XX

PI Borhani DW, Calderwood D, Dixon RW, Hirst GC, Hrnciar P, Loew A;
PI Leung A, Ritter K;
XX
DR WPI; 2003-300872/29.
XX
PT New crystalline polypeptide comprising ligand binding domain or catalytic
PT domain of Lck protein, for determining three-dimensional structure of
PT catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS Claim 5; Fig 1; 994pp; English.
XX
CC The present invention relates to a crystalline polypeptide (I),
CC comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC in T-cells and plays an essential role in immune response. The present
CC sequence is the full-length sequence of human Lck (1-509). (I) is useful
CC for identifying a compound which is an inhibitor of human Lck protein
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 41; DB 7; Length 509;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 340 KLLDMAAQI 348

RESULT 24
ADE40449
ID ADE40449 standard; protein; 509 AA.
XX
AC ADE40449;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human proto-oncogene Tyr protein kinase LCK (gene ID 1611) protein.
XX
KW AIDS; acquired immunodeficiency syndrome; human immunodeficiency virus;
KW HIV-related disorder; differential expression; drug screening;
KW viral replication modulation; diagnosis; prognosis; predisposition;
KW anti-HIV; gene therapy; antisense therapy; human;
KW proto-oncogene Tyr protein kinase LCK; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003070883-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004246.
XX
PR 15-FEB-2002; 2002US-0357391P.
PR 13-MAY-2002; 2002US-0380249P.
PR 25-JUN-2002; 2002US-0391306P.
PR 27-AUG-2002; 2002US-0406297P.
PR 19-SEP-2002; 2002US-0412007P.
PR 10-OCT-2002; 2002US-0417508P.
PR 10-DEC-2002; 2002US-0432318P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Powell DM, Weich NS;
XX
DR WPI; 2003-671808/63.
DR N-PSDB; ADE40448.
XX
PT Identifying a compound capable of diagnosing, preventing or treating AIDS
PT or an HIV-related disorder comprises assaying the ability of the compound
PT to modulate e.g. 1414, 1481 or 1553 nucleic acid expression or
PT polypeptide activity.
XX
PS Claim 1; SEQ ID NO 28; 167pp; English.
XX
CC The invention relates to a method of identifying a compound useful in the
CC treatment of AIDS (acquired immunodeficiency syndrome) or an HIV (human
CC immunodeficiency virus)-related disorder. The invention involves assaying
CC the ability of a test compound to modulate the activity or expression of
CC 26 human proteins. These proteins and nucleic acids encoding them
CC (ADE40422-ADE40473) are differentially expressed in tissues relating to
CC AIDS or an HIV-related disorder compared to their expression in normal
CC tissues. The invention also relates to the use of the compounds
CC identified to modulate viral replication in a cell and to treat a patient
CC with AIDS or an HIV-related disorder. The invention further discloses
CC methods for the diagnostic evaluation and prognosis of various HIV-
CC related disorders, and for the identification of individuals exhibiting a
CC predisposition to such conditions. The modulatory compounds identified
CC using the method of the invention may be small organic molecules,
CC peptides, antibodies or antisense nucleic acid molecules. The methods of
CC the invention are useful in diagnosing, preventing or treating AIDS or
CC HIV-related disorders. The present sequence represents a human protein
CC which is differentially expressed in AIDS or HIV-related disorders.
XX
SQ Sequence 509 AA;

Query Match 100.0%; Score 41; DB 7; Length 509;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 340 KLLDMAAQI 348

RESULT 25
ADL22907
ID ADL22907 standard; protein; 509 AA.
XX
AC ADL22907;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human MP2153 polypeptide sequence SEQ ID NO: 27.
XX
KW human; MP2153; p21; p53; cancer.
XX
OS Homo sapiens.
XX
PN WO2004015069-A2.
XX
PD 19-FEB-2004.
XX
PF 06-AUG-2003; 2003WO-US024505.
XX
PR 07-AUG-2002; 2002US-0401701P.
PR 16-SEP-2002; 2002US-0411017P.
PR 30-DEC-2002; 2002US-0437107P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Francis-Lang H, Friedman L, Kidd T, Roche S, Belvin M;
PI Plowman GD, Lickteig K, Zhang H, Amundsen CD;
XX
DR WPI; 2004-180653/17.
DR N-PSDB; ADL22890.
XX
PT Identifying a candidate p21 or p53 pathway modulating agent using an
PT assay system having a modulator of p21 or p53 (MP2153) polypeptide or
PT nucleic acid, useful for diagnosing or treating cancer, such as colon or
PT breast cancer.
XX
PS Example 3; Page 94-96; 110pp; English.
XX
CC The present invention relates to a method of identifying a candidate p21
CC or p53 pathway modulating agent. This comprises providing an assay system

```
CC   comprising a modulator of p21 or p53 (MP2153) polypeptide or nucleic
CC   acid, contacting the assay system with a test agent, where in its
CC   presence the system provides a reference activity, and detecting a test
CC   agent-biased activity of the assay system, wherein a difference between
CC   the test agent-biased activity and the reference activity identifies the
CC   test agent as a candidate p21 or p53 pathway modulating agent. The
CC   methods and compositions of the present invention are useful for the
CC   diagnosis and/or treatment of diseases or conditions associated with
CC   aberrant expression or activity of the p21 or p53 pathway, such as
CC   cancer, preferably colon or head and neck cancer. The present sequence is
CC   a human MP2153 protein sequence of the invention.
XX
SQ   Sequence 509 AA;

  Query Match             100.0%;  Score 41;  DB 8;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||||
Db        340 KLLDMAAQI 348


RESULT 26
ADP12458
ID   ADP12458 standard; protein; 509 AA.
XX
AC   ADP12458;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Protein encoded by mRNA of the invention #68.
XX
KW   transplant rejection; immune system; rheumatoid arthritis; lupus;
KW   inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
OS   Homo sapiens.
XX
PN   WO2004042346-A2.
XX
PD   21-MAY-2004.
XX
PF   24-APR-2003; 2003WO-US012946.
XX
PR   24-APR-2002; 2002US-00131831.
PR   20-DEC-2002; 2002US-00325899.
XX
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI   Wohlgemuth J,  Fry K,  Woodward R,  Ly N,  Prentice J,  Morris M;
PI   Rosenberg S;
XX
DR   WPI; 2004-400724/37.
XX
PT   Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT   pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT   rejection, in an individual, comprises detecting the expression level of
PT   the genes.
XX
PS   Claim 65; SEQ ID NO 2467; 1762pp; English.
XX
CC   The present invention relates to diagnosing or monitoring transplant
CC   rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC   comprises detecting the expression level of one or more genes. The
CC   methods, system and kits are useful in diagnosing or monitoring
CC   transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC   islet, lung, bone marrow or stem cell transplant rejection,
CC   xenotransplant rejection or mechanical organ replacement rejection, in an
CC   individual. The method is also useful in assessing the immune status of
CC   an individual. The methods are also useful in diagnosing and monitoring
CC   diseases that involve the immune system, e.g. rheumatoid arthritis,
CC   lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC   viral, bacterial or fungal infection. The present sequence represents a
CC   protein that is encoded by the mRNA of the invention.
XX
SQ   Sequence 509 AA;

  Query Match             100.0%;  Score 41;  DB 8;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||||
Db        340 KLLDMAAQI 348


RESULT 27
ADP48374
ID   ADP48374 standard; protein; 509 AA.
XX
AC   ADP48374;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human lymphocyte specific tyrosine kinase (Lck) polypeptide #1.
XX
KW   Human; lymphocyte specific tyrosine kinase; Lck;
KW   antisense oligonucleotide; phosphorothioate linkage;
KW   2'-O-methoxyethyl sugar moiety; 5-methylcytosine;
KW   hyperproliferative disorder; cancer; cytostatic; enzyme.
XX
OS   Homo sapiens.
XX
PN   US2004116365-A1.
XX
PD   17-JUN-2004.
XX
PF   10-DEC-2002; 2002US-00316515.
XX
PR   10-DEC-2002; 2002US-00316515.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Borchers AH,  Freier SM;
XX
DR   WPI; 2004-498280/47.
DR   N-PSDB; ADP48301.
XX
PT   New antisense oligonucleotide compounds, useful for diagnosing,
PT   preventing and/or treating diseases or conditions associated with
PT   aberrant expression or activity of Lck, such as hyperproliferative
PT   disorders.
XX
PS   Claim 1; SEQ ID NO 4; 40pp; English.
XX
CC   The invention relates to a compound targeted to a nucleic acid molecule
CC   encoding the human lymphocyte specific tyrosine kinase (Lck) polypeptide.
CC   The compound is an antisense oligonucleotide that specifically hybridises
CC   with the nucleic acid and inhibits expression of the polypeptide. The
CC   antisense oligonucleotide comprises at least one modified internucleoside
CC   linkage i.e. a phosphorothioate linkage, at least one modified sugar
CC   moiety, preferably a 2'-O-methoxyethyl sugar moiety, or at least one
CC   modified nucleobase comprising a 5-methylcytosine. The antisense
CC   compounds are useful for modulating the expression of the human Lck
CC   polypeptide and in preparation of a composition for treating
CC   hyperproliferative disorders, e.g. cancer. This sequence represents a
CC   human Lck polypeptide of the invention.
XX
SQ   Sequence 509 AA;

  Query Match             100.0%;  Score 41;  DB 8;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||||
```

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Db        340 KLLDMAAQI 348


RESULT 28
ADZ51107
ID   ADZ51107 standard; protein; 509 AA.
XX
AC   ADZ51107;
XX
DT   30-JUN-2005  (first entry)
XX
DE   Amino acid sequence of human Tyr kinase Lck.
XX
KW   protein kinase inhibitor; inactive conformation; Tethering; Tyr kinase;
KW   Lck.
XX
OS   Homo sapiens.
XX
PN   WO2005034840-A2.
XX
PD   21-APR-2005.
XX
PF   17-SEP-2003; 2003WO-US029870.
XX
PR   17-SEP-2003; 2003WO-US029870.
XX
PA   (SUNE-) SUNESIS PHARM INC.
XX
PI   Prescoot JC;
XX
DR   WPI; 2005-315455/32.
XX
PT   Identifying ligand binding to inactive conformation of target protein
PT   kinase, by contacting inactive conformation of target with ligand
PT   candidates specific to target, detecting formation of kinase-ligand
PT   conjugate and identifying ligand.
XX
PS   Example 1; SEQ ID NO 9; 101pp; English.
XX
CC   The specification describes a method for identifying protein kinase
CC   inhibitors that preferentially bind to the inactive conformation of a
CC   target protein kinase. The inhibitors are identified by locking the
CC   target protein kinase in an inactive conformation, and using Tethering to
CC   identify inhibitors preferentially targeting the inactive conformation.
CC   The method of the invention is useful for identifying a ligand which
CC   binds to an inactive conformation of a target protein kinase. The present
CC   sequence represents the human Tyr kinase Lck. Lck variants were used to
CC   demonstrate the method of the invention.
XX
SQ   Sequence 509 AA;

  Query Match             100.0%;  Score 41;  DB 9;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||||
Db        340 KLLDMAAQI 348


RESULT 29
AEA35921
ID   AEA35921 standard; protein; 509 AA.
XX
AC   AEA35921;
XX
DT   25-AUG-2005  (first entry)
XX
DE   Human Lck kinase amino acid sequence SEQ ID NO:8.
XX
KW   Src family kinase; Lck kinase.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 273
FT                   /note= "constant amino acid K in domain SH2"
FT   Misc-difference 316
FT                   /note= "constant amino acid T in domain SH2"
FT   Misc-difference 505
FT                   /note= "constant amino acid Y in domain SH1"
XX
PN   EP1541694-A1.
XX
PD   15-JUN-2005.
XX
PF   12-DEC-2003; 2003EP-00028713.
XX
PR   12-DEC-2003; 2003EP-00028713.
XX
PA   (SIRE-) SIRENADE PHARM AG.
XX
PI   Obermeier A,  Bieger B;
XX
DR   WPI; 2005-428084/44.
XX
PT   Identifying compound which modulates Src family kinase (SFK) activity, by
PT   contacting cells expressed with SFK or mutated SFK with test compound,
PT   where change in phenotype of cells indicates that test compound modulates
PT   SFK activity.
XX
PS   Disclosure; SEQ ID NO 8; 114pp; English.
XX
CC   The invention relates to a method (M1) for identifying, selecting and/or
CC   characterizing a compound which modulates Src family kinase (SFK)
CC   activity, by expressing nucleic acids encoding SFK or mutated SFK in
CC   cells, contacting cells with test compound and determining whether
CC   phenotype of cells is changed as compared with phenotype of cells not
CC   expressed with above nucleic acids, where difference in phenotype
CC   indicates that test compound modulate SFK activity. Also described: (1) a
CC   compound (I) identified, selected and/or characterized by (M1); and (2) a
CC   pharmaceutical composition (PC1) containing (I), and a carrier, adjuvant
CC   or vehicle. (I) is useful as a medicament, particularly for the treatment
CC   of diseases, which are at least in part caused by a Src family kinase.
CC   (I) and PC1 are useful for producing a medicament for the treatment of
CC   diseases, which are at least in part caused by a Src family kinase,
CC   particularly by a dysfunction of a Src family kinase, in particular
CC   cancer, hypercalcemia, restenosis, osteoporosis, osteoarthritis,
CC   symptomatic treatment of bone metastasis, rheumatoid arthritis,
CC   inflammatory bowel disease, multiple sclerosis, psoriasis, lupus, graft
CC   versus host disease, T-cell mediated hypersensitivity disease,
CC   Hashimoto's thyroiditis, Guillain-Barre syndrome, chronic obstructive
CC   pulmonary disorder, contact dermatitis, Paget's disease, asthma, ischemic
CC   or reperfusion injury, allergic disease, atopic dermatitis, transplant
CC   rejection or allergic rhinitis. The present sequence represents human Lck
CC   kinase, which is given in the exemplification of the present invention.
XX
SQ   Sequence 509 AA;

  Query Match             100.0%;  Score 41;  DB 9;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||||
Db        340 KLLDMAAQI 348


RESULT 30
ABM82981
ID   ABM82981 standard; protein; 539 AA.
XX
AC   ABM82981;
XX
DT   18-NOV-2004  (first entry)
XX
```

DE Human diagnostic and therapeutic pprotein SEQ ID NO:3230.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN41633.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 539 AA;

Query Match 100.0%; Score 41; DB 8; Length 539;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KLLDMAAQI 9
              |||||||||
Db        370 KLLDMAAQI 378
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Search completed: June 29, 2006, 09:13:11
Job time : 89.8313 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 09:13:45 ; Search time 13.3373 Seconds
(without alignments)
64.927 Million cell updates/sec

Title: US-10-062-257A-14
Perfect score: 41
Sequence: 1 KLLDMAAQI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	100.0	507	1	A39939	protein-tyrosine k
2	41	100.0	509	1	I48845	protein-tyrosine k
3	41	100.0	509	1	OKHULK	protein-tyrosine k
4	34	82.9	362	2	S24551	protein-tyrosine k
5	34	82.9	526	1	OKFVYR	protein-tyrosine k
6	34	82.9	526	1	TVFV60	protein-tyrosine k
7	34	82.9	526	1	TVFVR	protein-tyrosine k
8	34	82.9	526	2	S15582	protein-tyrosine k
9	34	82.9	526	2	S20808	protein-tyrosine k
10	34	82.9	526	2	S26420	protein-tyrosine k
11	34	82.9	528	1	TVFVG9	protein-tyrosine k
12	34	82.9	532	1	B34104	protein-tyrosine k
13	34	82.9	532	1	A34104	protein-tyrosine k
14	34	82.9	533	1	TVCHS	protein-tyrosine k
15	34	82.9	536	2	S33569	protein-tyrosine k
16	34	82.9	537	1	A45501	protein-tyrosine k
17	34	82.9	539	2	B49114	protein-tyrosine k
18	34	82.9	541	1	TVCHYS	protein-tyrosine k
19	34	82.9	541	2	S31645	protein-tyrosine k
20	34	82.9	542	1	TVHUSC	protein-tyrosine k
21	34	82.9	543	1	TVHUYS	protein-tyrosine k
22	34	82.9	545	2	S52313	protein-tyrosine k
23	34	82.9	546	2	S52314	protein-tyrosine k
24	34	82.9	557	1	TVFVS2	protein-tyrosine k
25	34	82.9	568	1	TVFVS1	protein-tyrosine k
26	34	82.9	587	1	TVFVPR	protein-tyrosine k
27	33	80.5	392	2	S04205	protein-tyrosine k
28	33	80.5	505	2	I37206	protein-tyrosine k
29	33	80.5	509	1	TVHAST	protein-tyrosine k
30	33	80.5	529	1	TVHUFR	protein-tyrosine k
31	33	80.5	663	1	TVMVRR	protein-tyrosine k
32	32	78.0	386	2	A83025	probable acyl-CoA
33	32	78.0	413	2	JC5178	probable starvatio
34	32	78.0	499	1	A40092	protein-tyrosine k
35	32	78.0	517	2	A43807	protein-tyrosine k
36	32	78.0	517	2	S24547	protein-tyrosine k
37	32	78.0	534	1	A44991	protein-tyrosine k
38	32	78.0	534	1	S33568	protein-tyrosine k
39	32	78.0	537	1	A43806	protein-tyrosine k
40	32	78.0	537	1	TVHUSY	protein-tyrosine k
41	32	78.0	537	2	I51592	protein-tyrosine k
42	32	78.0	542	2	A49114	protein-tyrosine k
43	31	75.6	178	2	E95994	hypothetical prote
44	31	75.6	334	2	G81744	hypothetical prote
45	31	75.6	335	2	E84422	hypothetical prote
46	31	75.6	503	1	JQ1321	protein-tyrosine k
47	31	75.6	503	1	TVMSHC	protein-tyrosine k
48	31	75.6	505	1	TVHUHC	protein-tyrosine k
49	31	75.6	512	1	A39719	protein-tyrosine k
50	31	75.6	512	1	I56160	protein-tyrosine k
51	31	75.6	512	1	TVHULY	protein-tyrosine k
52	31	75.6	527	2	E90740	probable enzyme [i
53	31	75.6	527	2	G85590	probable enzyme yb
54	31	75.6	527	2	G64818	probable membrane
55	31	75.6	541	1	A43610	protein-tyrosine k
56	31	75.6	544	2	I51593	protein-tyrosine k
57	31	75.6	576	2	AC2195	hypothetical prote
58	31	75.6	581	2	T23396	hypothetical prote
59	31	75.6	642	2	F72528	probable Glu-tRNA
60	31	75.6	693	2	T15728	hypothetical prote
61	30	73.2	134	2	A55580	dihydrodipicolinat
62	30	73.2	172	2	AH2456	hypothetical prote
63	30	73.2	182	2	A83289	2'-5' RNA ligase P
64	30	73.2	193	2	S70681	bplK protein - Bor
65	30	73.2	268	2	H83051	dihydrodipicolinat
66	30	73.2	338	2	F69232	conserved hypothet
67	30	73.2	348	2	AF1249	Recombination prot
68	30	73.2	348	2	AB1612	Recombination prot
69	30	73.2	448	2	AG2661	PmbA/TldD related
70	30	73.2	450	2	A84330	hypothetical prote
71	30	73.2	453	2	E97443	pmbA protein (AF17
72	30	73.2	462	2	S10397	finger protein kox
73	30	73.2	510	2	S68116	4-aminobutyrate tr
74	30	73.2	523	1	TVFVMT	protein-tyrosine k
75	30	73.2	560	2	D90571	conserved hypothet
76	30	73.2	770	2	T22944	hypothetical prote
77	30	73.2	773	2	T40694	probable rna matur
78	30	73.2	784	2	T22939	hypothetical prote
79	29	70.7	72	2	D95907	hypothetical prote
80	29	70.7	78	2	AG2080	hypothetical prote
81	29	70.7	94	2	AB2197	hypothetical prote
82	29	70.7	116	2	B97172	flagellin family p
83	29	70.7	175	2	AD1800	transcription regu
84	29	70.7	182	2	T08596	pollen-specific pr
85	29	70.7	187	2	T05570	pollen-specific pr
86	29	70.7	233	2	C75290	hypothetical prote
87	29	70.7	246	2	AE0583	glutamate/aspartat
88	29	70.7	246	2	H85565	glutamate/aspartat
89	29	70.7	246	2	E90715	glutamate/aspartat
90	29	70.7	246	2	D64800	glutamate/aspartat
91	29	70.7	251	2	AE1051	probable transcrip
92	29	70.7	255	2	C75594	phosphoadenosine p
93	29	70.7	268	2	AE0215	2,4-dihydroxyhept-
94	29	70.7	275	2	T35064	probable integral
95	29	70.7	293	2	AH2988	methyltransferase
96	29	70.7	305	2	F86744	tagatose-6-phospha
97	29	70.7	334	2	S24552	protein-tyrosine k
98	29	70.7	334	2	A24582	MHC class I histoc
99	29	70.7	353	2	D71526	hypothetical prote
100	29	70.7	357	2	A95190	hypothetical prote

ALIGNMENTS

RESULT 1
A39939
protein-tyrosine kinase (EC 2.7.1.112) tkl [similarity] - chicken
N;Alternate names: kinase-related transforming protein (tkl); T-cell surface antigen ass
C;Species: Gallus gallus (chicken)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C;Accession: A42126; A39939
R;Chow, L.M.; Ratcliffe, M.J.; Veillette, A.
Mol. Cell. Biol. 12, 1226-1233, 1992
A;Title: tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene.
A;Reference number: A42126; MUID:92186854; PMID:1545804
A;Accession: A42126
A;Molecule type: mRNA
A;Residues: 1-88 <CHO>
A;Cross-references: UNIPARC:UPI0000172587; GB:M85043
A;Experimental source: thymus, spleen
A;Note: sequence extracted from NCBI backbone (NCBIN:88831, NCBIP:88833)
R;Strebhardt, K.; Mullins, J.I.; Bruck, C.; Ruebsamen-Waigmann, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987
A;Title: Additional member of the protein-tyrosine kinase family: the src-and lck-relate
A;Reference number: A39939; MUID:88097370; PMID:3321053
A;Accession: A39939
A;Molecule type: mRNA
A;Residues: 52-507 <STR>
A;Cross-references: UNIPARC:UPI00001713B3; GB:J03579; NID:g212712; PIDN:AAA49081.1; PID:
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;66-114/Domain: SH3 homology <SH3>
F;125-222/Domain: SH2 homology <SH2>
F;241-499/Domain: protein kinase homology <KIN>
F;249-257/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match 100.0%; Score 41; DB 1; Length 507;
  Best Local Similarity 100.0%; Pred. No. 0.57;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 338 KLLDMAAQI 346

RESULT 2
I48845
protein-tyrosine kinase (EC 2.7.1.112) lck, lymphocyte - mouse
N;Alternate names: p56; protein-tyrosine kinase tck
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: I48845; A23639; I57629; I77452
R;Voronova, A.F.; Sefton, B.M.
Nature 319, 682-685, 1986
A;Title: Expression of a new tyrosine protein kinase is stimulated by retrovirus promote
A;Reference number: I48845; MUID:86146842; PMID:3081813
A;Accession: I48845
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-509 <VOR1>
A;Cross-references: UNIPROT:Q91X65; UNIPARC:UPI000000418D; EMBL:X03533; NID:g54813; PIDN
R;Marth, J.D.; Peet, R.; Krebs, E.G.; Perimutter, R.M.
Cell 43, 393-404, 1985
A;Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpres
A;Reference number: A23639; MUID:86079521; PMID:2416464
A;Accession: A23639
A;Molecule type: mRNA
A;Residues: 1-282,'VP',285-509 <MAR>
A;Cross-references: UNIPARC:UPI0000172586; GB:M12056; NID:g198763
A;Note: the sequence is revised in GenBank entry MUSLCK, release 116.0, (PIDN:AAB59674.1
R;Voronova, A.F.; Adler, H.T.; Sefton, B.M.
Mol. Cell. Biol. 7, 4407-4413, 1987
A;Title: Two lck transcripts containing different 5' untranslated regions are present in
A;Reference number: I57629; MUID:88142832; PMID:3501824
A;Accession: I57629
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <VOR>
A;Cross-references: UNIPARC:UPI000016CE9D; GB:M18098; NID:g198766; PIDN:AAA39421.1; PID:
R;Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
Mol. Cell. Biol. 8, 3058-3064, 1988
A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel
A;Reference number: I57636; MUID:89096891; PMID:2850479
A;Accession: I77452
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-35,'VR' <GAR>
A;Cross-references: UNIPARC:UPI000016CE9E; GB:M21511; NID:g198768; PIDN:AAA39422.1; PID:
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro
F;68-116/Domain: SH3 homology <SH3>
F;127-224/Domain: SH2 homology <SH2>
F;243-501/Domain: protein kinase homology <KIN>
F;251-259/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;273/Active site: Lys #status predicted
F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match 100.0%; Score 41; DB 1; Length 509;
  Best Local Similarity 100.0%; Pred. No. 0.57;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
|||||||||
Db 340 KLLDMAAQI 348

RESULT 3
OKHULK
protein-tyrosine kinase (EC 2.7.1.112) lck - human
N;Alternate names: kinase-related transforming protein (lck)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 05-Oct-2004
C;Accession: JQ0152; S07822; S07200; S01879; S07143; A32797; I57636
R;Rouer, E.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R.
Gene 84, 105-113, 1989
A;Title: Structure of the human lck gene: differences in genomic organisation within src
A;Reference number: JQ0152; MUID:90108697; PMID:2558056
A;Accession: JQ0152
A;Molecule type: DNA
A;Residues: 1-509 <ROU>
A;Cross-references: UNIPROT:P06239; UNIPARC:UPI0000151F17; EMBL:X14053
R;Perlmutter, R.M.; Marth, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, C.B.
J. Cell. Biochem. 38, 117-126, 1988
A;Title: Structure and expression of lck transcripts in human lymphoid cells.
A;Reference number: S07822; MUID:89123626; PMID:3265417
A;Accession: S07822
A;Molecule type: mRNA
A;Residues: 1-86,'P',88-509 <PER>
A;Cross-references: UNIPARC:UPI0000163BD5; EMBL:X13529; NID:g34294; PIDN:CAA31884.1; PID
R;Koga, Y.; Caccia, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikai, Y.; Mak, T.W.
Eur. J. Immunol. 16, 1643-1646, 1986
A;Title: A human T cell-specific cDNA clone (YT16) encodes a protein with extensive homo
A;Reference number: S07200; MUID:87133831; PMID:3493153
A;Accession: S07200
A;Molecule type: mRNA
A;Residues: 1-205,'ASAITPI',212-257,'RCGW',262,'TTT',266,'T',268-281,'AGRLP',287-503,'ST
A;Cross-references: UNIPARC:UPI000016B09E; EMBL:X05027; NID:g36807; PIDN:CAA28691.1; PID
R;Veillette, A.; Foss, F.M.; Sausville, E.A.; Bolen, J.B.; Rosen, N.
Oncogene Res. 1, 357-374, 1987
A;Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other n
A;Reference number: S01879; MUID:88217332; PMID:2835736
A;Accession: S01879
A;Molecule type: mRNA
A;Residues: 368-471,'H',473-509 <VEI>

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A;Cross-references: UNIPARC:UPI000016ABFC; EMBL:X06369; NID:g34288; PIDN:CAA29667.1; PID
R;Trevillyan, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Linna, T.J.
Biochim. Biophys. Acta 888, 286-295, 1986
A;Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56(LSTRA).
A;Reference number: S07143; MUID:87000726; PMID:3489486
A;Accession: S07143
A;Molecule type: mRNA
A;Residues: 'A',376-509 <TRE>
A;Cross-references: UNIPARC:UPI000016AF39; EMBL:X04476; NID:g35779; PIDN:CAA28165.1; PID
R;Takadera, T.; Leung, S.; Gernone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.W
Mol. Cell. Biol. 9, 2173-2180, 1989
A;Title: Structure of the two promoters of the human lck gene: differential accumulation
A;Reference number: A32797; MUID:89313764; PMID:2787474
A;Accession: A32797
A;Molecule type: DNA
A;Residues: 1-35 <TAK>
A;Cross-references: UNIPARC:UPI000016ABFF; GB:M26692; NID:g341523; PIDN:AAA59503.1; PID:
R;Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
Mol. Cell. Biol. 8, 3058-3064, 1988
A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel
A;Reference number: I57636; MUID:89096891; PMID:2850479
A;Accession: I57636
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-35,'VR' <RES>
A;Cross-references: UNIPARC:UPI000016ABFD; GB:M21510; NID:g187031; PIDN:AAA59501.1; PID:
C;Comment: Protein tyrosine kinases play important roles in the control of cell growth a
C;Genetics:
A;Gene: GDB:LCK
A;Cross-references: GDB:119360; OMIM:153390
A;Map position: 1p35-1p34.3
A;Introns: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;2-509/Product: protein-tyrosine kinase lck #status predicted <MAT>
F;68-116/Domain: SH3 homology <SH3>
F;127-224/Domain: SH2 homology <SH2>
F;243-501/Domain: protein kinase homology <KIN>
F;251-259/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3,5/Binding site: palmitate (Cys) (covalent) #status predicted
F;273/Active site: Lys #status predicted
F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             100.0%;  Score 41;  DB 1;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 0.57;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||||
Db        340 KLLDMAAQI 348


RESULT 4
S24551
protein-tyrosine kinase (EC 2.7.1.112) 2 - freshwater sponge (Spongilla lacustris) (frag
N;Alternate names: src-type tyrosine kinase 2
C;Species: Spongilla lacustris
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 05-Oct-2004
C;Accession: S24551
R;Raulf, F.
submitted to the EMBL Data Library, September 1991
A;Reference number: S24550
A;Accession: S24551
A;Molecule type: mRNA
A;Residues: 1-362 <RAU>
A;Cross-references: UNIPROT:P42688; UNIPARC:UPI0000135F48; EMBL:X61602; NID:g10151; PIDN
C;Genetics:
A;Gene: srk2
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; tyrosine-speci
F;1-70/Domain: SH2 homology (fragment) <SH2>
F;93-351/Domain: protein kinase homology <KIN>
F;101-109/Region: protein kinase ATP-binding motif
F;123/Active site: Lys #status predicted
F;355/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             82.9%;  Score 34;  DB 2;  Length 362;
  Best Local Similarity   66.7%;  Pred. No. 14;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:|||||:
Db        190 QLIDMAAQV 198


RESULT 5
OKFVYR
protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain H-19)
N;Alternate names: kinase-related transforming protein src
C;Species: Rous sarcoma virus
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004
C;Accession: S09609
R;Bodor, J.; Poliak, E.; Pichrtova, J.; Geryk, J.; Svoboda, J.
Nucleic Acids Res. 17, 8869, 1989
A;Title: Complete nucleotide sequence of LTR, v-src, LTR provirus H-19.
A;Reference number: S09609; MUID:90067864; PMID:2587228
A;Accession: S09609
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-526 <BOD>
A;Cross-references: UNIPROT:P25020; UNIPARC:UPI0000135F2A; EMBL:X15345; NID:g61706; PIDN
C;Genetics:
A;Gene: src
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             82.9%;  Score 34;  DB 1;  Length 526;
  Best Local Similarity   77.8%;  Pred. No. 20;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||||||
Db        362 QLVDMAAQI 370


RESULT 6
TVFV60
protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
C;Species: Rous sarcoma virus
C;Date: 22-May-1981 #sequence_revision 17-Dec-1982 #text_change 05-Oct-2004
C;Accession: A38017; A00631; S02726; A38018
R;Czernilofsky, A.P.; Levinson, A.D.; Varmus, H.E.; Bishop, J.M.; Tischer, E.; Goodman,
Nature 301, 736-738, 1983
A;Title: Corrections to the nucleotide sequence of the src gene of Rous sarcoma virus.
A;Reference number: A38017; MUID:83141780; PMID:6298633
A;Accession: A38017
A;Molecule type: DNA
A;Residues: 1-526 <CZE>
A;Cross-references: UNIPROT:P00524; UNIPARC:UPI0000170DC3; GB:L29199; GB:J02018; GB:J020
A;Experimental source: strain Schmidt-Ruppin
R;Takeya, T.; Hanafusa, H.
Cell 32, 881-890, 1983
A;Title: Structure and sequence of the cellular gene homologous to the RSV sec gene and
A;Reference number: A00630; MUID:83155664; PMID:6299580
A;Accession: A00631
A;Molecule type: DNA
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A;Residues: 1-62,'D',64-95,'T',97-123,'V',125-300,'N',302-526 <TAK>
A;Cross-references: UNIPARC:UPI0000172582
A;Experimental source: strain Schmidt-Ruppin
R;Barnier, J.V.; Dezelee, P.; Marx, M.; Calothy, G.
Nucleic Acids Res. 17, 1252, 1989
A;Title: Nucleotide sequence of the src gene of the Schmidt-Ruppin strain of Rous Sarcom
A;Reference number: S02726; MUID:89160256; PMID:2537953
A;Accession: S02726
A;Molecule type: DNA
A;Residues: 1-9,'G',11-62,'D',64-123,'V',125-319,'K',321-495,'S',497-526 <BAR>
A;Cross-references: UNIPARC:UPI0000135F2C; EMBL:X13745; NID:g61908; PIDN:CAA32012.1; PID
R;Takeya, T.; Feldman, R.A.; Hanafusa, H.
J. Virol. 44, 1-11, 1982
A;Title: DNA sequence of the viral and cellular src gene of chickens: I. Complete nuclec
A;Reference number: A38018; MUID:83059858; PMID:6292477
A;Accession: A38018
A;Molecule type: DNA
A;Residues: 1-15,'C',17-94,'RT',97-116,'D',118-337,'T',339-526 <TA2>
A;Cross-references: UNIPARC:UPI0000135F24; GB:K00928; NID:g210187; PIDN:AAA42565.1; PID:
A;Experimental source: strain rASV1441
R;Neil, J.C.; Ghysdael, J.; Vogt, P.K.; Smart, J.E.
Nature 291, 675-677, 1981
A;Title: Homologous tyrosine phosphorylation sites in transformation-specific gene produ
A;Reference number: A38019; MUID:81220979; PMID:6264320
A;Contents: annotation; phosphorylation site
C;Comment: The sequence from the Schmidt-Ruppin strain is shown.
C;Genetics:
A;Gene: src
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experime

Query Match 82.9%; Score 34; DB 1; Length 526;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
:|:||||||
Db 362 QLVDMAAQI 370

RESULT 7
TVFVR
protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain Prague C)
C;Species: Rous sarcoma virus
C;Date: 01-Sep-1981 #sequence_revision 17-Dec-1982 #text_change 05-Oct-2004
C;Accession: A00632
R;Schwartz, D.; Tizard, R.; Gilbert, W.
submitted to the Nucleic Acid Sequence Database, September 1982
A;Reference number: A00632
A;Accession: A00632
A;Molecule type: genomic RNA
A;Residues: 1-526 <SCH>
A;Cross-references: UNIPROT:P00526; UNIPROT:O92806; UNIPARC:UPI000002BA63
A;Note: as a result of base variations, residues 242 and 288 may be replaced by Thr and
R;Neil, J.C.; Ghysdael, J.; Vogt, P.K.; Smart, J.E.
Nature 291, 675-677, 1981
A;Title: Homologous tyrosine phosphorylation sites in transformation-specific gene produ
A;Reference number: A38019; MUID:81220979; PMID:6264320
A;Contents: annotation; phosphorylation site
C;Genetics:
A;Gene: src
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experime

Query Match 82.9%; Score 34; DB 1; Length 526;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
:|:||||||
Db 362 QLVDMAAQI 370

RESULT 8
S15582
protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain Prague A)
C;Species: Rous sarcoma virus
A;Variety: strain Prague A
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Oct-2004
C;Accession: S15582; S09665
R;Liu, Z.; Hackett, P.B.
Nucleic Acids Res. 17, 3986, 1989
A;Title: Sequence variation of the Rous sarcoma virus PrA src gene.
A;Reference number: S15582; MUID:89282411; PMID:2543959
A;Accession: S15582
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-526 <LIU>
A;Cross-references: UNIPROT:Q64994; UNIPROT:O92806; UNIPROT:Q60567; UNIPROT:Q07461; UNIP
A;Experimental source: strain Prague A
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989
A;Note: only a list of differences from sequence S09665 is given; however, the list is i
R;Fincham, V.J.; Wyke, J.A.
J. Virol. 58, 694-699, 1986
A;Title: Localization of temperature-sensitive transformation mutations and back mutatio
A;Reference number: S09665; MUID:86200422; PMID:3009882
A;Accession: S09665
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 231-241,'TH',244-287,'G',289-463,'P',465-501,'N',503-526 <FIN>
A;Cross-references: UNIPARC:UPI00001755F1
C;Genetics:
A;Gene: src
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match 82.9%; Score 34; DB 2; Length 526;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
:|:||||||
Db 362 QLVDMAAQI 370

RESULT 9
S20808
protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
C;Species: Rous sarcoma virus
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004
C;Accession: S20808; S32774
R;Bodor, J.; Rozkot, F.; Svoboda, J.
submitted to the EMBL Data Library, May 1990
A;Description: Sequence organization of the adjacent chromosomal flanks the LTR.
A;Reference number: S20808

A;Accession: S20808
A;Molecule type: DNA
A;Residues: 1-526 <BOD>
A;Cross-references: UNIPROT:Q60567; UNIPARC:UPI00001068B2; EMBL:X52822; NID:g49656; PIDN
A;Experimental source: Mesocricetus auratus (golden hamster) provirus
C;Genetics:
A;Gene: src
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; tran
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match 82.9%; Score 34; DB 2; Length 526;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
:|:||||||
Db 362 QLVDMAAQI 370

RESULT 10
S26420
protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
C;Species: Rous sarcoma virus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Oct-2004
C;Accession: S26420; S20676
R;Kashuba, V.I.; Rynditch, A.V.; Dostalova, V.; Hlozanek, I.; Zubak, S.V.; Kavsan, V.M.
submitted to the EMBL Data Library, September 1992
A;Description: Molecular cloning and DNA sequence analysis of duck-adapted variant of Rc
A;Reference number: S26417
A;Accession: S26420
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-526 <KAS>
A;Cross-references: UNIPROT:Q07461; UNIPARC:UPI0000010512B; EMBL:X68524; NID:g61903; PIDN
R;Kashuba, V.I.; Serge, Z.V.; Rynditch, A.V.; Kavsan, V.M.; Hlozanek, I.
submitted to the EMBL Data Library, March 1990
A;Reference number: S20676
A;Accession: S20676
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-526 <KA2>
A;Cross-references: UNIPARC:UPI0000010512B; EMBL:X51861; NID:g61896; PIDN:CAA36154.1; PID
C;Genetics:
A;Gene: src
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match 82.9%; Score 34; DB 2; Length 526;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
:|:||||||
Db 362 QLVDMAAQI 370

RESULT 11
TVFVG9
protein-tyrosine kinase (EC 2.7.1.112) yes - avian sarcoma virus Y73
C;Species: avian sarcoma virus Y73
A;Note: host Gallus gallus (chicken)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 05-Oct-2004
C;Accession: A00633
R;Kitamura, N.; Kitamura, A.; Toyoshima, K.; Hirayama, Y.; Yoshida, M.
Nature 297, 205-208, 1982
A;Title: Avian sarcoma virus Y73 genome sequence and structural similarity of its transf
A;Reference number: A00633; MUID:82195528; PMID:6281656
A;Accession: A00633
A;Molecule type: genomic RNA
A;Residues: 1-528 <KIT>
A;Cross-references: UNIPARC:UPI000017258B
C;Comment: This protein is synthesized as a gag-yes polyprotein.
C;Genetics:
A;Gene: yes
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; tran
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match 82.9%; Score 34; DB 1; Length 528;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
:|:||||||
Db 362 QLVDMAAQI 370

RESULT 12
B34104
protein-tyrosine kinase (EC 2.7.1.112) src 2 [similarity] - African clawed frog
N;Alternate names: kinase-related transforming protein (src); kinase-related transformin
C;Species: Xenopus laevis (African clawed frog)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C;Accession: B34104; I51563
R;Steele, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B.
J. Biol. Chem. 264, 10649-10653, 1989
A;Title: The two Xenopus laevis SRC genes are co-expressed and each produces functional
A;Reference number: A34104; MUID:89278134; PMID:2499582
A;Accession: B34104
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-532 <STE>
A;Cross-references: UNIPROT:P13116; UNIPARC:UPI000017159F; GB:M23422; GB:J04822; NID:g21
R;Steele, R.E.
Nucleic Acids Res. 13, 1747-1761, 1985
A;Title: Two divergent cellular src genes are expressed in Xenopus laevis.
A;Reference number: I51563; MUID:85215578; PMID:2987836
A;Accession: I51563
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 439-492 <ST2>
A;Cross-references: UNIPARC:UPI00001715A0; GB:M30858; NID:g214799; PIDN:AAA51644.1; PID:
C;Genetics:
A;Gene: src
A;Introns: 464/1
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;87-136/Domain: SH3 homology <SH3>
F;147-244/Domain: SH2 homology <SH2>
F;264-522/Domain: protein kinase homology <KIN>
F;272-280/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;294/Active site: Lys #status predicted
F;415,526/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 82.9%; Score 34; DB 1; Length 532;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 KLLDMAAQI 9
              :|:||||||
Db        361 QLVDMAAQI 369


RESULT 13
A34104
protein-tyrosine kinase (EC 2.7.1.112) src 1 [similarity] - African clawed frog
N;Alternate names: kinase-related transforming protein (src); kinase-related transformin
C;Species: Xenopus laevis (African clawed frog)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 31-Dec-2004
C;Accession: A34104; I51564
R;Steele, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B.
J. Biol. Chem. 264, 10649-10653, 1989
A;Title: The two Xenopus laevis SRC genes are co-expressed and each produces functional
A;Reference number: A34104; MUID:89278134; PMID:2499582
A;Accession: A34104
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-532 <STE>
A;Cross-references: UNIPROT:Q91851; UNIPARC:UPI0000172581; GB:M24704; GB:J04822; NID:g21
R;Steele, R.E.; Chosn, R.; Ral, B.B.A.; Winokur, S.T.; Unger, T.F.
Oncogene 7, 2345-2350, 1992
A;Title: Structural organization of a src gene from xenopus laevis.
A;Reference number: I51564; MUID:93064714; PMID:1437158
A;Accession: I51564
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-113 <ST2>
A;Cross-references: UNIPARC:UPI00000FD97A; GB:M33646; NID:g214808; PIDN:AAA49963.1; PID:
C;Genetics:
A;Introns: 80/1
C;Superfamily: protein kinase homology; SH2 homology; SH3 homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phc
F;87-136/Domain: SH3 homology <SH3>
F;147-244/Domain: SH2 homology <SH2>
F;264-522/Domain: protein kinase homology <KIN>
F;272-280/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;294/Active site: Lys #status predicted
F;415,526/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             82.9%;  Score 34;  DB 1;  Length 532;
  Best Local Similarity   77.8%;  Pred. No. 20;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||||||
Db        361 QLVDMAAQI 369


RESULT 14
TVCHS
protein-tyrosine kinase (EC 2.7.1.112) src - chicken
N;Alternate names: kinase-related transforming protein src
C;Species: Gallus gallus (chicken)
C;Date: 19-Feb-1984 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C;Accession: A00630; I50217; A41256; C35650; A32432
R;Takeya, T.; Hanafusa, H.
Cell 32, 881-890, 1983
A;Title: Structure and sequence of the cellular gene homologous to the RSV sec gene and
A;Reference number: A00630; MUID:83155664; PMID:6299580
A;Accession: A00630
A;Molecule type: DNA
A;Residues: 1-500,'R',502-533 <TAK>
A;Cross-references: UNIPROT:P00523; UNIPROT:Q90993; UNIPARC:UPI000017257F; GB:J00844; NI
R;Takeya, T.; Hanafusa, H.
Cell 34, 319, 1983
A;Reference number: A90838
A;Contents: annotation; erratum, correct translation of residue 526
R;Takeya, T.; Hanafusa, H.
J. Virol. 44, 12-18, 1982
A;Title: DNA sequence of the viral and cellular src gene of chickens: II comparison of t
A;Reference number: I50217; MUID:83059861; PMID:6292480
A;Accession: I50217
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7 <TA2>
A;Cross-references: UNIPARC:UPI000011E887; GB:J00908; NID:g211690; PIDN:AAA48732.1; PID:
A;Note: the authors translated the codons AAC and CAG for residues 301 and 526 as Thr an
R;Dorai, T.; Levy, J.B.; Kang, L.; Brugge, J.S.; Wang, L.H.
Mol. Cell. Biol. 11, 4165-4176, 1991
A;Title: Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5' exons and po
A;Reference number: A41256; MUID:91304409; PMID:1712905
A;Accession: A41256
A;Molecule type: mRNA
A;Residues: 484-533 <DOR1>
A;Cross-references: UNIPARC:UPI0000171468; GB:S43579; NID:g1679964; PIDN:AAB19353.1; PID
A;Note: the authors translated the codon CAG for residue 527 as Glu
R;Dorai, T.; Wang, L.H.
Mol. Cell. Biol. 10, 4068-4079, 1990
A;Title: An alternative non-tyrosine protein kinase product of the c-src gene in chicken
A;Reference number: A35650; MUID:90318371; PMID:2115117
A;Accession: C35650
A;Molecule type: mRNA
A;Residues: 1-182,'DPCIPLPSCLC' <DOR2>
A;Cross-references: UNIPARC:UPI00000FD3A4; GB:M57290; NID:g212703; PIDN:AAA49078.1; PID:
A;Note: alternatively spliced mRNA exclusively replaces the long form in skeletal muscle
A;Note: this ORF appears not to be translated
R;Shenoy, S.; Choi, J.K.; Bagrodia, S.; Copeland, T.D.; Maller, J.L.; Shalloway, D.
Cell 57, 763-774, 1989
A;Title: Purified maturation promoting factor phosphorylates pp60(c-src) at the sites ph
A;Reference number: A32432; MUID:89249341; PMID:2470512
A;Accession: A32432
A;Molecule type: protein
A;Residues: 2-88 <SHE>
A;Cross-references: UNIPARC:UPI0000172580
A;Note: 34-Thr, 46-Thr, and 72-Ser are phosphorylated during mitosis
C;Genetics:
A;Gene: src
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;12,48/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;17/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F;34,46/Binding site: phosphate (Thr) (covalent) #status experimental
F;72/Binding site: phosphate (Ser) (covalent) #status experimental
F;295/Active site: Lys #status predicted
F;416,527/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             82.9%;  Score 34;  DB 1;  Length 533;
  Best Local Similarity   77.8%;  Pred. No. 20;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||||||
Db        362 QLVDMAAQI 370


RESULT 15
S33569
protein-tyrosine kinase (EC 2.7.1.112) yrk - chicken
C;Species: Gallus gallus (chicken)
C;Date: 08-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C;Accession: S33569; S29626
R;Sudol, M.; Greulich, H.; Newman, L.; Sarkar, A.; Sukegawa, J.; Yamamoto, T.
Oncogene 8, 823-831, 1993
A;Title: A novel Yes-related kinase, Yrk, is expressed at elevated levels in neural and
A;Reference number: S33568; MUID:93205395; PMID:8455940
A;Accession: S33569
A;Molecule type: mRNA
```

```
A;Residues: 1-536 <SUD>
A;Cross-references: UNIPROT:Q02977; UNIPARC:UPI0000151F15; EMBL:X67786; NID:g63895; PIDN
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;268-526/Domain: protein kinase homology <KIN>
F;276-284/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;298/Active site: Lys #status predicted
F;419,530/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             82.9%;  Score 34;  DB 2;  Length 536;
  Best Local Similarity   77.8%;  Pred. No. 20;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||||||
Db        365 QLVDMAAQI 373


RESULT 16
A45501
protein-tyrosine kinase (EC 2.7.1.112) yes [similarity] - African clawed frog
N;Alternate names: kinase-related transforming protein (yes)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C;Accession: A45501; S08517
R;Steele, R.E.; Irwin, M.Y.; Knudsen, C.L.; Collett, J.W.; Fero, J.B.
Oncogene Res. 1, 223-233, 1989
A;Title: The yes proto-oncogene is present in amphibians and contributes to the maternal
A;Reference number: A45501
A;Accession: A45501
A;Molecule type: mRNA
A;Residues: 1-537 <STE>
A;Cross-references: UNIPROT:P10936; UNIPARC:UPI0000172588; GB:X14377
R;Steele, R.E.; Irwin, M.Y.; Knudsen, C.L.; Collett, J.W.; Fero, J.B.
submitted to the EMBL Data Library, February 1989
A;Reference number: S08517
A;Accession: S08517
A;Molecule type: mRNA
A;Residues: 1-250,'S',252-537 <ST2>
A;Cross-references: UNIPARC:UPI000013ACB9; EMBL:X14377; NID:g65272; PIDN:CAA32551.1; PID
C;Genetics:
A;Gene: yes
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro
F;92-141/Domain: SH3 homology <SH3>
F;152-249/Domain: SH2 homology <SH2>
F;269-527/Domain: protein kinase homology <KIN>
F;277-285/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;299/Active site: Lys #status predicted
F;420,531/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             82.9%;  Score 34;  DB 1;  Length 537;
  Best Local Similarity   77.8%;  Pred. No. 21;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||||||
Db        366 QLVDMAAQI 374


RESULT 17
B49114
protein-tyrosine kinase (EC 2.7.1.112) fyk - Pacific electric ray
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 05-Oct-2004
C;Accession: B49114
R;Swope, S.L.; Huganir, R.L.
J. Biol. Chem. 268, 25152-25161, 1993
A;Title: Molecular cloning of two abundant protein tyrosine kinases in Torpedo electric
A;Reference number: A49114; MUID:94043386; PMID:8227079
A;Accession: B49114
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-539 <SWO>
A;Cross-references: UNIPROT:Q7LZH0; UNIPARC:UPI00001755F6; GB:U01350
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;91-140/Domain: SH3 homology <SH3>
F;151-248/Domain: SH2 homology <SH2>
F;271-529/Domain: protein kinase homology <KIN>
F;279-287/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;301/Active site: Lys #status predicted
F;422,533/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             82.9%;  Score 34;  DB 2;  Length 539;
  Best Local Similarity   77.8%;  Pred. No. 21;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||||||
Db        368 QLVDMAAQI 376


RESULT 18
TVCHYS
protein-tyrosine kinase (EC 2.7.1.112) yes - chicken
N;Alternate names: kinase-related transforming protein yes
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004
C;Accession: S03324; S05283; S01689
R;Zheng, X.; Podell, S.; Sefton, B.M.; Kaplan, P.L.
Oncogene 4, 99-104, 1989
A;Title: The sequence of chicken c-yes and p61(c-yes).
A;Reference number: S03324; MUID:89128204; PMID:2464785
A;Accession: S03324
A;Molecule type: mRNA
A;Residues: 1-541 <ZHE>
A;Cross-references: UNIPROT:P09324; UNIPARC:UPI0000047A82; EMBL:X13207
R;Kaplan, P.L.
submitted to the EMBL Data Library, October 1988
A;Reference number: S05283
A;Accession: S05283
A;Molecule type: mRNA
A;Residues: 1-66,'IHPLR',72-81,'Q',83-541 <KAP>
A;Cross-references: UNIPARC:UPI0000171303; EMBL:X13207; NID:g63362; PIDN:CAA31595.1; PID
R;Sudol, M.; Kieswetter, C.; Zhao, Y.H.; Dorai, T.; Wang, L.H.; Hanafusa, H.
Nucleic Acids Res. 16, 9876, 1988
A;Title: Nucleotide sequence of a cDNA for the chick yes proto-oncogene: comparison with
A;Reference number: S01689; MUID:89041591; PMID:3054816
A;Accession: S01689
A;Molecule type: mRNA
A;Residues: 1-237,'S',239-541 <SUD>
A;Cross-references: UNIPARC:UPI000017258C; EMBL:X12461
C;Genetics:
A;Gene: yes
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;2-541/Product: protein-tyrosine kinase yes #status predicted <MAT>
F;96-145/Domain: SH3 homology <SH3>
F;156-253/Domain: SH2 homology <SH2>
F;273-531/Domain: protein kinase homology <KIN>
F;281-289/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;303/Active site: Lys #status predicted
F;424,535/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             82.9%;  Score 34;  DB 1;  Length 541;
  Best Local Similarity   77.8%;  Pred. No. 21;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 KLLDMAAQI 9
              :|:||||||
Db        370 QLVDMAAQI 378


RESULT 19
S31645
protein-tyrosine kinase (EC 2.7.1.112) yes - mouse
N;Alternate names: gene c-yes protein
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1994 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C;Accession: I48318; S31645
R;Klages, S.; Adam, D.; Eiseman, E.; Fargnoli, J.; Dymecki, S.M.; Desiderio, S.V.; Bolen
Oncogene 8, 713-719, 1993
A;Title: Molecular cloning and analysis of cDNA encoding the murine c-yes tyrosine prote
A;Reference number: I48318; MUID:93173515; PMID:8437854
A;Accession: I48318
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-541 <RES>
A;Cross-references: UNIPROT:Q04736; UNIPARC:UPI00000018E2; EMBL:X67677; NID:g50623; PIDN
C;Genetics:
A;Gene: c-yes
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;96-145/Domain: SH3 homology <SH3>
F;156-253/Domain: SH2 homology <SH2>
F;273-531/Domain: protein kinase homology <KIN>
F;281-289/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;303/Active site: Lys #status predicted
F;424,535/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             82.9%;  Score 34;  DB 2;  Length 541;
  Best Local Similarity   77.8%;  Pred. No. 21;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||||||
Db        370 QLVDMAAQI 378


RESULT 20
TVHUSC
protein-tyrosine kinase (EC 2.7.1.112) src, neuronal - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C;Accession: A26891; A61083; B61083; A23287; A28832; B34704
R;Tanaka, A.; Gibbs, C.P.; Arthur, R.R.; Anderson, S.K.; Kung, H.J.; Fujita, D.J.
Mol. Cell. Biol. 7, 1978-1983, 1987
A;Title: DNA sequence encoding the amino-terminal region of the human c-src protein: imp
A;Reference number: A26891; MUID:87257903; PMID:3299057
A;Accession: A26891
A;Molecule type: mRNA
A;Residues: 1-117;124-191 <TAN>
A;Cross-references: UNIPROT:P12931; UNIPARC:UPI0000172578; UNIPARC:UPI0000172579; GB:M16
R;Pyper, J.M.; Bolen, J.B.
J. Neurosci. Res. 24, 89-96, 1989
A;Title: Neuron-specific splicing of C-SRC RNA in human brain.
A;Reference number: A61083; MUID:90040822; PMID:2681803
A;Accession: A61083
A;Molecule type: mRNA
A;Residues: 98-145 <PYP>
A;Cross-references: UNIPARC:UPI000017257A
A;Accession: B61083
A;Molecule type: mRNA
A;Residues: 98-117;124-145 <PY2>
A;Cross-references: UNIPARC:UPI000017257A
R;Anderson, S.K.; Gibbs, C.P.; Tanaka, A.; Kung, H.J.; Fujita, D.J.
Mol. Cell. Biol. 5, 1122-1129, 1985
A;Title: Human cellular src gene: Nucleotide sequence and derived amino acid sequence of
A;Reference number: A23287; MUID:85213483; PMID:2582238
A;Accession: A23287
A;Molecule type: mRNA
A;Residues: 192-542 <AND>
A;Cross-references: UNIPARC:UPI000016B068; GB:X02647; NID:g36588; PIDN:CAA26485.1; PID:g
R;Parker, R.C.; Mardon, G.; Lebo, R.V.; Varmus, H.E.; Bishop, J.M.
Mol. Cell. Biol. 5, 831-838, 1985
A;Title: Isolation of duplicated human c-src genes located on chromosomes 1 and 20.
A;Reference number: A28832; MUID:85187981; PMID:2581127
A;Accession: A28832
A;Molecule type: mRNA
A;Residues: 382-542 <PAR>
A;Cross-references: UNIPARC:UPI000017257D
R;Pyper, J.M.; Bolen, J.B.
Mol. Cell. Biol. 10, 2035-2040, 1990
A;Title: Identification of a novel neurcnal C-SRC exon expressed in human brain.
A;Reference number: A34704; MUID:90220588; PMID:1691439
A;Accession: B34704
A;Molecule type: mRNA
A;Residues: 118-123 <PY3>
A;Cross-references: UNIPARC:UPI000017257E
C;Genetics:
A;Gene: GDB:SRC
A;Cross-references: GDB:120750; OMIM:190090
A;Map position: 20q11.2-20q11.2
A;Introns: 84/1; 117/2; 123/2; 156/2; 191/1; 241/1; 293/1; 353/1; 378/3; 430/1; 474/1
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;1-542/Product: protein-tyrosine kinase src, neuronal #status predicted <MAT>
F;1-117,124-542/Product: protein-tyrosine kinase src, short form #status predicted <MA2>
F;91-146/Domain: SH3 homology <SH3>
F;157-254/Domain: SH2 homology <SH2>
F;274-532/Domain: protein kinase homology <KIN>
F;282-290/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;304/Active site: Lys #status predicted
F;425,536/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             82.9%;  Score 34;  DB 1;  Length 542;
  Best Local Similarity   77.8%;  Pred. No. 21;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||||||
Db        371 QLVDMAAQI 379


RESULT 21
TVHUYS
protein-tyrosine kinase (EC 2.7.1.112) yes-1 - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Oct-2004
C;Accession: A26714
R;Sukegawa, J.; Semba, K.; Yamanashi, Y.; Nishizawa, M.; Miyajima, N.; Yamamoto, T.; Toy
Mol. Cell. Biol. 7, 41-47, 1987
A;Title: Characterization of cDNA clones for the human c-yes gene.
A;Reference number: A26714; MUID:87172733; PMID:2436037
A;Accession: A26714
A;Molecule type: mRNA
A;Residues: 1-543 <SUK>
A;Cross-references: UNIPROT:P07947; UNIPARC:UPI0000062316; GB:M15990; NID:g181267; PIDN:
C;Genetics:
A;Gene: GDB:YES1
A;Cross-references: GDB:119637; OMIM:164880
A;Map position: 18p11.31-18p11.22
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
in kinase
F;2-543/Product: protein-tyrosine kinase yes-1 #status predicted <MAT>
F;98-147/Domain: SH3 homology <SH3>
F;158-255/Domain: SH2 homology <SH2>
```

```
F;275-533/Domain: protein kinase homology <KIN>
F;283-291/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;305/Active site: Lys #status predicted
F;426/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             82.9%;  Score 34;  DB 1;  Length 543;
  Best Local Similarity   77.8%;  Pred. No. 21;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||||||
Db        372 QLVDMAAQI 380


RESULT 22
S52313
protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
C;Species: Rous sarcoma virus
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Oct-2004
C;Accession: S52313
R;Tatosyan, A.; Yatsula, B.; Shtutman, M.; Moinova, E.; Kaverina, I.; Musatkina, E.; Les
submitted to the EMBL Data Library, January 1995
A;Description: Two new isoforms of v-src oncogene isolated from low and high metastatic
A;Reference number: S52313
A;Accession: S52313
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-545 <TAT>
A;Cross-references: UNIPROT:Q86362; UNIPARC:UPI0000105D06; EMBL:X84074; NID:g663083; PID
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;108-157/Domain: SH3 homology <SH3>
F;168-265/Domain: SH2 homology <SH2>
F;285-543/Domain: protein kinase homology <KIN>
F;293-301/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;315/Active site: Lys #status predicted
F;436/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             82.9%;  Score 34;  DB 2;  Length 545;
  Best Local Similarity   77.8%;  Pred. No. 21;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||||||
Db        382 QLVDMAAQI 390


RESULT 23
S52314
protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
C;Species: Rous sarcoma virus
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Oct-2004
C;Accession: S52314
R;Tatosyan, A.; Yatsula, B.; Shtutman, M.; Moinova, E.; Kaverina, I.; Musatkina, E.; Les
submitted to the EMBL Data Library, January 1995
A;Description: Two new isoforms of v-src oncogene isolated from low and high metastatic
A;Reference number: S52313
A;Accession: S52314
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-546 <TAT>
A;Cross-references: UNIPROT:Q86363; UNIPARC:UPI0000106213; EMBL:X84073; NID:g663085; PID
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;108-157/Domain: SH3 homology <SH3>
F;168-265/Domain: SH2 homology <SH2>
F;285-543/Domain: protein kinase homology <KIN>
F;293-301/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;315/Active site: Lys #status predicted
F;436/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             82.9%;  Score 34;  DB 2;  Length 546;
  Best Local Similarity   77.8%;  Pred. No. 21;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||||||
Db        382 QLVDMAAQI 390


RESULT 24
TVFVS2
protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus S2
C;Species: avian sarcoma virus S2
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C;Accession: B25375
R;Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.; Toyoshima, K.
Mol. Cell. Biol. 6, 2420-2428, 1986
A;Title: Activation of the cellular src gene by transducing retrovirus.
A;Reference number: A25375; MUID:87064539; PMID:3097513
A;Accession: B25375
A;Molecule type: DNA
A;Residues: 1-557 <IKA>
A;Cross-references: UNIPROT:P14085; UNIPARC:UPI0000135F26
C;Genetics:
A;Gene: src
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             82.9%;  Score 34;  DB 1;  Length 557;
  Best Local Similarity   77.8%;  Pred. No. 21;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||||||
Db        362 QLVDMAAQI 370


RESULT 25
TVFVS1
protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus S1
C;Species: avian sarcoma virus S1
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C;Accession: A25375
R;Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.; Toyoshima, K.
Mol. Cell. Biol. 6, 2420-2428, 1986
A;Title: Activation of the cellular src gene by transducing retrovirus.
A;Reference number: A25375; MUID:87064539; PMID:3097513
A;Accession: A25375
A;Molecule type: DNA
A;Residues: 1-568 <IKA>
A;Cross-references: UNIPROT:P14084; UNIPARC:UPI0000135F25
C;Genetics:
A;Gene: src
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             82.9%;  Score 34;  DB 1;  Length 568;
```

```
  Best Local Similarity   77.8%;  Pred. No. 22;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||||||
Db        362 QLVDMAAQI 370


RESULT 26
TVFVPR
protein-tyrosine kinase (EC 2.7.1.112) src - avian sarcoma virus PR2257
C;Species: avian sarcoma virus PR2257
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C;Accession: A30174
R;Geryk, J.; Dezelee, P.; Barnier, J.V.; Svoboda, J.; Nehyba, J.; Karakoz, I.; Rynditch,
J. Virol. 63, 481-492, 1989
A;Title: Transduction of the cellular src gene and 3' adjacent sequences in avian sarcom
A;Reference number: A30174; MUID:89094972; PMID:2463376
A;Accession: A30174
A;Molecule type: DNA
A;Residues: 1-587 <GER>
A;Cross-references: UNIPROT:P15054; UNIPARC:UPI0000135F23; GB:M21526; NID:g210264; PIDN:
C;Genetics:
A;Gene: src
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             82.9%;  Score 34;  DB 1;  Length 587;
  Best Local Similarity   77.8%;  Pred. No. 23;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||||||
Db        362 QLVDMAAQI 370


RESULT 27
S04205
protein-tyrosine kinase (EC 2.7.1.112) - feline sarcoma virus (fragment)
N;Alternate names: gag-onc fusion protein
C;Species: feline sarcoma virus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S04205
R;Kappes, B.; Ziemiecki, A.; Mueller, R.G.; Theilen, G.H.; Bauer, H.; Barnekow, A.
Oncogene 4, 363-372, 1989
A;Title: The TP1 isolate of feline sarcoma virus encodes a fgr-related oncogene lacking
A;Reference number: S04205; MUID:89201884; PMID:2539576
A;Accession: S04205
A;Molecule type: DNA
A;Residues: 1-392 <KAP>
A;Cross-references: UNIPROT:Q28414; UNIPARC:UPI00001046DB; EMBL:X14842; NID:g1089; PIDN:
C;Superfamily: feline sarcoma virus protein-tyrosine kinase fgr; protein kinase homology
C;Keywords: ATP; autophosphorylation; myristylation; oncogene; phosphoprotein; phosphotr
F;7-104/Domain: SH2 homology <SH2>
F;124-382/Domain: protein kinase homology <KIN>
F;132-140/Region: protein kinase ATP-binding motif
F;154/Active site: Lys #status predicted
F;275,386/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             80.5%;  Score 33;  DB 2;  Length 392;
  Best Local Similarity   66.7%;  Pred. No. 24;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:|||||:
Db        221 QLVDMAAQV 229


RESULT 28
I37206
protein-tyrosine kinase (EC 2.7.1.112) blk - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Oct-2004
C;Accession: I37206; S51647
R;Islam, K.B.; Rabbani, H.; Larsson, C.; Sanders, R.; Smith, C.I.
J. Immunol. 154, 1265-1272, 1995
A;Title: Molecular cloning, characterization, and chromosomal localization of a human ly
A;Reference number: I37206; MUID:95123078; PMID:7822795
A;Accession: I37206
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-505 <RES>
A;Cross-references: UNIPROT:P51451; UNIPARC:UPI0000163B22; EMBL:Z33998; NID:g601951; PID
C;Genetics:
A;Gene: GDB:BLK
A;Cross-references: GDB:454114; OMIM:191305
A;Map position: 8p23-8p22
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; tyro
F;65-113/Domain: SH3 homology <SH3>
F;124-220/Domain: SH2 homology <SH2>
F;239-497/Domain: protein kinase homology <KIN>
F;247-255/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;269/Active site: Lys #status predicted

  Query Match             80.5%;  Score 33;  DB 2;  Length 505;
  Best Local Similarity   66.7%;  Pred. No. 32;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||:|||
Db        336 RLIDMSAQI 344


RESULT 29
TVHAST
protein-tyrosine kinase (EC 2.7.1.112) stk - Hydra attenuata
C;Species: Hydra attenuata
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Oct-2004
C;Accession: A34094
R;Bosch, T.C.G.; Unger, T.F.; Fisher, D.A.; Steele, R.E.
Mol. Cell. Biol. 9, 4141-4151, 1989
A;Title: Structure and expression of STK, a src-related gene in the simple metazoan Hydr
A;Reference number: A34094; MUID:90066418; PMID:2479820
A;Accession: A34094
A;Molecule type: mRNA
A;Residues: 1-509 <BOS>
A;Cross-references: UNIPROT:P17713; UNIPARC:UPI000013610D; GB:M25245; NID:g159273; PIDN:
C;Genetics:
A;Gene: stk
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;66-115/Domain: SH3 homology <SH3>
F;126-218/Domain: SH2 homology <SH2>
F;238-497/Domain: protein kinase homology <KIN>
F;246-254/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;4/Binding site: palmitate (Cys) (covalent) #status predicted
F;268/Active site: Lys #status predicted
F;390/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             80.5%;  Score 33;  DB 1;  Length 509;
  Best Local Similarity   75.0%;  Pred. No. 32;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LLDMAAQI 9
              |:|||||:
Db        337 LIDMAAQV 344
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RESULT 30
TVHUFR
protein-tyrosine kinase (EC 2.7.1.112) fgr - human
N;Alternate names: kinase-related transforming protein (fgr)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 30-Sep-1989 #text_change 05-Oct-2004
C;Accession: A27676; A28353; A24842; A45930; S24306
R;Katamine, S.; Notario, V.; Rao, C.D.; Miki, T.; Cheah, M.S.C.; Tronick, S.R.; Robbins,
Mol. Cell. Biol. 8, 259-266, 1988
A;Title: Primary structure of the human fgr proto-oncogene product p55(c-fgr).
A;Reference number: A27676; MUID:88094395; PMID:3275868
A;Accession: A27676
A;Molecule type: mRNA
A;Residues: 1-529 <REA>
A;Cross-references: UNIPROT:P09769; UNIPARC:UPI000012A72F; GB:M19722; GB:J03429; NID:g18
R;Inoue, K.; Ikawa, S.; Semba, K.; Sukegawa, J.; Yamamoto, T.; Toyoshima, K.
Oncogene 1, 301-304, 1987
A;Title: Isolation and sequencing of cDNA clones homologous to the v-fgr oncogene from a
A;Reference number: A28353; MUID:88262220; PMID:3330776
A;Accession: A28353
A;Molecule type: mRNA
A;Residues: 1-143 <INO>
A;Cross-references: UNIPARC:UPI000017258D
R;Nishizawa, M.; Semba, K.; Yoshida, M.C.; Yamamoto, T.; Sasaki, M.; Toyoshima, K.
Mol. Cell. Biol. 6, 511-517, 1986
A;Title: Structure, expression, and chromosomal location of the human c-fgr gene.
A;Reference number: A24842; MUID:87064334; PMID:3023853
A;Accession: A24842
A;Molecule type: DNA
A;Residues: 111-416 <REB>
A;Cross-references: UNIPARC:UPI000016A8FC; GB:M12724; NID:g182581; PIDN:AAA52762.1; PID:
R;Brickell, P.M.; Patel, M.
Br. J. Cancer 58, 704-709, 1988
A;Title: Structure and expression of c-fgr protooncogene mRNA in Epstein-Barr virus conv
A;Reference number: A45930; MUID:89134667; PMID:2852026
A;Accession: A45930
A;Molecule type: mRNA
A;Residues: 1-177;524-529 <BRI>
A;Cross-references: UNIPARC:UPI000006D52E; UNIPARC:UPI000017258E; GB:M27454
R;Patel, M.; Leevers, S.J.; Brickell, P.M.
Oncogene 5, 201-206, 1990
A;Title: Structure of the complete human c-fgr proto-oncogene and identification of mult
A;Reference number: S24306; MUID:90206622; PMID:1690869
A;Accession: S24306
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-142 <PAT>
A;Cross-references: UNIPARC:UPI0000070DB5; EMBL:X52207; NID:g29893; PIDN:CAA36457.2; PID
C;Genetics:
A;Gene: GDB:FGR
A;Cross-references: GDB:120615; OMIM:164940
A;Map position: 1p36.2-1p36.1
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
in kinase
F;84-133/Domain: SH3 homology <SH3>
F;144-241/Domain: SH2 homology <SH2>
F;261-519/Domain: protein kinase homology <KIN>
F;269-277/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3,6/Binding site: palmitate (Cys) (covalent) #status predicted
F;291/Active site: Lys #status predicted
F;523/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match 80.5%; Score 33; DB 1; Length 529;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLLDMAAQI 9
:|:|||||:
Db 358 QLVDMAAQV 366

Search completed: June 29, 2006, 09:31:37
Job time : 14.3373 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:39 ; Search time 105.831 Seconds
(without alignments)
78.664 Million cell updates/sec

Title: US-10-062-257A-14
Perfect score: 41
Sequence: 1 KLLDMAAQI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	100.0	368	2	Q3TLX4_MOUSE	Q3tlx4 mus musculu
2	41	100.0	379	2	Q4FZR6_RAT	Q4fzr6 rattus norv
3	41	100.0	507	1	LCK_CHICK	P42683 gallus gall
4	41	100.0	508	1	LCK_AOTNA	Q5pxs1 aotus nancy
5	41	100.0	508	1	LCK_HUMAN	P06239 homo sapien
6	41	100.0	508	1	LCK_MOUSE	P06240 mus musculu
7	41	100.0	508	1	LCK_SAISC	Q95kr7 saimiri sci
8	41	100.0	509	2	Q7RTZ3_HUMAN	Q7rtz3 homo sapien
9	41	100.0	509	2	Q95M32_9PRIM	Q95m32 hylobates s
10	41	100.0	509	2	Q3ZCM0_BOVIN	Q3zcm0 bos taurus
11	41	100.0	516	2	Q573B4_HUMAN	Q573b4 homo sapien
12	39	95.1	322	2	Q4RR72_TETNG	Q4rr72 tetraodon n
13	37	90.2	263	2	Q2KW85_BORAV	Q2kw85 bordetella
14	37	90.2	269	1	DAPB_BORBR	Q7wgh5 bordetella
15	37	90.2	269	1	DAPB_BORPA	Q7w510 bordetella
16	37	90.2	269	1	DAPB_BORPE	Q9x6y9 bordetella
17	36	87.8	267	1	DAPB_CHRVO	Q7nx34 chromobacte
18	36	87.8	267	1	DAPB_PSEPK	Q88du4 pseudomonas
19	36	87.8	267	2	Q2XEZ8_PSEPU	Q2xez8 pseudomonas
20	36	87.8	268	2	Q3KI98_PSEPF	Q3ki98 pseudomonas
21	36	87.8	268	2	Q4KIG9_PSEF5	Q4kig9 pseudomonas
22	35	85.4	434	2	Q5L9P3_BACFN	Q5l9p3 bacteroides
23	35	85.4	434	2	Q64PY6_BACFR	Q64py6 bacteroides
24	35	85.4	434	2	Q7MUW1_PORGI	Q7muw1 porphyromon
25	35	85.4	434	2	Q8A681_BACTN	Q8a681 bacteroides
26	35	85.4	485	2	Q5TYU7_BRARE	Q5tyu7 brachydanio
27	35	85.4	508	2	Q7PPB4_ANOGA	Q7ppb4 anopheles g
28	34	82.9	183	2	Q3MYH2_9DELT	Q3myh2 syntrophoba
29	34	82.9	235	2	Q5U175_DROME	Q5u175 drosophila
30	34	82.9	245	2	Q9PVU9_LAMRE	Q9pvu9 lampetra re
31	34	82.9	249	2	Q9U8V6_EPTBU	Q9u8v6 eptatretus
32	34	82.9	251	2	Q9H7V3_HUMAN	Q9h7v3 homo sapien
33	34	82.9	362	1	SRK2_SPOLA	P42688 spongilla l
34	34	82.9	379	2	Q36QP8_MARHY	Q36qp8 marinobacte
35	34	82.9	408	2	Q4RAT6_TETNG	Q4rat6 tetraodon n
36	34	82.9	430	2	Q5PAI3_ANAMM	Q5pai3 anaplasma m
37	34	82.9	489	2	Q6AXQ3_RAT	Q6axq3 rattus norv
38	34	82.9	498	2	Q7NX24_CHRVO	Q7nx24 chromobacte
39	34	82.9	504	2	Q8WSU2_9METZ	Q8wsu2 ephydatia f
40	34	82.9	509	2	Q4RNL0_TETNG	Q4rnl0 tetraodon n
41	34	82.9	517	1	SRC42_DROME	Q9v9j3 drosophila
42	34	82.9	523	2	Q85477_9RETR	Q85477 rous sarcom
43	34	82.9	525	1	SRC_AVISR	P00525 avian sarco
44	34	82.9	525	1	SRC_RSVH1	P25020 rous sarcom
45	34	82.9	525	1	SRC_RSVP	P00526 rous sarcom
46	34	82.9	525	1	SRC_RSVSA	P00524 rous sarcom
47	34	82.9	525	1	SRC_RSVSE	P63185 rous sarcom
48	34	82.9	525	2	Q8AWF1_BRARE	Q8awf1 brachydanio
49	34	82.9	526	2	O92806_9RETR	O92806 rous sarcom
50	34	82.9	526	2	O93080_9RETR	O93080 rous sarcom
51	34	82.9	526	2	Q07461_9RETR	Q07461 rous sarcom
52	34	82.9	526	2	Q60567_9RETR	Q60567 rous sarcom
53	34	82.9	526	2	Q64993_RSVSR	Q64993 rous sarcom
54	34	82.9	528	1	YES_AVISY	P00527 avian sarco
55	34	82.9	528	2	Q66HZ1_BRARE	Q66hz1 brachydanio
56	34	82.9	531	1	SRC1_XENLA	P13115 xenopus lae
57	34	82.9	531	1	SRC2_XENLA	P13116 xenopus lae
58	34	82.9	532	1	SRC_CHICK	P00523 gallus gall
59	34	82.9	532	2	Q2TAR1_XENLA	Q2tar1 xenopus lae
60	34	82.9	532	2	Q5MAS9_XENTR	Q5mas9 xenopus tro
61	34	82.9	535	1	SRC_HUMAN	P12931 homo sapien
62	34	82.9	535	1	YRK_CHICK	Q02977 gallus gall
63	34	82.9	535	2	O92957_RSVSB	O92957 rous sarcom
64	34	82.9	536	1	YES_XENLA	P10936 xenopus lae
65	34	82.9	537	2	Q498G3_XENLA	Q498g3 xenopus lae
66	34	82.9	537	2	Q640S9_XENTR	Q640s9 xenopus tro
67	34	82.9	537	2	Q6PF70_XENLA	Q6pf70 xenopus lae
68	34	82.9	537	2	Q7ZX73_XENLA	Q7zx73 xenopus lae
69	34	82.9	538	1	YES_CANFA	Q28923 canis famil
70	34	82.9	539	2	Q7LZH0_TORCA	Q7lzh0 torpedo cal
71	34	82.9	540	1	YES_CHICK	P09324 gallus gall
72	34	82.9	540	1	YES_MOUSE	Q04736 mus musculu
73	34	82.9	541	2	Q3TJI7_MOUSE	Q3tji7 mus musculu
74	34	82.9	541	2	Q8C762_MOUSE	Q8c762 mus musculu
75	34	82.9	541	2	Q8CBP1_MOUSE	Q8cbp1 mus musculu
76	34	82.9	541	2	Q99PW1_RAT	Q99pw1 rattus norv
77	34	82.9	542	1	YES_HUMAN	P07947 homo sapien
78	34	82.9	542	2	Q76P87_HUMAN	Q76p87 homo sapien
79	34	82.9	545	2	Q86362_9RETR	Q86362 rous sarcom
80	34	82.9	546	2	Q6EWH1_BRARE	Q6ewh1 brachydanio
81	34	82.9	546	2	Q86363_9RETR	Q86363 rous sarcom
82	34	82.9	556	1	SRC_AVIST	P14085 avian sarco
83	34	82.9	567	1	SRC_AVISS	P14084 avian sarco
84	34	82.9	586	1	SRC_AVIS2	P15054 avian sarco
85	34	82.9	587	2	Q64817_9RETR	Q64817 avian sarco
86	34	82.9	656	2	Q3SGA9_THIDA	Q3sga9 thiobacillu
87	34	82.9	716	2	Q2R196_ORYSA	Q2r196 oryza sativ
88	33	80.5	103	2	Q6JAC8_MAIZE	Q6jac8 zea mays (m
89	33	80.5	106	2	Q75GQ1_ORYSA	Q75gq1 oryza sativ
90	33	80.5	134	2	Q75GQ0_ORYSA	Q75gq0 oryza sativ
91	33	80.5	184	2	Q35E95_9BRAD	Q35e95 bradyrhizob
92	33	80.5	218	2	Q7QQG4_GIALA	Q7qqg4 giardia lam
93	33	80.5	232	2	Q35M74_9BRAD	Q35m74 bradyrhizob
94	33	80.5	267	1	DAPB_PSEFL	Q84cp9 pseudomonas
95	33	80.5	304	2	Q5FI89_LACAC	Q5fi89 lactobacill
96	33	80.5	304	2	Q74HP0_LACJO	Q74hp0 lactobacill
97	33	80.5	378	2	Q7YZH8_MONBE	Q7yzh8 monosiga br
98	33	80.5	382	2	Q7VS22_BORPE	Q7vs22 bordetella
99	33	80.5	382	2	Q7WEC4_BORBR	Q7wec4 bordetella
100	33	80.5	392	2	Q28414_FLV	Q28414 feline sarc

ALIGNMENTS

```
RESULT 1
Q3TLX4_MOUSE
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AC   Q3TLX4;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched
DE   library, clone:G830026O06 product:lymphocyte protein tyrosine kinase,
DE   full insert sequence. (Fragment).
GN   Name=Lck;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
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RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
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RC   TISSUE=Mammary gland;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
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RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
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RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
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RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
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RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
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RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK166263; BAE38668.1; -; mRNA.
DR   MGI; MGI:96756; Lck.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   368 AA;  42018 MW;  7AB6AE53AF1A5059 CRC64;

  Query Match             100.0%;  Score 41;  DB 2;  Length 368;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||||
Db        199 KLLDMAAQI 207


RESULT 2
Q4FZR6_RAT
ID   Q4FZR6_RAT     PRELIMINARY;   PRT;   379 AA.
AC   Q4FZR6;
DT   30-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   30-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Lck_mapped protein (Fragment).
GN   Name=Lck_mapped;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC099218; AAH99218.1; -; mRNA.
DR   SMR; Q4FZR6; 2-379.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   379 AA;  43336 MW;  7CDEB573BAFB53AB CRC64;

  Query Match             100.0%;  Score 41;  DB 2;  Length 379;
  Best Local Similarity   100.0%;  Pred. No. 2.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
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Db        210 KLLDMAAQI 218
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RESULT 3
LCK_CHICK
ID   LCK_CHICK      STANDARD;      PRT;   507 AA.
AC   P42683; Q53WS8;
DT   01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1995, sequence version 1.
DT   07-MAR-2006, entry version 47.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (Protein-
DE   tyrosine kinase C-TKL) (p56tkl).
GN   Name=LCK;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Spleen;
RA   Gaertner T., Khnel H., Strebhardt K., Ruebsamen-Waigmann H.;
RL   Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 1-88.
RX   MEDLINE=92186854; PubMed=1545804;
RA   Chow L., Ratcliffe M., Veillette A.;
RT   "tkl is the avian homolog of the mammalian lck tyrosine protein kinase
RT   gene.";
RL   Mol. Cell. Biol. 12:1226-1233(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 46-507.
RX   MEDLINE=88097370; PubMed=3321053;
RA   Strebhardt K., Mullins J.I., Bruck C., Ruebsamen-Waigmann H.;
RT   "Additional member of the protein-tyrosine kinase family: the src- and
RT   lck-related protooncogene c-tkl.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:8778-8782(1987).
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD4, CD8 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Bound to the cytoplasmic domain of either
CC       CD4 or CD8 (By similarity).
CC   -!- PTM: Phosphorylated on Tyr-503. This phosphorylation downregulates
CC       catalytic activity. Phosphorylated on Tyr-392 either by itself or
CC       another kinase, leading to increased enzymatic activity.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X60380; CAA42930.1; -; mRNA.
DR   EMBL; M85043; AAA49003.1; -; mRNA.
DR   EMBL; J03579; AAA49081.1; ALT_INIT; mRNA.
DR   HSSP; P06239; 3LCK.
DR   SMR; P42683; 63-507.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    507       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088128.
FT   DOMAIN       59    119       SH3.
FT   DOMAIN      125    222       SH2.
FT   DOMAIN      243    496       Protein kinase.
FT   NP_BIND     249    257       ATP (By similarity).
FT   ACT_SITE    362    362       Proton acceptor (By similarity).
FT   BINDING     271    271       ATP (By similarity).
FT   MOD_RES     392    392       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     503    503       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   507 AA;  58009 MW;  BC83C4FA891B6170 CRC64;

  Query Match             100.0%;  Score 41;  DB 1;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||||
Db        338 KLLDMAAQI 346


RESULT 4
LCK_AOTNA
ID   LCK_AOTNA      STANDARD;      PRT;   508 AA.
AC   Q5PXS1;
DT   08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT   08-NOV-2005, sequence version 3.
DT   07-MAR-2006, entry version 13.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Aotus nancymaae (Ma's night monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=37293;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Perez-Quintero L.A., Vernot J.P.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways. Association of the TCR with a peptide
CC       antigen-bound MHC complex facilitates the interaction of CD4 and
CC       CD8 with MHC class II and class I molecules, respectively, and
CC       thereby recruits the associated LCK to the vicinity of the TCR/CD3
CC       complex. LCK then phosphorylates tyrosines residues within the
CC       immunoreceptor tyrosines-based activation motifs (ITAMs) in the
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CC       cytoplasmic tails of the TCRgamma chains and CD3 subunits,
CC       initiating the TCR/CD3 signaling pathway. In addition, contributes
CC       to signaling by other receptor molecules. Associates directly with
CC       the cytoplasmic tail of CD2, and upon engagement of the CD2
CC       molecule, LCK undergoes hyperphosphorylation and activation. Also
CC       plays a role in the IL2 receptor-linked signaling pathway that
CC       controls T-cell proliferative response. Binding of IL2 to its
CC       receptor results in increased activity of LCK. Is expressed at all
CC       stages of thymocyte development and is required for the regulation
CC       of maturation events that are governed by both pre-TCR and mature
CC       alpha beta TCR (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also
CC       binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to
CC       other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds
CC       to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes
CC       through its SH3 domain and to the tyrosine phosphorylated form of
CC       KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.
CC       Interacts with phosphorylated LIME1. Interacts with CBLB (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.
CC       Present in lipid rafts in an unactive form (By similarity).
CC   -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.
CC       Interaction is regulated by Ser-58 phosphorylation (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY821852; AAV70114.2; -; mRNA.
DR   SMR; Q5PXS1; 64-508.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    508       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088123.
FT   DOMAIN       60    120       SH3.
FT   DOMAIN      126    223       SH2.
FT   DOMAIN      244    497       Protein kinase.
FT   NP_BIND     250    258       ATP (By similarity).
FT   REGION        1     71       Interactions with CD4 and CD8 (By
FT                                similarity).
FT   ACT_SITE    363    363       Proton acceptor (By similarity).
FT   BINDING     272    272       ATP (By similarity).
FT   MOD_RES     393    393       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     504    504       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   508 AA;  58041 MW;  8B61951BC192A3A4 CRC64;

  Query Match             100.0%;  Score 41;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||||
Db        339 KLLDMAAQI 347


RESULT 5
LCK_HUMAN
ID   LCK_HUMAN      STANDARD;      PRT;   508 AA.
AC   P06239; P07100; Q12850; Q13152; Q5TDH8; Q5TDH9; Q96DW4; Q9NYT8;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1994, sequence version 5.
DT   07-MAR-2006, entry version 87.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase) (LSK) (T cell-
DE   specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=87133831; PubMed=3493153;
RA   Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
RA   Mak T.W.;
RT   "A human T cell-specific cDNA clone (YT16) encodes a protein with
RT   extensive homology to a family of protein-tyrosine kinases.";
RL   Eur. J. Immunol. 16:1643-1646(1986).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=89123626; PubMed=3265417;
RA   Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F.,
RA   Wilson C.B.;
RT   "Structure and expression of lck transcripts in human lymphoid
RT   cells.";
RL   J. Cell. Biochem. 38:117-126(1988).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=90108697; PubMed=2558056; DOI=10.1016/0378-1119(89)90144-3;
RA   Rouer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
RA   Benarous R.;
RT   "Structure of the human lck gene: differences in genomic organisation
RT   within src-related genes affect only N-terminal exons.";
RL   Gene 84:105-113(1989).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA], VARIANTS LEU-27; GLN-LYS-PRO-231 INS;
RP   VAL-352 AND LEU-446, AND PHOSPHORYLATION SITES TYR-393 AND TYR-504.
RC   TISSUE=Leukemia;
RX   MEDLINE=94187714; PubMed=8139546;
RA   Wright D.D., Sefton B.M., Kamps M.P.;
RT   "Oncogenic activation of the Lck protein accompanies translocation of
RT   the LCK gene in the human HSB2 T-cell leukemia.";
RL   Mol. Cell. Biol. 14:2429-2437(1994).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM SHORT), AND ALTERNATIVE SPLICING.
RC   TISSUE=Leukemic T-cell;
RX   MEDLINE=96085119; PubMed=7495859; DOI=10.1016/0167-4781(95)00162-A;
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RA Vogel L.B., Arthur R., Fujita D.J.;
RT "An aberrant lck mRNA in two human T-cell lines.";
RL Biochim. Biophys. Acta 1264:168-172(1995).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG Human chromosome 1 international sequencing consortium;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX MEDLINE=89096891; PubMed=2850479;
RA Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT "Structure of the murine lck gene and its rearrangement in a murine
RT lymphoma cell line.";
RL Mol. Cell. Biol. 8:3058-3064(1988).
RN [9]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX MEDLINE=89313764; PubMed=2787474;
RA Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
RA Miyamoto N.G., Mak T.W.;
RT "Structure of the two promoters of the human lck gene: differential
RT accumulation of two classes of lck transcripts in T cells.";
RL Mol. Cell. Biol. 9:2173-2180(1989).
RN [10]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 13-508.
RC TISSUE=Peripheral blood lymphocyte;
RX MEDLINE=20462621; PubMed=11009097;
RX DOI=10.1002/1521-4141(200009)30:9<2632::AID-IMMU2632>3.0.CO;2-C;
RA Boncristiano M., Majolini M.B., D'Elios M.M., Pacini S., Valensin S.,
RA Ulivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,
RA Baldari C.T.;
RT "Defective recruitment and activation of ZAP-70 in common variable
RT immunodeficiency patients with T cell defects.";
RL Eur. J. Immunol. 30:2632-2638(2000).
RN [11]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 367-508.
RX MEDLINE=88217332; PubMed=2835736;
RA Veillette A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.;
RT "Expression of the lck tyrosine kinase gene in human colon carcinoma
RT and other non-lymphoid human tumor cell lines.";
RL Oncogene Res. 1:357-374(1987).
RN [12]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 374-508.
RX MEDLINE=87000726; PubMed=3489486; DOI=10.1016/0167-4889(86)90228-4;
RA Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
RA Linna T.J.;
RT "Human T lymphocytes express a protein-tyrosine kinase homologous to
RT p56LSTRA.";
RL Biochim. Biophys. Acta 888:286-295(1986).
RN [13]
RP PHOSPHORYLATION SITE TYR-504.
RX MEDLINE=92347326; PubMed=1639064;
RA Bergman M., Mustelin T., Oetken C., Partanen J., Flint N.A.,
RA Amrein K.E., Autero M., Burn P., Alitalo K.;
RT "The human p50csk tyrosine kinase phosphorylates p56lck at Tyr-505 and
RT down regulates its catalytic activity.";
RL EMBO J. 11:2919-2924(1992).
RN [14]
RP INTERACTION WITH PI3K.
RX MEDLINE=94067101; PubMed=7504174;
RA Vogel L.B., Fujita D.J.;
RT "The SH3 domain of p56lck is involved in binding to
RT phosphatidylinositol 3'-kinase from T lymphocytes.";
RL Mol. Cell. Biol. 13:7408-7417(1993).
RN [15]
RP INTERACTION WITH KHDRBS1.
RX MEDLINE=95155308; PubMed=7852312; DOI=10.1074/jbc.270.6.2506;
RA Vogel L.B., Fujita D.J.;
RT "p70 phosphorylation and binding to p56lck is an early event in
RT interleukin-2-induced onset of cell cycle progression in T-
RT lymphocytes.";
RL J. Biol. Chem. 270:2506-2511(1995).
RN [16]
RP INTERACTION WITH SQSTM1, AND MUTAGENESIS OF SER-58 AND ARG-153.
RX PubMed=8618896;
RA Park I., Chung J., Walsh C.T., Yun Y., Strominger J.L., Shin J.;
RT "Phosphotyrosine-independent binding of a 62-kDa protein to the src
RT homology 2 (SH2) domain of p56lck and its regulation by
RT phosphorylation of Ser-59 in the lck unique N-terminal region.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:12338-12342(1995).
RN [17]
RP INTERACTION WITH HIV-1 NEF.
RX MEDLINE=96386556; PubMed=8794306;
RA Greenway A.L., Azad A., Mills J., McPhee D.A.;
RT "Human immunodeficiency virus type 1 Nef binds directly to LCK and
RT mitogen-activated protein kinase, inhibiting kinase activity.";
RL J. Virol. 70:6701-6708(1996).
RN [18]
RP REVIEW.
RX PubMed=10848956;
RA Isakov N., Biesinger B.;
RT "Lck protein tyrosine kinase is a key regulator of T-cell activation
RT and a target for signal intervention by Herpesvirus saimiri and other
RT viral gene products.";
RL Eur. J. Biochem. 267:3413-3421(2000).
RN [19]
RP SUBCELLULAR LOCATION.
RX PubMed=12218089;
RA Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT protein/phosphoprotein associated with glycolipid-enriched
RT microdomains in lipid rafts in resting T cells.";
RL J. Immunol. 169:2813-2817(2002).
RN [20]
RP MASS SPECTROMETRY.
RC TISSUE=Mammary cancer;
RX MEDLINE=21829512; PubMed=11840567;
RX DOI=10.1002/1615-9861(200202)2:2<212::AID-PROT212>3.0.CO;2-H;
RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
RA Zvelebil M.J.;
RT "Cluster analysis of an extensive human breast cancer cell line
RT protein expression map database.";
RL Proteomics 2:212-223(2002).
RN [21]
RP INTERACTION WITH LIME1.
RX PubMed=14610046; DOI=10.1084/jem.20031484;
RA Brdickova N., Brdicka T., Angelisova P., Horvath O., Spicka J.,
RA Hilgert I., Paces J., Simeoni L., Kliche S., Merten C., Schraven B.,
RA Horejsi V.;
RT "LIME: a new membrane raft-associated adaptor protein involved in CD4
RT and CD8 coreceptor signaling.";

```
RL   J. Exp. Med. 198:1453-1462(2003).
RN   [22]
RP   INTERACTION WITH LIME1.

  Query Match             100.0%;  Score 41;  DB 1;  Length 508;
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Qy          1 KLLDMAAQI 9
              |||||||||
Db        339 KLLDMAAQI 347


RESULT 6
LCK_MOUSE
ID   LCK_MOUSE      STANDARD;      PRT;   508 AA.
AC   P06240; Q61794; Q61795; Q62320; Q91X65;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   25-OCT-2005, sequence version 3.
DT   07-MAR-2006, entry version 74.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase) (LSK).
GN   Name=Lck; Synonyms=Lsk-t;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86079521; PubMed=2416464; DOI=10.1016/0092-8674(85)90169-2;
RA   Marth J.D., Peet R., Krebs E.G., Perlmutter R.M.;
RT   "A lymphocyte-specific protein-tyrosine kinase gene is rearranged and
RT   overexpressed in the murine T cell lymphoma LSTRA.";
RL   Cell 43:393-404(1985).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86146842; PubMed=3081813;
RA   Voronova A.F., Sefton B.M.;
RT   "Expression of a new tyrosine protein kinase is stimulated by
RT   retrovirus promoter insertion.";
RL   Nature 319:682-685(1986).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=NOD; TISSUE=Thymus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX   MEDLINE=89096891; PubMed=2850479;
RA   Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT   "Structure of the murine lck gene and its rearrangement in a murine
RT   lymphoma cell line.";
RL   Mol. Cell. Biol. 8:3058-3064(1988).
RN   [6]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-10.
RX   MEDLINE=88142832; PubMed=3501824;
RA   Voronova A.F., Adler H.T., Sefton B.M.;
RT   "Two lck transcripts containing different 5' untranslated regions are
RT   present in T cells.";
RL   Mol. Cell. Biol. 7:4407-4413(1987).
RN   [7]
RP   MUTAGENESIS OF TYR-504.
RX   MEDLINE=88248001; PubMed=3380790;
RA   Amrein K.E., Sefton B.M.;
RT   "Avian reovirus mRNAs are nonfunctional in infected mouse cells:
RT   translational basis for virus host-range restriction.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:4257-4261(1988).
RN   [8]
RP   INTERACTIONS WITH CD4 AND CD8, AND MUTAGENESIS OF 2-CYS--CYS-4; CYS-19
RP   AND CYS-22.
RX   MEDLINE=90182665; PubMed=2107025; DOI=10.1016/0092-8674(90)90090-2;
RA   Turner J.M., Brodsky M.H., Irving B.A., Levin S.D., Perlmutter R.M.,
RA   Littman D.R.;
RT   "Interaction of the unique N-terminal region of tyrosine kinase p56lck
RT   with cytoplasmic domains of CD4 and CD8 is mediated by cysteine
RT   motifs.";
RL   Cell 60:755-765(1990).
RN   [9]
RP   MUTAGENESIS.
RX   MEDLINE=93059694; PubMed=1279202;
RA   Hurley T.R., Amrein K.E., Sefton B.M.;
RT   "Creation and characterization of temperature-sensitive mutants of the
RT   lck tyrosine protein kinase.";
```

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RL   J. Virol. 66:7406-7413(1992).
RN   [10]
RP   MUTAGENESIS OF LYS-272.
RX   MEDLINE=91163633; PubMed=1706070; DOI=10.1038/350062a0;
RA   Abraham N., Miceli M.C., Parnes J.C., Veillette A.;
RT   "Enhancement of T-cell responsiveness by the lymphocyte-specific
RT   tyrosine protein kinase p56lck.";
RL   Nature 350:62-66(1991).
RN   [11]
RP   MUTAGENESIS OF TYR-504.
RX   MEDLINE=91219495; PubMed=1708890;
RA   Abraham K.M., Levin S.D., Marth J.D., Forbush K.A., Perlmutter R.M.;
RT   "Thymic tumorigenesis induced by overexpression of p56lck.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981(1991).
RN   [12]
RP   PHOSPHORYLATION BY CSK.
RX   PubMed=8371758; DOI=10.1038/365156a0;
RA   Chow L.M., Fournel M., Davidson D., Veillette A.;
RT   "Negative regulation of T-cell receptor signalling by tyrosine protein
RT   kinase p50csk.";
RL   Nature 365:156-160(1993).
RN   [13]
RP   MUTAGENESIS.
RX   MEDLINE=93133805; PubMed=8421674;
RA   Carrera A.C., Alexandrov K., Roberts T.M.;
RT   "The conserved lysine of the catalytic domain of protein kinases is
RT   actively involved in the phosphotransfer reaction and not required for
RT   anchoring ATP.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:442-446(1993).
RN   [14]
RP   PALMITOYLATION.
RX   MEDLINE=94019312; PubMed=8413237;
RA   Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;
RT   "Palmitylation of an amino-terminal cysteine motif of protein tyrosine
RT   kinases p56lck and p59fyn mediates interaction with glycosyl-
RT   phosphatidylinositol-anchored proteins.";
RL   Mol. Cell. Biol. 13:6385-6392(1993).
RN   [15]
RP   PALMITOYLATION.
RX   MEDLINE=95071286; PubMed=7980442;
RA   Koegl M., Zlatkine P., Ley S.C., Courtneidge S.A., Magee A.I.;
RT   "Palmitoylation of multiple Src-family kinases at a homologous N-
RT   terminal motif.";
RL   Biochem. J. 303:749-753(1994).
RN   [16]
RP   INTERACTION WITH CBLB.
RX   PubMed=10646608; DOI=10.1038/35003228;
RA   Bachmaier K., Krawczyk C., Kozieradzki I., Kong Y.-Y., Sasaki T.,
RA   Oliveira-dos-Santos A., Mariathasan S., Bouchard D., Wakeham A.,
RA   Itie A., Le J., Ohashi P.S., Sarosi I., Nishina H., Lipkowitz S.,
RA   Penninger J.M.;
RT   "Negative regulation of lymphocyte activation and autoimmunity by the
RT   molecular adaptor Cbl-b.";
RL   Nature 403:211-216(2000).
RN   [17]
RP   SUBCELLULAR LOCATION.
RX   PubMed=12218089;
RA   Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA   Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT   "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT   protein/phosphoprotein associated with glycolipid-enriched
RT   microdomains in lipid rafts in resting T cells.";
RL   J. Immunol. 169:2813-2817(2002).
RN   [18]
RP   PHOSPHORYLATION SITE TYR-393, AND MASS SPECTROMETRY.
RX   PubMed=15592455; DOI=10.1038/nbt1046;
RA   Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
RA   Zha X.-M., Polakiewicz R.D., Comb M.J.;
RT   "Immunoaffinity profiling of tyrosine phosphorylation in cancer

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Db        339 KLLDMAAQI 347


RESULT 7
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ID   LCK_SAISC      STANDARD;      PRT;   508 AA.
AC   Q95KR7;
DT   08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT   08-NOV-2005, sequence version 2.
DT   07-MAR-2006, entry version 26.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], ENZYME REGULATION, AND INTERACTION WITH
RP   SAIMIRINE HERPESVIRUS 2 TIP.
RC   TISSUE=T-cell;
RX   MEDLINE=21424508; PubMed=11533187;
RX   DOI=10.1128/JVI.75.19.9252-9261.2001;
RA   Greve T., Tamgueney G., Fleischer B., Fickenscher H., Broeker B.M.;
RT   "Downregulation of p56Lck tyrosine kinase activity in T cells of
RT   squirrel monkeys (Saimiri sciureus) correlates with the non-
RT   transforming and apathogenic properties of herpesvirus saimiri in its
RT   natural host.";
RL   J. Virol. 75:9252-9261(2001).
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways. Association of the TCR with a peptide
CC       antigen-bound MHC complex facilitates the interaction of CD4 and
CC       CD8 with MHC class II and class I molecules, respectively, and
CC       thereby recruits the associated LCK to the vicinity of the TCR/CD3
CC       complex. LCK then phosphorylates tyrosines residues within the
CC       immunoreceptor tyrosines-based activation motifs (ITAMs) in the
CC       cytoplasmic tails of the TCRgamma chains and CD3 subunits,
CC       initiating the TCR/CD3 signaling pathway. In addition, contributes
CC       to signaling by other receptor molecules. Associates directly with
CC       the cytoplasmic tail of CD2, and upon engagement of the CD2
CC       molecule, LCK undergoes hyperphosphorylation and activation. Also
CC       plays a role in the IL2 receptor-linked signaling pathway that
CC       controls T-cell proliferative response. Binding of IL2 to its
CC       receptor results in increased activity of LCK. Is expressed at all
CC       stages of thymocyte development and is required for the regulation
CC       of maturation events that are governed by both pre-TCR and mature
CC       alpha beta TCR (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a prctein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- ENZYME REGULATION: Regulated by phosphatases.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also
CC       binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to
CC       other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds
CC       to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes
CC       through its SH3 domain and to the tyrosine phosphorylated form of
CC       KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.
CC       Interacts with phosphorylated LIME1. Interacts with CBLB (By
CC       similarity). Interacts with saimirine herpesvirus 2 TIP.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.
CC       Present in lipid rafts in an unactive form (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed specificaly in lymphoid cells.
CC   -!- DEVELOPMENTAL STAGE: Levels remain relatively constant throughout
CC       T-cell ontogeny.
CC   -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.
```

```
CC       Interaction is regulated by Ser-58 phosphorylation (By
CC       similarity).
CC   -!- PTM: Phosphorylated on Tyr-504 presumably by CSK. This
CC       phosphorylation downregulates catalytic activity. Phosphorylated
CC       on Tyr-393 either by itself or another kinase, leading to
CC       increased enzymatic activity.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   -!- CAUTION: LCK seems to be active in all vertebrates, except in
CC       squirrel monkey T-cells, in which it is inactivated. The reason
CC       seems to be that squirrel monkey are the natural host for
CC       Saimiriine herpesvirus 2, which is able to efficiently transform
CC       T-cells through a mecanism involving viral Tip/ host LCK
CC       interaction. Its inactivation may a mecanism that specificaly
CC       counteracts the transformation effects of viral Tip.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ277921; CAC38871.1; -; mRNA.
DR   HSSP; P06239; 1LKK.
DR   SMR; Q95KR7; 64-508.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    508       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088127.
FT   DOMAIN       60    120       SH3.
FT   DOMAIN      126    223       SH2.
FT   DOMAIN      244    497       Protein kinase.
FT   NP_BIND     250    258       ATP (By similarity).
FT   REGION        1     71       Interactions with CD4 and CD8 (By
FT                                similarity).
FT   ACT_SITE    363    363       Proton acceptor (By similarity).
FT   BINDING     272    272       ATP (By similarity).
FT   MOD_RES     393    393       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     504    504       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   508 AA;  58122 MW;  5088C64061853819 CRC64;

  Query Match           100.0%;  Score 41;  DB 1;  Length 508;
  Best Local Similarity  100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||||
Db        339 KLLDMAAQI 347


RESULT 8
Q7RTZ3_HUMAN
ID   Q7RTZ3_HUMAN   PRELIMINARY;   PRT;   509 AA.
AC   Q7RTZ3;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Protein tyrosine kinase.
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22289034; PubMed=12401726;
RA   Nervi S., Nicodeme S., Gartioux C., Atlan C., Lathrop M., Reviron D.,
RA   Naquet P., Matsuda F., Imbert J., Vialettes B.;
RT   "No association between lck gene polymorphisms and protein level in
RT   type 1 diabetes.";
RL   Diabetes 51:3326-3330(2002).
CC   -!- MISCELLANEOUS: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ third party annotation (TPA) entry.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BN000073; CAD55807.1; -; Genomic_DNA.
DR   HSSP; P06239; 1BHF.
DR   SMR; Q7RTZ3; 65-509.
DR   Ensembl; ENSG00000182866; Homo sapiens.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
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DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   509 AA;  58001 MW;  44BFF0D43FFB420D CRC64;

  Query Match            100.0%;  Score 41;  DB 2;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||||
Db        340 KLLDMAAQI 348


RESULT 9
Q95M32_9PRIM
ID   Q95M32_9PRIM   PRELIMINARY;   PRT;   509 AA.
AC   Q95M32;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Lck protein.
GN   Name=lck;
OS   Hylobates sp. (gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Hylobatidae; Hylobates.
OX   NCBI_TaxID=9581;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22031236; PubMed=12033791; DOI=10.1006/viro.2002.1381;
RA   Picard C., Greenway A., Holloway G., Olive D., Collette Y.;
RT   "Interaction with simian Hck tyrosine kinase reveals convergent
RT   evolution of the Nef protein from simian and human immunodeficiency
RT   viruses despite differential molecular surface usage.";
RL   Virology 295:320-327(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Picard C.;
RL   Thesis (2001), Department of Experimental Oncology laboratory, U.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ320182; CAC44027.1; -; mRNA.
DR   HSSP; P06239; 1LCK.
DR   SMR; Q95M32; 65-509.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   509 AA;  57947 MW;  F1BFE5C237C8DB7E CRC64;

  Query Match            100.0%;  Score 41;  DB 2;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||||
Db        340 KLLDMAAQI 348


RESULT 10
Q3ZCM0_BOVIN
ID   Q3ZCM0_BOVIN   PRELIMINARY;   PRT;   509 AA.
AC   Q3ZCM0;
DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
DT   07-MAR-2006, entry version 6.
DE   Hypothetical protein MGC126900.
GN   Name=MGC126900;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Crossbred x Angus; TISSUE=Ileum;
RA   Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA   Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA   Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA   Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA   Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA   Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC102046; AAI02047.1; -; mRNA.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
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DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   509 AA;  58116 MW;  CE0E80DCD6D0F2F8 CRC64;

  Query Match             100.0%;  Score 41;  DB 2;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||||
Db        340 KLLDMAAQI 348


RESULT 11
Q573B4_HUMAN
ID   Q573B4_HUMAN   PRELIMINARY;   PRT;   516 AA.
AC   Q573B4;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Proto-oncogene tyrosine-protein kinase LCK.
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Blood;
RX   PubMed=16107303; DOI=10.1016/j.gene.2005.06.018;
RA   Nervi S., Guinamard R., Delaval B., Lecine P., Vialettes B.,
RA   Naquet P., Imbert J.;
RT   "A rare mRNA variant of the human lymphocyte-specific protein tyrosine
RT   kinaseLCK gene with intron B retention and exon 7 skipping encodes a
RT   putativeprotein with altered SH3-dependent molecular interactions.";
RL   Gene 359:18-25(2005).
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ865079; CAI23831.1; -; mRNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   516 AA;  58333 MW;  EB9A52D4EBDF14D2 CRC64;

  Query Match             100.0%;  Score 41;  DB 2;  Length 516;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||||
Db        347 KLLDMAAQI 355


RESULT 12
Q4RR72_TETNG
ID   Q4RR72_TETNG   PRELIMINARY;   PRT;   322 AA.
AC   Q4RR72;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   Chromosome 14 SCAF15003, whole genome shotgun sequence. (Fragment).
GN   ORFNames=GSTENG00030294001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC       cycle. It is required in higher cells for entry into S-phase and
CC       mitosis. Component of the kinase complex that phosphorylates the
```

```
CC       repetitive C-terminus of RNA polymerase II. Catalytic component of
CC       MPF (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC       mature oocytes (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CAAE01015003; CAG09110.1; -; Genomic_DNA.
DR   SMR; Q4RR72; 2-322.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER      1      1
SQ   SEQUENCE   322 AA;  36768 MW;  EC0ED0B6DB1CBB2F CRC64;

  Query Match             95.1%;  Score 39;  DB 2;  Length 322;
  Best Local Similarity   88.9%;  Pred. No. 5.4;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              ||:||||||
Db        128 KLIDMAAQI 136


RESULT 13
Q2KW85_BORAV
ID   Q2KW85_BORAV   PRELIMINARY;   PRT;   263 AA.
AC   Q2KW85;
DT   07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT   07-MAR-2006, sequence version 1.
DT   07-MAR-2006, entry version 1.
DE   Dihydrodipicolinate reductase (EC 1.3.1.26).
GN   Name=dapB; ORFNames=BAV2726;
OS   Bordetella avium 197N.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Alcaligenaceae; Bordetella.
OX   NCBI_TaxID=360910;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=197N;
RA   Sebaihia M.;
RT   "The genome sequence of the poultry pathogen Bordetella avium, and
RT   genomic comparisons with related species infecting mammals.";
RL   Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AM167904; CAJ50337.1; -; Genomic_DNA.
KW   Oxidoreductase.
SQ   SEQUENCE   263 AA;  27587 MW;  2F9C77E7982E13FC CRC64;

  Query Match             90.2%;  Score 37;  DB 2;  Length 263;
  Best Local Similarity   88.9%;  Pred. No. 13;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||:|
Db        131 KLLDMAARI 139


RESULT 14
DAPB_BORBR
ID   DAPB_BORBR     STANDARD;      PRT;   269 AA.
AC   Q7WGH5;
DT   15-DEC-2003, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-2003, sequence version 1.
DT   07-MAR-2006, entry version 17.
DE   Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR).
GN   Name=dapB; OrderedLocusNames=BB3944;
OS   Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Alcaligenaceae; Bordetella.
OX   NCBI_TaxID=518;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=RB50 / ATCC BAA-588;
RX   MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA   Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA   Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA   Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA   Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA   Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA   Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA   Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA   Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA   Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA   Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT   "Comparative analysis of the genome sequences of Bordetella pertussis,
RT   Bordetella parapertussis and Bordetella bronchiseptica.";
RL   Nat. Genet. 35:32-40(2003).
CC   -!- CATALYTIC ACTIVITY: 2,3,4,5-tetrahydrodipicolinate + NAD(P)(+) =
CC       2,3-dihydrodipicolinate + NAD(P)H.
CC   -!- PATHWAY: Amino-acid biosynthesis; L-lysine biosynthesis via DAP
CC       pathway; tetrahydrodipicolinate from L-aspartate: step 4.
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC   -!- SIMILARITY: Belongs to the dihydrodipicolinate reductase family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BX640449; CAE34307.1; -; Genomic_DNA.
DR   GenomeReviews; BX470250_GR; BB3944.
DR   BioCyc; BBRO518:BB3944-MONOMER; -.
DR   HAMAP; MF_00102; -; 1.
DR   InterPro; IPR000846; DapB.
DR   InterPro; IPR011770; DapB_bac.
DR   Pfam; PF05173; DapB_C; 1.
DR   Pfam; PF01113; DapB_N; 1.
DR   PIRSF; PIRSF000161; DHPR; 1.
DR   ProDom; PD004105; DapB; 1.
DR   TIGRFAMs; TIGR00036; dapB; 1.
DR   PROSITE; PS01298; DAPB; 1.
KW   Amino-acid biosynthesis; Complete proteome;
KW   Diaminopimelate biosynthesis; Lysine biosynthesis; NADP;
KW   Oxidoreductase.
FT   CHAIN         1    269       Dihydrodipicolinate reductase.
FT                                /FTId=PRO_0000141413.
SQ   SEQUENCE   269 AA;  28329 MW;  68D79CFD3AD76ADF CRC64;

  Query Match             90.2%;  Score 37;  DB 1;  Length 269;
  Best Local Similarity   88.9%;  Pred. No. 13;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||:|
Db        137 KLLDMAARI 145
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RESULT 15
DAPB_BORPA
ID   DAPB_BORPA     STANDARD;      PRT;   269 AA.
AC   Q7W5I0;
DT   15-DEC-2003, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-2003, sequence version 1.
DT   07-MAR-2006, entry version 17.
DE   Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR).
GN   Name=dapB; OrderedLocusNames=BPP3496;
OS   Bordetella parapertussis.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Alcaligenaceae; Bordetella.
OX   NCBI_TaxID=519;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=12822 / ATCC BAA-587;
RX   MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA   Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA   Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA   Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA   Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA   Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA   Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA   Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA   Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA   Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA   Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT   "Comparative analysis of the genome sequences of Bordetella pertussis,
RT   Bordetella parapertussis and Bordetella bronchiseptica.";
RL   Nat. Genet. 35:32-40(2003).
CC   -!- CATALYTIC ACTIVITY: 2,3,4,5-tetrahydrodipicolinate + NAD(P)(+) =
CC       2,3-dihydrodipicolinate + NAD(P)H.
CC   -!- PATHWAY: Amino-acid biosynthesis; L-lysine biosynthesis via DAP
CC       pathway; tetrahydrodipicolinate from L-aspartate: step 4.
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC   -!- SIMILARITY: Belongs to the dihydrodipicolinate reductase family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BX640433; CAE38780.1; -; Genomic_DNA.
DR   GenomeReviews; BX470249_GR; BPP3496.
DR   BioCyc; BPAR519:BPP3496-MONOMER; -.
DR   HAMAP; MF_00102; -; 1.
DR   InterPro; IPR000846; DapB.
DR   InterPro; IPR011770; DapB_bac.
DR   Pfam; PF05173; DapB_C; 1.
DR   Pfam; PF01113; DapB_N; 1.
DR   PIRSF; PIRSF000161; DHPR; 1.
DR   ProDom; PD004105; DapB; 1.
DR   TIGRFAMs; TIGR00036; dapB; 1.
DR   PROSITE; PS01298; DAPB; 1.
KW   Amino-acid biosynthesis; Complete proteome;
KW   Diaminopimelate biosynthesis; Lysine biosynthesis; NADP;
KW   Oxidoreductase.
FT   CHAIN         1    269       Dihydrodipicolinate reductase.
FT                                /FTId=PRO_0000141414.
SQ   SEQUENCE   269 AA;  28329 MW;  68D79CFD3AD76ADF CRC64;

  Query Match             90.2%;  Score 37;  DB 1;  Length 269;
  Best Local Similarity   88.9%;  Pred. No. 13;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||:|
Db        137 KLLDMAARI 145


RESULT 16
DAPB_BORPE
ID   DAPB_BORPE     STANDARD;      PRT;   269 AA.
AC   Q9X6Y9;
DT   30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1999, sequence version 1.
DT   07-MAR-2006, entry version 37.
DE   Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR).
GN   Name=dapB; OrderedLocusNames=BP2509;
OS   Bordetella pertussis.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Alcaligenaceae; Bordetella.
OX   NCBI_TaxID=520;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC   STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RA   Pradel E.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX   MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA   Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA   Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA   Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA   Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA   Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA   Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA   Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA   Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA   Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA   Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT   "Comparative analysis of the genome sequences of Bordetella pertussis,
RT   Bordetella parapertussis and Bordetella bronchiseptica.";
RL   Nat. Genet. 35:32-40(2003).
CC   -!- CATALYTIC ACTIVITY: 2,3,4,5-tetrahydrodipicolinate + NAD(P)(+) =
CC       2,3-dihydrodipicolinate + NAD(P)H.
CC   -!- PATHWAY: Amino-acid biosynthesis; L-lysine biosynthesis via DAP
CC       pathway; tetrahydrodipicolinate from L-aspartate: step 4.
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC   -!- SIMILARITY: Belongs to the dihydrodipicolinate reductase family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ238308; CAB41012.1; -; Genomic_DNA.
DR   EMBL; BX640418; CAE42781.1; -; Genomic_DNA.
DR   HSSP; P04036; 1DRW.
DR   GenomeReviews; BX470248_GR; BP2509.
DR   BioCyc; BPER520:BP2509-MONOMER; -.
DR   HAMAP; MF_00102; -; 1.
DR   InterPro; IPR000846; DapB.
DR   InterPro; IPR011770; DapB_bac.
DR   Pfam; PF05173; DapB_C; 1.
DR   Pfam; PF01113; DapB_N; 1.
DR   PIRSF; PIRSF000161; DHPR; 1.
DR   ProDom; PD004105; DapB; 1.
DR   TIGRFAMs; TIGR00036; dapB; 1.
DR   PROSITE; PS01298; DAPB; 1.
KW   Amino-acid biosynthesis; Complete proteome;
KW   Diaminopimelate biosynthesis; Lysine biosynthesis; NADP;
KW   Oxidoreductase.
FT   CHAIN         1    269       Dihydrodipicolinate reductase.
FT                                /FTId=PRO_0000141415.
SQ   SEQUENCE   269 AA;  28328 MW;  68DF3E7158BDAA31 CRC64;

  Query Match             90.2%;  Score 37;  DB 1;  Length 269;
  Best Local Similarity   88.9%;  Pred. No. 13;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||:|
Db        137 KLLDMAARI 145


RESULT 17
DAPB_CHRVO
ID   DAPB_CHRVO     STANDARD;      PRT;   267 AA.
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AC   Q7NX34;
DT   15-DEC-2003, integrated into UniProtKB/Swiss-Prot.
DT   15-DEC-2003, sequence version 1.
DT   07-MAR-2006, entry version 17.
DE   Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR).
GN   Name=dapB; OrderedLocusNames=CV1795;
OS   Chromobacterium violaceum.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC   Neisseriaceae; Chromobacterium.
OX   NCBI_TaxID=536;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=ATCC 12472 / DSM 30191;
RX   MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA   Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA   Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA   Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA   Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA   Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA   Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA   Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA   Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA   Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA   Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA   Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA   Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA   Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA   Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA   Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA   di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
RA   Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA   Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA   Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA   Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA   Santos E.B.P., Santos F.R., Schneider M.P.C., Seuanez H.N.,
RA   Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA   Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA   Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA   Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
RT   "The complete genome sequence of Chromobacterium violaceum reveals
RT   remarkable and exploitable bacterial adaptability.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
CC   -!- CATALYTIC ACTIVITY: 2,3,4,5-tetrahydrodipicolinate + NAD(P)(+) =
CC       2,3-dihydrodipicolinate + NAD(P)H.
CC   -!- PATHWAY: Amino-acid biosynthesis; L-lysine biosynthesis via DAP
CC       pathway; tetrahydrodipicolinate from L-aspartate: step 4.
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC   -!- SIMILARITY: Belongs to the dihydrodipicolinate reductase family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AE016825; AAQ59469.1; -; Genomic_DNA.
DR   GenomeReviews; AE016825_GR; CV1795.
DR   BioCyc; CVIO243365:CV1795-MONOMER; -.
DR   HAMAP; MF_00102; -; 1.
DR   InterPro; IPR000846; DapB.
DR   InterPro; IPR011770; DapB_bac.
DR   Pfam; PF05173; DapB_C; 1.
DR   Pfam; PF01113; DapB_N; 1.
DR   PIRSF; PIRSF000161; DHPR; 1.
DR   ProDom; PD004105; DapB; 1.
DR   TIGRFAMs; TIGR00036; dapB; 1.
DR   PROSITE; PS01298; DAPB; 1.
KW   Amino-acid biosynthesis; Complete proteome;
KW   Diaminopimelate biosynthesis; Lysine biosynthesis; NADP;
KW   Oxidoreductase.
FT   CHAIN         1    267       Dihydrodipicolinate reductase.
FT                                /FTId=PRO_0000141430.
SQ   SEQUENCE   267 AA;  28178 MW;  AB3EA3EFAE3E27ED CRC64;

  Query Match             87.8%;  Score 36;  DB 1;  Length 267;
  Best Local Similarity   77.8%;  Pred. No. 22;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||::
Db        134 KLLDMAARV 142


RESULT 18
DAPB_PSEPK
ID   DAPB_PSEPK     STANDARD;      PRT;   267 AA.
AC   Q88DU4;
DT   24-OCT-2003, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-2003, sequence version 1.
DT   07-MAR-2006, entry version 20.
DE   Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR).
GN   Name=dapB; OrderedLocusNames=PP4725;
OS   Pseudomonas putida (strain KT2440).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=160488;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=22423060; PubMed=12534463;
RX   DOI=10.1046/j.1462-2920.2002.00366.x;
RA   Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA   Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA   Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA   Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA   Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA   Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA   Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA   Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA   Fraser C.M.;
RT   "Complete genome sequence and comparative analysis of the
RT   metabolically versatile Pseudomonas putida KT2440.";
RL   Environ. Microbiol. 4:799-808(2002).
CC   -!- CATALYTIC ACTIVITY: 2,3,4,5-tetrahydrodipicolinate + NAD(P)(+) =
CC       2,3-dihydrodipicolinate + NAD(P)H.
CC   -!- PATHWAY: Amino-acid biosynthesis; L-lysine biosynthesis via DAP
CC       pathway; tetrahydrodipicolinate from L-aspartate: step 4.
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC   -!- SIMILARITY: Belongs to the dihydrodipicolinate reductase family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE015451; AAN70297.1; -; Genomic_DNA.
DR   HSSP; P04036; 1DRW.
DR   GenomeReviews; AE015451_GR; PP4725.
DR   TIGR; PP4725; -.
DR   HAMAP; MF_00102; -; 1.
DR   InterPro; IPR000846; DapB.
DR   InterPro; IPR011770; DapB_bac.
DR   Pfam; PF05173; DapB_C; 1.
DR   Pfam; PF01113; DapB_N; 1.
DR   PIRSF; PIRSF000161; DHPR; 1.
DR   ProDom; PD004105; DapB; 1.
DR   TIGRFAMs; TIGR00036; dapB; 1.
DR   PROSITE; PS01298; DAPB; 1.
KW   Amino-acid biosynthesis; Complete proteome;
KW   Diaminopimelate biosynthesis; Lysine biosynthesis; NADP;
KW   Oxidoreductase.
FT   CHAIN         1    267       Dihydrodipicolinate reductase.
FT                                /FTId=PRO_0000141470.
SQ   SEQUENCE   267 AA;  28424 MW;  2F5BB5545D754C7A CRC64;

  Query Match             87.8%;  Score 36;  DB 1;  Length 267;
  Best Local Similarity   77.8%;  Pred. No. 22;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||::
Db        134 KLLDMAARV 142
```

```
RESULT 19
Q2XEZ8_PSEPU
ID   Q2XEZ8_PSEPU   PRELIMINARY;   PRT;   267 AA.
AC   Q2XEZ8;
DT   10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT   10-JAN-2006, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Dihydrodipicolinate reductase, bacterial.
GN   ORFNames=PputDRAFT_2379;
OS   Pseudomonas putida F1.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=351746;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=F1;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome and assembly of Pseudomonas putida
RT   F1.";
RL   Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=F1;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Pseudomonas putida F1.";
RL   Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AALM01000017; EAP50349.1; -; Genomic_DNA.
SQ   SEQUENCE   267 AA;  28414 MW;  DF5BE5CD79E70417 CRC64;

  Query Match             87.8%;  Score 36;  DB 2;  Length 267;
  Best Local Similarity   77.8%;  Pred. No. 22;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||::
Db        134 KLLDMAARV 142


RESULT 20
Q3KI98_PSEPF
ID   Q3KI98_PSEPF   PRELIMINARY;   PRT;   268 AA.
AC   Q3KI98;
DT   08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT   08-NOV-2005, sequence version 1.
DT   21-FEB-2006, entry version 4.
DE   Dihydrodipicolinate reductase.
GN   OrderedLocusNames=Pfl_0765;
OS   Pseudomonas fluorescens (strain Pf0-1).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=205922;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG   US DOE Joint Genome Institute;
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Saunders E.H., Schmutz J.,
RA   Larimer F., Land M., Kyripides N., Anderson I., Richardson P.;
RT   "Complete sequence of Pseudomonas fluorescens Pf0-1.";
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; CP000094; ABA72508.1; -; Genomic_DNA.
DR   GO; GO:0005737; C:cytoplasm; IEA.
DR   GO; GO:0008839; F:dihydrodipicolinate reductase activity; IEA.
DR   GO; GO:0009089; P:lysine biosynthesis via diaminopimelate; IEA.
DR   InterPro; IPR000846; DapB.
DR   InterPro; IPR011770; DapB_bac.
DR   Pfam; PF05173; DapB_C; 1.
DR   Pfam; PF01113; DapB_N; 1.
DR   PIRSF; PIRSF000161; DHPR; 1.
DR   ProDom; PD004105; DapB; 1.
DR   TIGRFAMs; TIGR00036; dapB; 1.
DR   PROSITE; PS01298; DAPB; 1.
KW   Complete proteome.
SQ   SEQUENCE   268 AA;  28499 MW;  B6D702E0339A7AD1 CRC64;

  Query Match             87.8%;  Score 36;  DB 2;  Length 268;
  Best Local Similarity   77.8%;  Pred. No. 22;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||::
Db        135 KLLDMAARV 143


RESULT 21
Q4KIG9_PSEF5
ID   Q4KIG9_PSEF5   PRELIMINARY;   PRT;   268 AA.
AC   Q4KIG9;
DT   02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   02-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Dihydrodipicolinate reductase (EC 1.3.1.26).
GN   Name=dapB; OrderedLocusNames=PFL_0829;
OS   Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=220664;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15980861; DOI=10.1038/nbt1110;
RA   Paulsen I.T., Press C.M., Ravel J., Kobayashi D.Y., Myers G.S.A.,
RA   Mavrodi D.V., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA   Durkin A.S., Brinkac L.M., Daugherty S.C., Sullivan S.A.,
RA   Rosovitz M.J., Gwinn M.L., Zhou L., Schneider D.J., Cartinhour S.W.,
RA   Nelson W.C., Weidman J., Watkins K., Tran K., Khouri H., Pierson E.A.,
RA   Pierson L.S. III, Thomashow L.S., Loper J.E.;
RT   "Complete genome sequence of the plant commensal Pseudomonas
RT   fluorescens Pf-5.";
RL   Nat. Biotechnol. 23:873-878(2005).
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CC   ---------------------------------------------------------------------
DR   EMBL; CP000076; AAY96229.1; -; Genomic_DNA.
DR   GO; GO:0005737; C:cytoplasm; IEA.
DR   GO; GO:0008839; F:dihydrodipicolinate reductase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0009089; P:lysine biosynthesis via diaminopimelate; IEA.
DR   InterPro; IPR000846; DapB.
DR   InterPro; IPR011770; DapB_bac.
DR   Pfam; PF05173; DapB_C; 1.
DR   Pfam; PF01113; DapB_N; 1.
DR   PIRSF; PIRSF000161; DHPR; 1.
DR   ProDom; PD004105; DapB; 1.
DR   TIGRFAMs; TIGR00036; dapB; 1.
DR   PROSITE; PS01298; DAPB; 1.
KW   Complete proteome; Oxidoreductase.
SQ   SEQUENCE   268 AA;  28486 MW;  F971DCD451A4366D CRC64;

  Query Match             87.8%;  Score 36;  DB 2;  Length 268;
  Best Local Similarity   77.8%;  Pred. No. 22;
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  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              |||||||::
Db        135 KLLDMAARV 143


RESULT 22
Q5L9P3_BACFN
ID   Q5L9P3_BACFN   PRELIMINARY;   PRT;   434 AA.
AC   Q5L9P3;
DT   21-JUN-2005, integrated into UniProtKB/TrEMBL.
DT   21-JUN-2005, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   Putative peptidoglycan biosynthesis related protein.
GN   OrderedLocusNames=BF3495;
OS   Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
OC   Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC   Bacteroidaceae; Bacteroides.
OX   NCBI_TaxID=272559;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15746427; DOI=10.1126/science.1107008;
RA   Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
RA   Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Quail M.A.,
RA   Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
RA   Line A., Lord A., Norbertczak H., Ormond D., Price C.,
RA   Rabbinowitsch E., Woodward J., Barrell B.G., Parkhill J.;
RT   "Extensive DNA inversions in the B. fragilis genome control variable
RT   gene expression.";
RL   Science 307:1463-1465(2005).
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CC   ---------------------------------------------------------------------
DR   EMBL; CR626927; CAH09184.1; -; Genomic_DNA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0019277; P:UDP-N-acetylgalactosamine biosynthesis; IEA.
DR   InterPro; IPR005750; AcGlu_Tran_MurA.
DR   InterPro; IPR001986; EPSP_synth.
DR   Pfam; PF00275; EPSP_synthase; 1.
DR   ProDom; PD001867; EPSP_synth; 1.
DR   TIGRFAMs; TIGR01072; murA; 1.
KW   Complete proteome.
SQ   SEQUENCE   434 AA;  47298 MW;  432E1CF649E68096 CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 434;
  Best Local Similarity   77.8%;  Pred. No. 62;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              ||:|| |||
Db        351 KLIDMGAQI 359


RESULT 23
Q64PY6_BACFR
ID   Q64PY6_BACFR   PRELIMINARY;   PRT;   434 AA.
AC   Q64PY6;
DT   25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT   25-OCT-2004, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   UDP-N-acetylglucosamine 1-carboxyvinyltransferase.
GN   OrderedLocusNames=BF3702;
OS   Bacteroides fragilis.
OC   Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC   Bacteroidaceae; Bacteroides.
OX   NCBI_TaxID=817;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=YCH46;
RX   PubMed=15466707; DOI=10.1073/pnas.0404172101;
RA   Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA   Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RT   "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT   inversions regulating cell surface adaptation.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924(2004).
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CC   ---------------------------------------------------------------------
DR   EMBL; AP006841; BAD50445.1; -; Genomic_DNA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0019277; P:UDP-N-acetylgalactosamine biosynthesis; IEA.
DR   InterPro; IPR005750; AcGlu_Tran_MurA.
DR   InterPro; IPR001986; EPSP_synth.
DR   Pfam; PF00275; EPSP_synthase; 1.
DR   ProDom; PD001867; EPSP_synth; 1.
DR   TIGRFAMs; TIGR01072; murA; 1.
KW   Complete proteome; Transferase.
SQ   SEQUENCE   434 AA;  47298 MW;  432E1CF649E68096 CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 434;
  Best Local Similarity   77.8%;  Pred. No. 62;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              ||:|| |||
Db        351 KLIDMGAQI 359


RESULT 24
Q7MUW1_PORGI
ID   Q7MUW1_PORGI   PRELIMINARY;   PRT;   434 AA.
AC   Q7MUW1;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   UDP-N-acetylglucosamine 1-carboxyvinyltransferase.
GN   Name=murA; OrderedLocusNames=PG1366; ORFNames=PG_1366;
OS   Porphyromonas gingivalis (Bacteroides gingivalis).
OC   Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC   Porphyromonadaceae; Porphyromonas.
OX   NCBI_TaxID=837;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=W83;
RX   MEDLINE=22829867; PubMed=12949112;
RX   DOI=10.1128/JB.185.18.5591-5601.2003;
RA   Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA   Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA   Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA   Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA   Dewhirst F.E., Fraser C.M.;
RT   "Complete genome sequence of the oral pathogenic bacterium
RT   Porphyromonas gingivalis strain W83.";
RL   J. Bacteriol. 185:5591-5601(2003).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE015924; AAQ66430.1; -; Genomic_DNA.
DR   HSSP; P33038; 1DLG.
DR   TIGR; PG1366; -.
DR   BioCyc; PGIN242619:PG1366-MONOMER; -.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0019277; P:UDP-N-acetylgalactosamine biosynthesis; IEA.
DR   InterPro; IPR005750; AcGlu_Tran_MurA.
DR   InterPro; IPR001986; EPSP_synth.
DR   Pfam; PF00275; EPSP_synthase; 1.
DR   ProDom; PD001867; EPSP_synth; 1.
DR   TIGRFAMs; TIGR01072; murA; 1.
KW   Complete proteome; Transferase.
SQ   SEQUENCE   434 AA;  47248 MW;  1C31097B40DD1D8B CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 434;
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  Best Local Similarity   77.8%;  Pred. No. 62;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              ||:|| |||
Db        351 KLIDMGAQI 359


RESULT 25
Q8A681_BACTN
ID   Q8A681_BACTN   PRELIMINARY;   PRT;   434 AA.
AC   Q8A681;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   UDP-N-acetylglucosamine 1-carboxyvinyltransferase.
GN   OrderedLocusNames=BT2005; ORFNames=BT_2005;
OS   Bacteroides thetaiotaomicron.
OC   Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC   Bacteroidaceae; Bacteroides.
OX   NCBI_TaxID=818;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=VPI-5482 / ATCC 29148;
RX   MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA   Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA   Chiang H.C., Hooper L.V., Gordon J.I.;
RT   "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL   Science 299:2074-2076(2003).
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CC   ---------------------------------------------------------------------
DR   EMBL; AE015928; AAO77112.1; -; Genomic_DNA.
DR   HSSP; P33038; 1EJD.
DR   BioCyc; BTHE226186:BT2005-MONOMER; -.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0019277; P:UDP-N-acetylgalactosamine biosynthesis; IEA.
DR   InterPro; IPR005750; AcGlu_Tran_MurA.
DR   InterPro; IPR001986; EPSP_synth.
DR   Pfam; PF00275; EPSP_synthase; 1.
DR   ProDom; PD001867; EPSP_synth; 1.
DR   TIGRFAMs; TIGR01072; murA; 1.
KW   Complete proteome; Transferase.
SQ   SEQUENCE   434 AA;  47416 MW;  86A3AE33AFD946AA CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 434;
  Best Local Similarity   77.8%;  Pred. No. 62;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              ||:|| |||
Db        351 KLIDMGAQI 359


RESULT 26
Q5TYU7_BRARE
ID   Q5TYU7_BRARE   PRELIMINARY;   PRT;   485 AA.
AC   Q5TYU7;
DT   07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   07-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   Novel protein tyrosine kinase.
GN   Name=si:dkey-33i22.2; Synonyms=OTTDARP00000004623;
GN   ORFNames=DKEY-33I22.2-001;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Dunn M.;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; BX842684; CAH69080.1; -; Genomic_DNA.
DR   SMR; Q5TYU7; 42-485.
DR   Ensembl; ENSDARG00000007783; Danio rerio.
DR   ZFIN; ZDB-GENE-040724-106; si:dkey-33i22.2.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   485 AA;  55644 MW;  3ED1878453666747 CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 485;
  Best Local Similarity   77.8%;  Pred. No. 70;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              ||:|| |||
Db        317 KLIDMTAQI 325


RESULT 27
Q7PPB4_ANOGA
ID   Q7PPB4_ANOGA   PRELIMINARY;   PRT;   508 AA.
AC   Q7PPB4;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   ENSANGP00000005994.
GN   ORFNames=ENSANGG00000004562;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Anophelinae; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RT   "Anopheles gambiae re-annotation.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
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CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
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CC   ---------------------------------------------------------------------
DR   EMBL; AAAB01008960; EAA10750.2; -; Genomic_DNA.
DR   HSSP; P06241; 1A0N.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   508 AA;  57965 MW;  DC6B6B65201B12F8 CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 508;
  Best Local Similarity   77.8%;  Pred. No. 74;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||||||
Db        337 QLIDMAAQI 345


RESULT 28
Q3MYH2_9DELT
ID   Q3MYH2_9DELT   PRELIMINARY;   PRT;   183 AA.
AC   Q3MYH2;
DT   25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   25-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Similar to transcriptional regulator.
GN   ORFNames=SfumDRAFT_0309;
OS   Syntrophobacter fumaroxidans MPOB.
OC   Bacteria; Proteobacteria; Deltaproteobacteria; Syntrophobacterales;
OC   Syntrophobacteraceae; Syntrophobacter.
OX   NCBI_TaxID=335543;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=MPOB;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome and assembly of Syntrophobacter
RT   fumaroxidans MPOB.";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=MPOB;
RG   US DOE Joint Genome Institute (JGI_ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Syntrophobacter
RT   fumaroxidans MPOB.";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AAJF01000042; EAO20012.1; -; Genomic_DNA.
SQ   SEQUENCE   183 AA;  20001 MW;  1065FDF64EE9B32D CRC64;

  Query Match             82.9%;  Score 34;  DB 2;  Length 183;
  Best Local Similarity   77.8%;  Pred. No. 42;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              ||||:||:|
Db          4 KLLDIAAEI 12


RESULT 29
Q5U175_DROME
ID   Q5U175_DROME   PRELIMINARY;   PRT;   235 AA.
AC   Q5U175;
DT   07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   07-DEC-2004, sequence version 1.
DT   21-FEB-2006, entry version 13.
DE   RE19378p.
GN   Name=Src42A;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Berkeley;
RA   Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA   Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
RL   Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC       protein (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BT016017; AAV36902.1; -; mRNA.
DR   FlyBase; FBgn0004603; Src42A.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   ATP-binding; Developmental protein; Kinase; Membrane;
KW   Nucleotide-binding; Receptor; Transferase; Transmembrane;
KW   Tyrosine-protein kinase.
SQ   SEQUENCE   235 AA;  27038 MW;  8B9F65DB2EE15B9A CRC64;

  Query Match             82.9%;  Score 34;  DB 2;  Length 235;
  Best Local Similarity   87.5%;  Pred. No. 55;
```

```
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LLDMAAQI 9
              |:||||||
Db         65 LIDMAAQI 72


RESULT 30
Q9PVU9_LAMRE
ID   Q9PVU9_LAMRE   PRELIMINARY;   PRT;   245 AA.
AC   Q9PVU9;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 28.
DE   Src-like B (Fragment).
OS   Lampetra reissneri (Far Eastern brook lamprey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC   Petromyzontiformes; Petromyzontidae; Lethenteron.
OX   NCBI_TaxID=7753;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20020330; PubMed=10552041;
RA   Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
RT   "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey:
RT   isoform duplications around the divergence of cyclostomes and
RT   gnathostomes.";
RL   J. Mol. Evol. 49:601-608(1999).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB025550; BAA84740.1; -; mRNA.
DR   HSSP; P12931; 1FMK.
DR   SMR; Q9PVU9; 1-245.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Tyrosine-protein kinase.
FT   NON_TER       1       1
SQ   SEQUENCE   245 AA;  28028 MW;  E73B5C2B64AA0FD5 CRC64;

  Query Match             82.9%;  Score 34;  DB 2;  Length 245;
  Best Local Similarity   77.8%;  Pred. No. 57;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLLDMAAQI 9
              :|:||||||
Db         74 QLVDMAAQI 82


Search completed: June 29, 2006, 09:29:39
Job time : 107.942 secs
```

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:14 ; Search time 87.8313 Seconds
(without alignments)
46.851 Million cell updates/sec

Title: US-10-062-257A-15
Perfect score: 43
Sequence: 1 QIAEGMAFI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	100.0	9	4	AAB73131	Aab73131 Tumour an
2	43	100.0	85	4	ABG22262	Abg22262 Novel hum
3	43	100.0	250	9	ADY52570	Ady52570 Human onc
4	43	100.0	259	2	AAY43957	Aay43957 Human pro
5	43	100.0	259	2	AAY43956	Aay43956 Mouse pro
6	43	100.0	259	2	AAY43955	Aay43955 Human pro
7	43	100.0	263	8	ADR88385	Adr88385 LCK tyros
8	43	100.0	265	7	ABR56203	Abr56203 Mutant Ly
9	43	100.0	271	7	ABR56204	Abr56204 Mutant Ly
10	43	100.0	271	8	ADR88384	Adr88384 HCK tyros
11	43	100.0	272	5	ABB81188	Abb81188 Human KIT
12	43	100.0	279	9	ADY85449	Ady85449 Catalytic
13	43	100.0	300	9	ADY85468	Ady85468 Catalytic
14	43	100.0	316	9	ADY85448	Ady85448 Catalytic
15	43	100.0	346	3	AAY76750	Aay76750 Human pro
16	43	100.0	346	4	AAE06208	Aae06208 Human pro
17	43	100.0	346	5	ABB84435	Abb84435 Human pro
18	43	100.0	355	8	ABM82980	Abm82980 Human dia
19	43	100.0	383	7	ADJ68978	Adj68978 Human hea
20	43	100.0	417	2	AAR14201	Aar14201 (Beta-gal
21	43	100.0	436	8	ADN61468	Adn61468 Human KPP
22	43	100.0	437	5	ABG79672	Abg79672 Tumour in
23	43	100.0	438	9	ADY52642	Ady52642 Human tra
24	43	100.0	458	7	ADC99048	Adc99048 Human KPP
25	43	100.0	458	8	ADJ71657	Adj71657 Human NOV
26	43	100.0	465	9	ADY52641	Ady52641 Human tra
27	43	100.0	471	9	ADY52640	Ady52640 Human tra
28	43	100.0	504	9	AEE05159	Aee05159 Cancer-as
29	43	100.0	505	4	AAB99332	Aab99332 Human tyr
30	43	100.0	505	7	ABW01407	Abw01407 Human hae
31	43	100.0	505	7	ADL71039	Adl71039 Type II c
32	43	100.0	505	8	ADI04092	Adi04092 Human HCK
33	43	100.0	505	8	ADJ71659	Adj71659 Human NOV
34	43	100.0	505	8	ADL22905	Adl22905 Human MP2
35	43	100.0	505	8	ADP12982	Adp12982 Protein e
36	43	100.0	505	8	ADQ88186	Adq88186 Human 146
37	43	100.0	505	8	ADR14261	Adr14261 Human NF-
38	43	100.0	505	9	ADY52575	Ady52575 Human onc
39	43	100.0	505	9	ADZ70757	Adz70757 Hemopoiet
40	43	100.0	505	9	AEE05161	Aee05161 Cancer-as
41	43	100.0	505	9	AEE05163	Aee05163 Cancer-as
42	43	100.0	508	3	AAB37700	Aab37700 Human lym
43	43	100.0	508	7	ADE58802	Ade58802 Human Pro
44	43	100.0	508	7	ADE58799	Ade58799 Human Pro
45	43	100.0	508	7	ADF45072	Adf45072 Human kin
46	43	100.0	508	7	ADL34479	Adl34479 Human lym
47	43	100.0	508	8	ADS88148	Ads88148 Human pro
48	43	100.0	509	3	AAY49420	Aay49420 PKA subst
49	43	100.0	509	6	ABR58699	Abr58699 Human can
50	43	100.0	509	7	ABR56202	Abr56202 Human Lym
51	43	100.0	509	7	ADE40449	Ade40449 Human pro
52	43	100.0	509	8	ADL22907	Adl22907 Human MP2
53	43	100.0	509	8	ADP12458	Adp12458 Protein e
54	43	100.0	509	8	ADP48374	Adp48374 Human lym
55	43	100.0	509	9	ADZ51107	Adz51107 Amino aci
56	43	100.0	509	9	AEA35921	Aea35921 Human Lck
57	43	100.0	525	9	AEA35919	Aea35919 Human Hck
58	43	100.0	526	7	ADF45062	Adf45062 Human kin
59	43	100.0	539	8	ABM82981	Abm82981 Human dia
60	43	100.0	539	8	ABM82982	Abm82982 Human dia
61	43	100.0	551	4	ABG22264	Abg22264 Novel hum
62	43	100.0	563	9	ADY52639	Ady52639 Human tra
63	43	100.0	567	5	ABG79673	Abg79673 Tumour in
64	43	100.0	610	9	ADY52638	Ady52638 Human tra
65	43	100.0	618	9	ADY52637	Ady52637 Human tra
66	40	93.0	251	9	ADY52569	Ady52569 Human onc
67	40	93.0	260	2	AAY43954	Aay43954 Human pro
68	40	93:0	439	9	ADY52636	Ady52636 Human tra
69	40	93.0	440	9	ADY52635	Ady52635 Human tra
70	40	93.0	444	9	ADY52634	Ady52634 Human tra
71	40	93.0	447	9	ADY52633	Ady52633 Human tra
72	40	93.0	452	9	ADY52632	Ady52632 Human tra
73	40	93.0	454	8	ADH48367	Adh48367 Human KPP
74	40	93.0	459	9	ADY52631	Ady52631 Human tra
75	40	93.0	467	9	ADY52630	Ady52630 Human tra
76	40	93.0	472	9	ADY52629	Ady52629 Human tra
77	40	93.0	473	9	ADY52628	Ady52628 Human tra
78	40	93.0	481	9	ADY52627	Ady52627 Human tra
79	40	93.0	483	9	ADY52626	Ady52626 Human tra
80	40	93.0	493	9	ADY52625	Ady52625 Human tra
81	40	93.0	503	7	ADL71037	Adl71037 Type II c
82	40	93.0	503	8	ADS85093	Ads85093 Mouse ato
83	40	93.0	503	9	ADZ70731	Adz70731 Hemopoiet
84	40	93.0	503	9	AEE05156	Aee05156 Cancer-as
85	40	93.0	504	7	ADF45035	Adf45035 Human kin
86	40	93.0	505	8	ADK70442	Adk70442 Respirato
87	40	93.0	505	8	ADL22909	Adl22909 Human MP2
88	40	93.0	505	8	ADQ97517	Adq97517 Human can
89	40	93.0	505	9	AEA35922	Aea35922 Human Blk
90	40	93.0	511	7	ADF45073	Adf45073 Human kin
91	40	93.0	512	7	ADD19014	Add19014 Human dis
92	40	93.0	512	7	ADN95430	Adn95430 Human BEC
93	40	93.0	512	8	ADL22908	Adl22908 Human MP2
94	40	93.0	512	8	ADN04498	Adn04498 Antipsori
95	40	93.0	512	8	ADP12483	Adp12483 Protein e
96	40	93.0	512	8	ADR14269	Adr14269 Human NF-

97	40	93.0	512	8	ADS88430	Ads88430 Human pro
98	40	93.0	512	8	ADP23372	Adp23372 PRO polyp
99	40	93.0	512	9	ADY16487	Ady16487 PRO polyp
100	40	93.0	512	9	ADY19685	Ady19685 PRO polyp

ALIGNMENTS

RESULT 1
AAB73131
ID AAB73131 standard; peptide; 9 AA.
XX
AC AAB73131;
XX
DT 09-MAY-2001 (first entry)
XX
DE Tumour antigen peptide #15.
XX
KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS Homo sapiens.
XX
PN WO200111044-A1.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-JP005220.
XX
PR 05-AUG-1999; 99JP-00222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT polynucleotides encoding them for treatment of cancer.
XX
PS Claim 1; Page 70; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 43; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 1 QIAEGMAFI 9

RESULT 2
ABG22262
ID ABG22262 standard; protein; 85 AA.
XX
AC ABG22262;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22253.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS86449.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 52621; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 85 AA;

Query Match 100.0%; Score 43; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 5 QIAEGMAFI 13

RESULT 3
ADY52570
ID ADY52570 standard; protein; 250 AA.
XX
AC ADY52570;
XX
DT 19-MAY-2005 (first entry)
XX
DE Human oncogene screening method-related HCK kinase domain protein.
XX
KW oncogene; cancer; cytostatic; neoplasm; hck tyrosine kinase; enzyme.
XX
OS Homo sapiens.
XX
PN JP2005052018-A.
XX
PD 03-MAR-2005.

XX
PF 07-AUG-2003; 2003JP-00206534.
XX
PR 07-AUG-2003; 2003JP-00206534.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
DR WPI; 2005-187380/20.
XX
PT Screening oncogene, by producing cDNA library having fusion DNA
PT comprising cDNA encoding PNT region of TEL connected to downstream of
PT promoter, introducing library into host cell, expressing fusion DNA and
PT selecting transformed cells.
XX
PS Claim 5; SEQ ID NO 2; 216pp; Japanese.
XX
CC The invention relates to a novel method for screening an oncogene. The
CC method comprises producing a cDNA library for a fusion DNA, comprising a
CC cDNA encoding the PNT region of TEL connected downstream of a vector
CC promoter, introducing the produced cDNA library into a host cell,
CC expressing the fusion DNA, selecting the transformed cells and analyzing
CC the base sequence of the fusion DNA in the transformed cell, and thus
CC identifying the fusion DNA as an oncogene. TEL is a transcription factor
CC which belongs to the Ets family and is known to form various genes and
CC fusion genes via a chromosomal translocation in cancer cells, such as
CC occurs in some cases of leukemia. The method of the invention may be
CC useful for screening a substance which suppresses the proliferative
CC property of a cancer cell, screening a substance which inhibits the
CC activity of a kinase gene introduced into the cell and screening a
CC substance for the treatment of cancer. The current sequence is that of
CC the human HCK kinase domain protein of the invention.
XX
SQ Sequence 250 AA;

Query Match 100.0%; Score 43; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 103 QIAEGMAFI 111

RESULT 4
AAY43957
ID AAY43957 standard; protein; 259 AA.
XX
AC AAY43957;
XX
DT 21-DEC-1999 (first entry)
XX
DE Human protein kinase #16.
XX
KW Prediction; secondary structure; alignment; evolutionary conservation;
KW homology; periodicity; co-variation analysis; antigenic site;
KW site directed mutagenesis; interaction.
XX
OS Homo sapiens.
XX
PN US5958784-A.
XX
PD 28-SEP-1999.
XX
PF 25-MAR-1992; 92US-00857224.
XX
PR 25-MAR-1992; 92US-00857224.
XX
PA (BENN/) BENNER S A.
XX
PI Benner SA;
XX
DR WPI; 1999-570766/48.
XX
PT Predicting the folded structure of proteins.
XX
PS Disclosure; Col 257-260; 113pp; English.
XX
CC Sequences AAY43902-Y44015 represent proteins used in a novel method of
CC predicting the folded structure of proteins, by aligning sequences of
CC homologous proteins and using patterns of evolutionarily conserved and
CC varied sequences to assign positions. Positions in the alignment are
CC assigned to the surface or inside of the folded structure, active sites,
CC and parsing segments. Secondary structural units are assigned by
CC identifying periodicity in the assignments, and assembled into globular
CC form using distance constraints imposed by disulfide bridges, active site
CC assignments and co-variation analysis. The predicted secondary structures
CC are useful for identifying antigenic sites on a protein molecule, as
CC guides for site directed mutagenesis studies, and for understanding the
CC interaction of a protein with other molecules
XX
SQ Sequence 259 AA;

Query Match 100.0%; Score 43; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 105 QIAEGMAFI 113

RESULT 5
AAY43956
ID AAY43956 standard; protein; 259 AA.
XX
AC AAY43956;
XX
DT 21-DEC-1999 (first entry)
XX
DE Mouse protein kinase #6.
XX
KW Prediction; secondary structure; alignment; evolutionary conservation;
KW homology; periodicity; co-variation analysis; antigenic site;
KW site directed mutagenesis; interaction.
XX
OS Mus sp.
XX
PN US5958784-A.
XX
PD 28-SEP-1999.
XX
PF 25-MAR-1992; 92US-00857224.
XX
PR 25-MAR-1992; 92US-00857224.
XX
PA (BENN/) BENNER S A.
XX
PI Benner SA;
XX
DR WPI; 1999-570766/48.
XX
PT Predicting the folded structure of proteins.
XX
PS Disclosure; Col 255-258; 113pp; English.
XX
CC Sequences AAY43902-Y44015 represent proteins used in a novel method of
CC predicting the folded structure of proteins, by aligning sequences of
CC homologous proteins and using patterns of evolutionarily conserved and
CC varied sequences to assign positions. Positions in the alignment are
CC assigned to the surface or inside of the folded structure, active sites,
CC and parsing segments. Secondary structural units are assigned by
CC identifying periodicity in the assignments, and assembled into globular
CC form using distance constraints imposed by disulfide bridges, active site
CC assignments and co-variation analysis. The predicted secondary structures
CC are useful for identifying antigenic sites on a protein molecule, as
CC guides for site directed mutagenesis studies, and for understanding the

```
CC   interaction of a protein with other molecules
XX
SQ   Sequence 259 AA;

  Query Match             100.0%;  Score 43;  DB 2;  Length 259;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        105 QIAEGMAFI 113


RESULT 6
AAY43955
ID   AAY43955 standard; protein; 259 AA.
XX
AC   AAY43955;
XX
DT   21-DEC-1999  (first entry)
XX
DE   Human protein kinase #15.
XX
KW   Prediction; secondary structure; alignment; evolutionary conservation;
KW   homology; periodicity; co-variation analysis; antigenic site;
KW   site directed mutagenesis; interaction.
XX
OS   Homo sapiens.
XX
PN   US5958784-A.
XX
PD   28-SEP-1999.
XX
PF   25-MAR-1992;   92US-00857224.
XX
PR   25-MAR-1992;   92US-00857224.
XX
PA   (BENN/) BENNER S A.
XX
PI   Benner SA;
XX
DR   WPI; 1999-570766/48.
XX
PT   Predicting the folded structure of proteins.
XX
PS   Disclosure; Col 253-256; 113pp; English.
XX
CC   Sequences AAY43902-Y44015 represent proteins used in a novel method of
CC   predicting the folded structure of proteins, by aligning sequences of
CC   homologous proteins and using patterns of evolutionarily conserved and
CC   varied sequences to assign positions. Positions in the alignment are
CC   assigned to the surface or inside of the folded structure, active sites,
CC   and parsing segments. Secondary structural units are assigned by
CC   identifying periodicity in the assignments, and assembled into globular
CC   form using distance constraints imposed by disulfide bridges, active site
CC   assignments and co-variation analysis. The predicted secondary structures
CC   are useful for identifying antigenic sites on a protein molecule, as
CC   guides for site directed mutagenesis studies, and for understanding the
CC   interaction of a protein with other molecules
XX
SQ   Sequence 259 AA;

  Query Match             100.0%;  Score 43;  DB 2;  Length 259;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        105 QIAEGMAFI 113


RESULT 7
ADR88385
ID   ADR88385 standard; protein; 263 AA.
XX
AC   ADR88385;
XX
DT   18-NOV-2004  (first entry)
XX
DE   LCK tyrosine kinase protein.
XX
KW   Molecular scaffold; nuclear hormone receptor; TNF receptor;
KW   G-protein coupled receptor; methyl transferase; ligase;
KW   LCK tyrosine kinase; enzyme.
XX
OS   Unidentified.
XX
PN   US2004171062-A1.
XX
PD   02-SEP-2004.
XX
PF   28-FEB-2003; 2003US-00377268.
XX
PR   28-FEB-2002; 2002US-0360651P.
PR   16-SEP-2002; 2002US-0411398P.
PR   20-SEP-2002; 2002US-0412341P.
PR   02-JAN-2003; 2003US-0437929P.
XX
PA   (PLEX-) PLEXXIKON INC.
XX
PI   Hirth K,  Milburn MV;
XX
DR   WPI; 2004-642017/62.
XX
PT   Designing a ligand binding to a target molecule, comprises identifying as
PT   molecular scaffolds compounds binding to members of a molecular family,
PT   detecting orientation of scaffolds at a binding site of target, and
PT   synthesizing ligand.
XX
PS   Disclosure; SEQ ID NO 24; 186pp; English.
XX
CC   The present invention relates to a method of designing a ligand binding
CC   to a target molecule. The method involves identifying as molecular
CC   scaffolds compounds binding to members of a molecular family, detecting
CC   orientation of scaffolds at a binding site of target, and synthesising
CC   ligand. The invention is useful for designing drug products and for
CC   designing ligand binding to target molecules such as nuclear hormone
CC   receptors, TNF receptors, G-protein coupled receptors, methyl
CC   transferases, ligases, etc. The present sequence is the LCK tyrosine
CC   kinase protein. This sequence is used to illustrate the method of
CC   invention.
XX
SQ   Sequence 263 AA;

  Query Match             100.0%;  Score 43;  DB 8;  Length 263;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        109 QIAEGMAFI 117


RESULT 8
ABR56203
ID   ABR56203 standard; protein; 265 AA.
XX
AC   ABR56203;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Mutant Lymphocyte Cell Kinase, Lck, fragment (237-501, D364N).
XX
KW   Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW   Src-family protein tyrosine kinase; T-cell; immune response; mutein;
KW   mutant.
```

```
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 128
FT                   /note= "Wild-type D substituted with N. This position is
FT                   364 in the full-length sequence (see ABR56202 for the
FT                   wild-type full length sequence"
FT   Modified-site   158
FT                   /note= "Phosphorylation site"
XX
PN   WO2003020880-A2.
XX
PD   13-MAR-2003.
XX
PF   02-AUG-2002; 2002WO-US024546.
XX
PR   03-AUG-2001; 2001US-0310051P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Borhani DW,  Calderwood D,  Dixon RW,  Hirst GC,  Hrnciar P,  Loew A;
PI   Leung A,  Ritter K;
XX
DR   WPI; 2003-300872/29.
XX
PT   New crystalline polypeptide comprising ligand binding domain or catalytic
PT   domain of Lck protein, for determining three-dimensional structure of
PT   catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS   Claim 12; Fig 2; 994pp; English.
XX
CC   The present invention relates to a crystalline polypeptide (I),
CC   comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC   protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC   in T-cells and plays an essential role in immune response. (I) is useful
CC   for identifying a compound which is an inhibitor of human Lck protein.
CC   The present sequence is a mutated fragment of the human Lck sequence,
CC   which approximately comprises the catalytic domain
XX
SQ   Sequence 265 AA;

  Query Match             100.0%;  Score 43;  DB 7;  Length 265;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        111 QIAEGMAFI 119


RESULT 9
ABR56204
ID   ABR56204 standard; protein; 271 AA.
XX
AC   ABR56204;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Mutant Lymphocyte Cell Kinase, Lck, fragment (231-501, D364N).
XX
KW   Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;
KW   Src-family protein tyrosine kinase; T-cell; immune response; mutein;
KW   mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 134
FT                   /note= "Wild-type D substituted with N. This position is
FT                   364 in the full-length sequence (see ABR56202 for the
FT                   wild-type full length sequence"
FT   Modified-site   164
FT                   /note= "Phosphorylation site"
XX
PN   WO2003020880-A2.
XX
PD   13-MAR-2003.
XX
PF   02-AUG-2002; 2002WO-US024546.
XX
PR   03-AUG-2001; 2001US-0310051P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Borhani DW,  Calderwood D,  Dixon RW,  Hirst GC,  Hrnciar P,  Loew A;
PI   Leung A,  Ritter K;
XX
DR   WPI; 2003-300872/29.
XX
PT   New crystalline polypeptide comprising ligand binding domain or catalytic
PT   domain of Lck protein, for determining three-dimensional structure of
PT   catalytic domain of Lck, has predetermined unit cell parameters.
XX
PS   Example 1; Fig 3; 994pp; English.
XX
CC   The present invention relates to a crystalline polypeptide (I),
CC   comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)
CC   protein. Lck is a Src-family protein tyrosine kinase expressed primarily
CC   in T-cells and plays an essential role in immune response. (I) is useful
CC   for identifying a compound which is an inhibitor of human Lck protein.
CC   The present sequence is a mutated fragment of the human Lck sequence,
CC   which approximately comprises the catalytic domain
XX
SQ   Sequence 271 AA;

  Query Match             100.0%;  Score 43;  DB 7;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        117 QIAEGMAFI 125


RESULT 10
ADR88384
ID   ADR88384 standard; protein; 271 AA.
XX
AC   ADR88384;
XX
DT   18-NOV-2004  (first entry)
XX
DE   HCK tyrosine kinase protein.
XX
KW   Molecular scaffold; nuclear hormone receptor; TNF receptor;
KW   G-protein coupled receptor; methyl transferase; ligase;
KW   HCK tyrosine kinase; enzyme.
XX
OS   Unidentified.
XX
PN   US2004171062-A1.
XX
PD   02-SEP-2004.
XX
PF   28-FEB-2003; 2003US-00377268.
XX
PR   28-FEB-2002; 2002US-0360651P.
PR   16-SEP-2002; 2002US-0411398P.
PR   20-SEP-2002; 2002US-0412341P.
PR   02-JAN-2003; 2003US-0437929P.
XX
PA   (PLEX-) PLEXXIKON INC.
XX
```

PI Hirth K, Milburn MV;
XX
DR WPI; 2004-642017/62.
XX
PT Designing a ligand binding to a target molecule, comprises identifying as
PT molecular scaffolds compounds binding to members of a molecular family,
PT detecting orientation of scaffolds at a binding site of target, and
PT synthesizing ligand.
XX
PS Disclosure; SEQ ID NO 23; 186pp; English.
XX
CC The present invention relates to a method of designing a ligand binding
CC to a target molecule. The method involves identifying as molecular
CC scaffolds compounds binding to members of a molecular family, detecting
CC orientation of scaffolds at a binding site of target, and synthesising
CC ligand. The invention is useful for designing drug products and for
CC designing ligand binding to target molecules such as nuclear hormone
CC receptors, TNF receptors, G-protein coupled receptors, methyl
CC transferases, ligases, etc. The present sequence is the HCK tyrosine
CC kinase protein. This sequence is used to illustrate the method of
CC invention.
XX
SQ Sequence 271 AA;

Query Match 100.0%; Score 43; DB 8; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 109 QIAEGMAFI 117

RESULT 11
ABB81188
ID ABB81188 standard; protein; 272 AA.
XX
AC ABB81188;
XX
DT 25-NOV-2002 (first entry)
XX
DE Human KIT protein sequence.
XX
KW Receptor tyrosine kinase; RTK; kinase domain; cytostatic; antiarthritic;
KW antiinflammatory; immunosuppressive; antirheumatic; virucide; nootropic;
KW neuroprotective; cerebroprotective; antiparkinsonian; dermatological;
KW nephrotropic; tranquilizer; vulnerary; anticonvulsant; human; KIT.
XX
OS Homo sapiens.
XX
PN WO200261055-A2.
XX
PD 08-AUG-2002.
XX
PF 31-JAN-2002; 2002WO-CA000114.
XX
PR 31-JAN-2001; 2001US-0265510P.
XX
PA (MOUN) MOUNT SINAI HOSPITAL.
XX
PI Sicheri F, Wybenga-Groot L, Pawson T;
XX
DR WPI; 2002-643365/69.
XX
PT Novel isolated binding pocket of receptor tyrosine kinase that regulates
PT the kinase domain of the receptor, useful for identifying modulator of
PT the receptor for treating lymphoproliferative conditions.
XX
PS Disclosure; Fig 1; 116pp; English.
XX
CC The invention relates to an isolated binding pocket (I) of a receptor
CC tyrosine kinase (RTK) that regulates the kinase domain of RTK. A crystal
CC (II) comprising a binding pocket of an RTK that regulates the kinase
CC domain of the RTK, or comprising a juxtamembrane region and/or kinase
CC domain of an RTK or its part, or formed by a juxtamembrane region and a
CC kinase region of an RTK in an autoinhibited state and a model (III) of
CC (I) made using (I); are useful for determining the secondary and/or
CC tertiary structure of a polypeptide, or for screening for a ligand
CC capable of binding to a binding pocket and/or inhibiting or enhancing the
CC atomic contacts of interactions in a binding pocket. (I) is useful for
CC identifying a modulator of an RTK. (II) is useful for designing,
CC modelling, identifying, evaluating and/or synthesizing mimetics of a
CC binding pocket, or ligands that associate with the binding pocket, to
CC make a model for (I) or its complexes or parts, in X-ray crystallography
CC techniques, or for determining three-dimensional structures of
CC polypeptides with unknown structures. Pharmaceutical compositions
CC comprising the ligand or modulator is useful for treating
CC lymphoproliferative conditions, malignant and pre-malignant conditions
CC (such as cancer), arthritis, inflammation, autoimmune disorder (such as
CC lupus erythematosus, immune-related glomerulonephritis, rheumatoid
CC arthritis), viral infection, inflammation, graft versus host disease,
CC neurodegenerative diseases and conditions involving trauma and injury to
CC the nervous system (e.g., Alzheimer's disease, Parkinson's disease,
CC Huntington's disease and multiple sclerosis). The present sequence
CC represents a human KIT protein sequence
XX
SQ Sequence 272 AA;

Query Match 100.0%; Score 43; DB 5; Length 272;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 110 QIAEGMAFI 118

RESULT 12
ADY85449
ID ADY85449 standard; protein; 279 AA.
XX
AC ADY85449;
XX
DT 16-JUN-2005 (first entry)
XX
DE Catalytic domain of PIM kinase-like protein LCK.
XX
KW Kinase; protein co-ordinate data; protein structure; cancer; cytostatic;
KW neoplasm; inflammation; antiinflammatory.
XX
OS Unidentified.
XX
PN WO2005028624-A2.
XX
PD 31-MAR-2005.
XX
PF 15-SEP-2004; 2004WO-US030360.
XX
PR 15-SEP-2003; 2003US-0503277P.
XX
PA (PLEX-) PLEXXIKON INC.
XX
PI Artis DR, Bremer RE, Gillette SJ, Hurt CR, Ibrahim PL;
PI Zuckerman RL;
XX
DR WPI; 2005-273155/28.
XX
PT New scaffold library used for identifying and developing ligands for
PT protein kinases and treating kinase associated disorders e.g. cancer,
PT comprises set of compounds comprising N-heterocyclic compounds.
XX
PS Disclosure; Page 170-174; 236pp; English.
XX
CC The invention relates to a new kinase scaffold library comprises at least
CC 1 set of compounds, each set comprising at least 1 N-heterocyclic
CC compound of formulae (I)-(VII) given in the specification. Also included

CC are a system for fitting compounds in binding sites of protein kinases
CC (comprising an electronic kinase scaffold, and a scaffold library
CC comprising at least 1 collection of electronic representations of (I)-
CC (VII), where the scaffold library is embedded in a computer device and
CC the electronic representations of the compounds can be selectively
CC retrieved and functionally connected with computer software adapted to
CC fit electronic representations of compounds in an electronic
CC representation of a binding site of a kinase), obtaining improved ligands
CC binding to a protein kinase (which comprises determining if a derivative
CC of (I)-(VII) binds to the kinase with greater affinity and/or specificity
CC than (I)-(VII)), developing ligands specific for a particular kinase
CC (which comprises determining if a derivative of (I)-(VII) that binds to
CC kinases has greater for specificity for the particular kinase than (I)-
CC (VII), developing ligands binding to a kinase (which comprises
CC determining the orientation of at least 1 molecular scaffold of (I)-(VII)
CC in co-crystals with the kinase, identifying chemical structures of the
CC scaffolds, that, when modified, change the binding affinity and/or
CC specificity between the scaffold and kinase and synthesizing a ligand in
CC which at least 1 chemical structure of the scaffold is modified),
CC developing ligands with increased specificity on a kinase (which
CC comprises testing a derivative of a kinase binding compound (I)-(VII) for
CC increased specificity on the kinase), identifying a ligand binding to a
CC kinase (which comprises determining if a derivative compound including a
CC core structure (I)-(VII) binds to the kinase with changed binding
CC affinity and/or specificity), a co-crystal of a kinase and a binding
CC compound (I)-(VII), preparation of co-crystals of Pim-1 with (I)-(VII),
CC identifying potential kinase binding compounds (which comprises fitting
CC electronic representations of (I)-(VII) in an electronic representation
CC of a kinase binding site), attaching a kinase binding compound to an
CC attachment component (which comprises identifying energetically allowed
CC sites for attachment of the component on a kinase binding compound (I)-
CC (VII) and attaching the compound or derivative to the attachment
CC component at the allowed site), modified compounds (comprising (I)-(VIII)
CC with an attached linker group, and developing a ligand for a kinase
CC comprising conserved residues matching at least on of Pim-1 residues 49,
CC 52, 67, 121, 128 and 186 which comprises determining if (I)-(VII) binds
CC to the kinase. The kinases comprise Pim-1, Pyk2, c-Abl, Her2, cMet,
CC vascular endothelial growth factor receptor, endothelial growth factor
CC receptor, cKit, Pkcbeta, p38, Cdk2, Akt or Gsk3beta. The kinase scaffold
CC library is used for identifying and developing ligands binding to
CC kinases, for modulating kinase activity and for treating disease
CC condition associated with abnormal kinase activity e.g. cancer,
CC inflammatory disease. The method identifies improved ligands binding to a
CC kinase resulting in ligands having high affinity and specificity towards
CC kinase. The co-crystals of kinase and the binding compound are of
CC sufficient size and quality to allow structural determination of at least
CC 2 Angstroms. The present sequence is a catalytic domain from a PIM-like
CC kinase. NOTE: It is not clear whether the sequence as presented
CC represents a continuous amino acid sequence.
XX
SQ Sequence 279 AA;

Query Match 100.0%; Score 43; DB 9; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 117 QIAEGMAFI 125

RESULT 13
ADY85468
ID ADY85468 standard; protein; 300 AA.
XX
AC ADY85468;
XX
DT 16-JUN-2005 (first entry)
XX
DE Catalytic domain of PIM kinase-like protein Src-2.
XX
KW Kinase; protein co-ordinate data; protein structure; cancer; cytostatic;
KW neoplasm; inflammation; antiinflammatory.
XX
OS Unidentified.
XX
PN WO2005028624-A2.
XX
PD 31-MAR-2005.
XX
PF 15-SEP-2004; 2004WO-US030360.
XX
PR 15-SEP-2003; 2003US-0503277P.
XX
PA (PLEX-) PLEXXIKON INC.
XX
PI Artis DR, Bremer RE, Gillette SJ, Hurt CR, Ibrahim PL;
PI Zuckerman RL;
XX
DR WPI; 2005-273155/28.
XX
PT New scaffold library used for identifying and developing ligands for
PT protein kinases and treating kinase associated disorders e.g. cancer,
PT comprises set of compounds comprising N-heterocyclic compounds.
XX
PS Disclosure; Page 170-174; 236pp; English.
XX
CC The invention relates to a new kinase scaffold library comprises at least
CC 1 set of compounds, each set comprising at least 1 N-heterocyclic
CC compound of formulae (I)-(VII) given in the specification. Also included
CC are a system for fitting compounds in binding sites of protein kinases
CC (comprising an electronic kinase scaffold, and a scaffold library
CC comprising at least 1 collection of electronic representations of (I)-
CC (VII), where the scaffold library is embedded in a computer device and
CC the electronic representations of the compounds can be selectively
CC retrieved and functionally connected with computer software adapted to
CC fit electronic representations of compounds in an electronic
CC representation of a binding site of a kinase), obtaining improved ligands
CC binding to a protein kinase (which comprises determining if a derivative
CC of (I)-(VII) binds to the kinase with greater affinity and/or specificity
CC than (I)-(VII)), developing ligands specific for a particular kinase
CC (which comprises determining if a derivative of (I)-(VII) that binds to
CC kinases has greater for specificity for the particular kinase than (I)-
CC (VII), developing ligands binding to a kinase (which comprises
CC determining the orientation of at least 1 molecular scaffold of (I)-(VII)
CC in co-crystals with the kinase, identifying chemical structures of the
CC scaffolds, that, when modified, change the binding affinity and/or
CC specificity between the scaffold and kinase and synthesizing a ligand in
CC which at least 1 chemical structure of the scaffold is modified),
CC developing ligands with increased specificity on a kinase (which
CC comprises testing a derivative of a kinase binding compound (I)-(VII) for
CC increased specificity on the kinase), identifying a ligand binding to a
CC kinase (which comprises determining if a derivative compound including a
CC core structure (I)-(VII) binds to the kinase with changed binding
CC affinity and/or specificity), a co-crystal of a kinase and a binding
CC compound (I)-(VII), preparation of co-crystals of Pim-1 with (I)-(VII),
CC identifying potential kinase binding compounds (which comprises fitting
CC electronic representations of (I)-(VII) in an electronic representation
CC of a kinase binding site), attaching a kinase binding compound to an
CC attachment component (which comprises identifying energetically allowed
CC sites for attachment of the component on a kinase binding compound (I)-
CC (VII) and attaching the compound or derivative to the attachment
CC component at the allowed site), modified compounds (comprising (I)-(VIII)
CC with an attached linker group, and developing a ligand for a kinase
CC comprising conserved residues matching at least on of Pim-1 residues 49,
CC 52, 67, 121, 128 and 186 which comprises determining if (I)-(VII) binds
CC to the kinase. The kinases comprise Pim-1, Pyk2, c-Abl, Her2, cMet,
CC vascular endothelial growth factor receptor, endothelial growth factor
CC receptor, cKit, Pkcbeta, p38, Cdk2, Akt or Gsk3beta. The kinase scaffold
CC library is used for identifying and developing ligands binding to
CC kinases, for modulating kinase activity and for treating disease
CC condition associated with abnormal kinase activity e.g. cancer,
CC inflammatory disease. The method identifies improved ligands binding to a
CC kinase resulting in ligands having high affinity and specificity towards
CC kinase. The co-crystals of kinase and the binding compound are of
CC sufficient size and quality to allow structural determination of at least

CC 2 Angstroms. The present sequence is a catalytic domain from a PIM-like
CC kinase. NOTE: It is not clear whether the sequence as presented
CC represents a continuous amino acid sequence.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 43; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 138 QIAEGMAFI 146

RESULT 14
ADY85448
ID ADY85448 standard; protein; 316 AA.
XX
AC ADY85448;
XX
DT 16-JUN-2005 (first entry)
XX
DE Catalytic domain of PIM kinase-like protein HCK.
XX
KW Kinase; protein co-ordinate data; protein structure; cancer; cytostatic;
KW neoplasm; inflammation; antiinflammatory.
XX
OS Unidentified.
XX
PN WO2005028624-A2.
XX
PD 31-MAR-2005.
XX
PF 15-SEP-2004; 2004WO-US030360.
XX
PR 15-SEP-2003; 2003US-0503277P.
XX
PA (PLEX-) PLEXXIKON INC.
XX
PI Artis DR, Bremer RE, Gillette SJ, Hurt CR, Ibrahim PL;
PI Zuckerman RL;
XX
DR WPI; 2005-273155/28.
XX
PT New scaffold library used for identifying and developing ligands for
PT protein kinases and treating kinase associated disorders e.g. cancer,
PT comprises set of compounds comprising N-heterocyclic compounds.
XX
PS Disclosure; Page 170-174; 236pp; English.
XX
CC The invention relates to a new kinase scaffold library comprises at least
CC 1 set of compounds, each set comprising at least 1 N-heterocyclic
CC compound of formulae (I)-(VII) given in the specification. Also included
CC are a system for fitting compounds in binding sites of protein kinases
CC (comprising an electronic kinase scaffold, and a scaffold library
CC comprising at least 1 collection of electronic representations of (I)-
CC (VII), where the scaffold library is embedded in a computer device and
CC the electronic representations of the compounds can be selectively
CC retrieved and functionally connected with computer software adapted to
CC fit electronic representations of compounds in an electronic
CC representation of a binding site of a kinase), obtaining improved ligands
CC binding to a protein kinase (which comprises determining if a derivative
CC of (I)-(VII) binds to the kinase with greater affinity and/or specificity
CC than (I)-(VII)), developing ligands specific for a particular kinase
CC (which comprises determining if a derivative of (I)-(VII) that binds to
CC kinases has greater for specificity for the particular kinase than (I)-
CC (VII), developing ligands binding to a kinase (which comprises
CC determining the orientation of at least 1 molecular scaffold of (I)-(VII)
CC in co-crystals with the kinase, identifying chemical structures of the
CC scaffolds, that, when modified, change the binding affinity and/or
CC specificity between the scaffold and kinase and synthesizing a ligand in
CC which at least 1 chemical structure of the scaffold is modified),
CC developing ligands with increased specificity on a kinase (which
CC comprises testing a derivative of a kinase binding compound (I)-(VII) for
CC increased specificity on the kinase), identifying a ligand binding to a
CC kinase (which comprises determining if a derivative compound including a
CC core structure (I)-(VII) binds to the kinase with changed binding
CC affinity and/or specificity), a co-crystal of a kinase and a binding
CC compound (I)-(VII), preparation of co-crystals of Pim-1 with (I)-(VII),
CC identifying potential kinase binding compounds (which comprises fitting
CC electronic representations of (I)-(VII) in an electronic representation
CC of a kinase binding site), attaching a kinase binding compound to an
CC attachment component (which comprises identifying energetically allowed
CC sites for attachment of the component on a kinase binding compound (I)-
CC (VII) and attaching the compound or derivative to the attachment
CC component at the allowed site), modified compounds (comprising (I)-(VIII)
CC with an attached linker group, and developing a ligand for a kinase
CC comprising conserved residues matching at least on of Pim-1 residues 49,
CC 52, 67, 121, 128 and 186 which comprises determining if (I)-(VII) binds
CC to the kinase. The kinases comprise Pim-1, Pyk2, c-Abl, Her2, cMet,
CC vascular endothelial growth factor receptor, endothelial growth factor
CC receptor, cKit, Pkcbeta, p38, Cdk2, Akt or Gsk3beta. The kinase scaffold
CC library is used for identifying and developing ligands binding to
CC kinases, for modulating kinase activity and for treating disease
CC condition associated with abnormal kinase activity e.g. cancer,
CC inflammatory disease. The method identifies improved ligands binding to a
CC kinase resulting in ligands having high affinity and specificity towards
CC kinase. The co-crystals of kinase and the binding compound are of
CC sufficient size and quality to allow structural determination of at least
CC 2 Angstroms. The present sequence is a catalytic domain from a PIM-like
CC kinase. NOTE: It is not clear whether the sequence as presented
CC represents a continuous amino acid sequence.
XX
SQ Sequence 316 AA;

Query Match 100.0%; Score 43; DB 9; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 154 QIAEGMAFI 162

RESULT 15
AAY76750
ID AAY76750 standard; protein; 346 AA.
XX
AC AAY76750;
XX
DT 17-APR-2000 (first entry)
XX
DE Human protein kinase homologue, PKH-3.
XX
KW Protein kinase homologue; human; PKH; diagnosis; therapy; cancer; AIDS;
KW autoimmune disorder; inflammatory disorder; reproductive defect; asthma;
KW diabetes mellitus; infertility; ovulatory defect; endometriosis;
KW polycystic ovary syndrome.
XX
OS Homo sapiens.
XX
PN US6013455-A.
XX
PD 11-JAN-2000.
XX
PF 15-OCT-1998; 98US-00173581.
XX
PR 15-OCT-1998; 98US-00173581.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Hillman JL, Yue H, Yang YT, Corley NC, Gorgone GA, Azimzai Y;
PI Lu DAM, Bandman O, Guegler KJ;
XX
DR WPI; 2000-136321/12.

DR N-PSDB; AAZ86794.
XX
PT Nucleic acids encoding a human protein kinase homolog useful for
PT preventing, diagnosing and treating cancer, autoimmune/inflammatory
PT disorders and reproductive defects.
XX
PS Claim 1; Col 47-50; 38pp; English.
XX
CC This sequence represents a human protein kinase homolog (PKH) of the
CC invention. The PKH sequences may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate PKH expression such
CC as cancers, autoimmune/inflammatory disorders and reproductive defects.
CC They may be used to treat disorders associated with decreased PKH
CC expression such as cancers (e.g. lymphoma, melanoma and cancers of the
CC breast lung and prostate), autoimmune/inflammatory disorders (e.g. AIDS,
CC asthma and diabetes mellitus), and reproductive defects (e.g.
CC infertility, ovulatory defects, endometriosis and polycystic ovary
CC syndrome). The DNA may be administered to treat diseases by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC PKH by expressing inactive proteins or to supplement the patients own
CC production of PKH polypeptides. Additionally, the DNA may be used to
CC produce PKH, according to standard recombinant DNA methodology, by
CC inserting the nucleic acids into a host cell and culturing the cell to
CC express the protein. Conversely, antisense nucleic acid molecules may be
CC administered to down regulate PKH expression by binding with the cells
CC own PKH genes and preventing their expression. The DNA, and antisense
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acid sequences in samples,
CC and hence which patients may be in need of restorative therapy. They may
CC also be used to study the expression and function of PKH polypeptides and
CC their role in metabolism. The PKH polypeptides may be used as antigens in
CC the production of antibodies against PKH and in assays to identify
CC modulators (agonists and antagonists) of PKH expression and activity. The
CC anti-PKH antibodies and PKH antagonists may also be used to down regulate
CC PKH expression and activity. The anti-PKH antibodies may also be used as
CC diagnostic agents for detecting the presence of PKH polypeptides in
CC samples
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 43; DB 3; Length 346;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 184 QIAEGMAFI 192

RESULT 16
AAE06208
ID AAE06208 standard; protein; 346 AA.
XX
AC AAE06208;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human protein kinase homolog-3 (PKH-3).
XX
KW Human; protein kinase homolog-3; PKH-3; cytostatic; protein therapy;
KW vaccine; immunosuppressive; antisclerotic; antiabortive; adenocarcinoma;
KW Acquired Immune deficiency Syndrome; AIDS; melanoma; cancer; bone; liver;
KW breast; autoimmune disorder; multiple sclerosis; drug screening; anaemia;
KW Crohn's disease; ectopic pregnancy; tubal disease; inflammatory disorder;
KW reproductive disorder; polycystic ovary syndrome; asthma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 125. .333
FT /note= "Signature sequence"
XX
PN US6264947-B1.
XX
PD 24-JUL-2001.
XX
PF 20-OCT-1999; 99US-00420915.
XX
PR 15-OCT-1998; 98US-00173581.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Bandman O, Tang YT, Hillman JL, Yue H, Guegler KJ, Corley NC;
PI Gorgone GA, Azimzai Y, Lu DAM;
XX
DR WPI; 2001-450728/48.
DR N-PSDB; AAD11845.
XX
PT Human protein kinase proteins and homologs, useful for preventing,
PT diagnosing and treating cancers, autoimmune/inflammatory disorders and
PT reproductive disorders.
XX
PS Claim 1; Col 47-50; 38pp; English.
XX
CC The present sequence is human protein kinase homolog-3 (PKH-3). Human
CC protein kinase homologs (PKH) and their cDNA molecules are used in the
CC prevention, diagnosis and treatment of diseases associated with increased
CC or decreased expression of PKH. Examples of such disorders include,
CC cancer (e.g. adenocarcinoma, melanoma and bone, breast and liver cancer),
CC autoimmune/inflammatory disorders (e.g. Acquired Immune deficiency
CC Syndrome (AIDS), anaemia, asthma, Crohn's disease and multiple sclerosis)
CC and reproductive disorders (e.g. tubal disease, ectopic pregnancy and
CC polycystic ovary syndrome). PKH, its catalytic or immunogenic fragment
CC are used for screening libraries of compounds in any of the drug
CC screening techniques. PKH nucleic acids are used to generate
CC hybridisation probes useful in mapping the naturally occurring genomic
CC sequences. PKH are also used as antigens in the production of antibodies
CC against protein kinases (PK) and in assays to identify modulators of PK
CC expression and activity. PKH is also used in protein therapy
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 43; DB 4; Length 346;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 184 QIAEGMAFI 192

RESULT 17
ABB84435
ID ABB84435 standard; protein; 346 AA.
XX
AC ABB84435;
XX
DT 08-NOV-2002 (first entry)
XX
DE Human protein kinase homologue from clone 507669.
XX
KW Protein kinase homologue; PKH; cytostatic; immunosuppressive; antifungal;
KW antiinflammatory; antiallergic; antiasthmatic; antianaemic; antidiabetic;
KW antiarteriosclerotic; antithyroid; dermatological; nephrotropic; human;
KW antigout; thyromimetic; nootropic; osteopathic; antiarthritic; allergy;
KW antirheumatic; ophthalmological; antiulcer; antiviral; antibacterial;
KW antiprotozoal; antiparasitic; antihelmintic; ankylosing spondylitis;
KW acquired immunodeficiency syndrome; AIDS; Addison's disease; amyloidosis;
KW adult respiratory distress syndrome; anaemia; asthma; atherosclerosis;
KW autoimmune haemolytic anaemia; autoimmune thyroiditis; bronchitis;
KW cholecystitis; contact dermatitis; Crohn's disease; atopic dermatitis;
KW dermatomyositis; diabetes mellitus; emphysema; atrophic gastritis; gout;
KW glomerulonephritis; Goodpasture's syndrome; Graves' disease; psoriasis;
KW Hashimoto's thyroiditis; hypereosinophilia; irritable bowel syndrome;
KW multiple sclerosis; myasthenia gravis; myocardial inflammation; uveitis;
KW pericardial inflammation; osteoarthritis; osteoporosis; pancreatitis;

KW polymyositis; Reiter's syndrome; rheumatoid arthritis; scleroderma; SLE;
KW Sjogren's syndrome; systemic lupus erythematosus; systemic sclerosis;
KW thrombocytopenic purpura; ulcerative colitis; Werner syndrome; infection;
KW haemodialysis; extracorporeal circulation; infertility; tubal disease;
KW ovulatory defect; endometriosis; oestrous; menstrual cycle; gene therapy;
KW uterine fibroid; autoimmune disorder; polycystic ovary syndrome; enzyme;
KW ovarian hyperstimulation syndrome; ectopic pregnancy; teratogenesis;
KW cancer.
XX
OS Homo sapiens.
XX
PN US2002081290-A1.
XX
PD 27-JUN-2002.
XX
PF 30-MAY-2001; 2001US-00870962.
XX
PR 15-OCT-1998; 98US-00173581.
PR 20-OCT-1999; 99US-00420915.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Tang YT, Hillman JL, Yue H, Guegler KJ, Corley NC;
PI Gorgone GA, Azimzai Y, Lu DAM;
XX
DR WPI; 2002-655433/70.
DR N-PSDB; ABQ76288.
XX
PT Nucleic acids encoding a human protein kinase homolog useful for
PT preventing, diagnosing and treating cancer, autoimmune/inflammatory
PT disorders and reproductive defects.
XX
PS Claim 47; Page 27; 43pp; English.
XX
CC This invention describes a novel protein kinase homologue (PKH)
CC polypeptides which have cytostatic, immunosuppressive, antiinflammatory,
CC antiallergic, antiasthmatic, antianaemic, antiarteriosclerotic,
CC antithyroid, dermatological, antidiabetic, nephrotropic, antigout,
CC thyromimetic, nootropic, osteopathic, antiarthritic, antirheumatic,
CC ophthalmological, antiulcer, antiviral, antibacterial, antifungal,
CC antiprotozoal, antiparasitic and antihelmintic activity. The polypeptide
CC is used for treating a disease or condition associated with decreased
CC expression of functional PKH. The polypeptide is used to screen for
CC agonists and antagonists of PKH which can also be used in disease
CC treatment. The polypeptide and polynucleotide are used for treating
CC acquired immunodeficiency syndrome (AIDS), Addison's disease, adult
CC respiratory distress syndrome, allergies, ankylosing spondylitis,
CC amyloidosis, anaemia, asthma, atherosclerosis, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, bronchitis, cholecystitis, cancer,
CC contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis,
CC diabetes mellitus, emphysema, atrophic gastritis, glomerulonephritis,
CC Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis,
CC hypereosinophilia, irritable bowel syndrome, multiple sclerosis,
CC myasthenia gravis, myocardial or pericardial inflammation,
CC osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis,
CC Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's syndrome,
CC systemic lupus erythematosus (SLE), systemic sclerosis, thrombocytopenic
CC purpura, ulcerative colitis, uveitis, Werner syndrome, complications of
CC cancer, haemodialysis, and extracorporeal circulation, viral, bacterial,
CC fungal, parasitic, protozoal, and helminthic infections, infertility,
CC including tubal disease, ovulatory defects, and endometriosis,
CC disruptions of the oestrous cycle, disruptions of the menstrual cycle,
CC polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial
CC and ovarian tumours, uterine fibroids, autoimmune disorders, ectopic
CC pregnancies, and teratogenesis. The polypeptides of the invention can be
CC used for gene therapy. This sequence represents a PKH from clone ID
CC 507669 isolated from TMLR3DT02, a library constructed using RNA isolated
CC from non-adherent peripheral blood mononuclear cells collected from a
CC pool of male and female donors
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 43; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 184 QIAEGMAFI 192

RESULT 18
ABM82980
ID ABM82980 standard; protein; 355 AA.
XX
AC ABM82980;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3229.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN41632.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 355 AA;

Query Match 100.0%; Score 43; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 2.1;

```
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        193 QIAEGMAFI 201


RESULT 19
ADJ68978
ID   ADJ68978 standard; protein; 383 AA.
XX
AC   ADJ68978;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human heat mitochondrial protein as a therapeutic target SeqID784.
XX
KW   mitochondrial; human; screening assay; diabetes mellitus;
KW   Huntington's disease; osteoarthritis;
KW   Leber's hereditary optic neuropathy; LHON;
KW   mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW   myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW   neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW   osteopathic; ophthalmological; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2003087768-A2.
XX
PD   23-OCT-2003.
XX
PF   04-APR-2003; 2003WO-US010870.
XX
PR   12-APR-2002; 2002US-0372843P.
PR   17-JUN-2002; 2002US-0389987P.
PR   20-SEP-2002; 2002US-0412418P.
XX
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
XX
PI   Ghosh SS,  Fahy ED,  Zhang B,  Gibson BW,  Taylor SW,  Glenn GM;
PI   Warnock DE;
XX
DR   WPI; 2003-845369/78.
XX
PT   Identifying a mitochondrial target for drug screening assays and for
PT   treating diseases associated with altered mitochondrial function,
PT   comprises detecting a modified polypeptide in a sample and correlating
PT   with the disease.
XX
PS   Claim 1; SEQ ID NO 784; 180pp; English.
XX
CC   This invention relates to novel mitochondrial targets that can be used
CC   for therapeutic intervention in treating a disease associated with
CC   altered mitochondrial function. Specifically, it refers to a method for
CC   identifying proteins of the human heart mitochondrial proteome that are
CC   useful for drug screening assays, as well as therapeutic targets. The
CC   present invention describes a method for identifying such proteins that
CC   can be used in the treatment of various diseases associated with altered
CC   mitochondrial function including diabetes mellitus, Huntington's disease,
CC   osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC   encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC   ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC   compositions have neuroprotective, nootropic, antidiabetic,
CC   anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC   cytostatic activities. This polypeptide sequence is a human heart
CC   mitochondrial protein of the invention.
XX
SQ   Sequence 383 AA;

  Query Match            100.0%;  Score 43;  DB 7;  Length 383;
  Best Local Similarity   100.0%;  Pred. No. 2.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        221 QIAEGMAFI 229


RESULT 20
AAR14201
ID   AAR14201 standard; protein; 417 AA.
XX
AC   AAR14201;
XX
DT   13-DEC-1991  (first entry)
XX
DE   (Beta-galactosidase N-terminal)-(lck gene prod.) fusion protein.
XX
KW   Multi-cloning site.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .26
FT                   /note= "beta-galactosidase fragment"
FT   Region          27. .417
FT                   /note= "lck gene polypeptide"
XX
PN   JP03201994-A.
XX
PD   03-SEP-1991.
XX
PF   28-DEC-1989;   89JP-00338268.
XX
PR   28-DEC-1989;   89JP-00338268.
XX
PA   (TOKU ) TOKUYAMA SODA KK.
XX
DR   WPI; 1991-300980/41.
DR   N-PSDB; AAQ14201.
XX
PT   Fused polypeptide - has amino acid sequence of beta-galactosidase with a
PT   LCK gene conjugated to the N-terminal via DNA having multi-cloning site.
XX
PS   Claim 1; Fig 4,2; 15pp; Japanese.
XX
CC   The sequence consists of the N-terminal amino acids of the beta-
CC   galactosidase gene fused with the lck gene. It is produced by E.coli
CC   transformed with a recombinant vector (see AAQ13983). It is useful for
CC   producing an antibody specifically immunoreactive with only a lck gene-
CC   derived polypeptide in T cells. The antibody may recognise lck gene-
CC   derived polypeptides in human cells
XX
SQ   Sequence 417 AA;

  Query Match            100.0%;  Score 43;  DB 2;  Length 417;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        255 QIAEGMAFI 263


RESULT 21
ADN61468
ID   ADN61468 standard; protein; 436 AA.
XX
AC   ADN61468;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human KPP-34 protein SEQ ID NO:34.
XX
KW   human; kinase; phosphatase; enzyme; KPP; cytostatic;
```

KW antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;
KW cerebroprotective; anti-HIV; antiallergic; antiinflammatory;
KW thyromimetic; gene therapy; cell proliferative disorder; cancer;
KW atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
KW stroke; immune disorder; inflammatory disorder; AIDS; allergy;
KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection.
XX
OS Homo sapiens.
XX
PN WO2004042022-A2.
XX
PD 21-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034809.
XX
PR 01-NOV-2002; 2002US-0423226P.
PR 15-NOV-2002; 2002US-0426713P.
PR 26-NOV-2002; 2002US-0429766P.
PR 11-FEB-2003; 2003US-0447043P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Hafalia AJA, Lee S, Murage J, Swarnakar A, Chawla NK, Khare R;
PI Elliott VS, Tran UK, Ramkumar J, Gururajan R, Baughn MR, Gietzen KJ;
PI Yang YG, Chien D, Wang JT, Favero KD, Becha SD, Richardson TW;
PI Jin P, Hawkins PR, Yue H, Lee EA, Marquis JP;
XX
DR WPI; 2004-390608/36.
DR N-PSDB; ADN61524.
XX
PT New human kinases and phosphatases (KPP), useful for diagnosing, treating
PT and preventing diseases or conditions associated with the aberrant KPP
PT expression e.g. cancer, AIDS, epilepsy, or infections.
XX
PS Claim 1; SEQ ID NO 34; 320pp; English.
XX
CC The present sequence represents a human kinase and phosphatase protein
CC designated KPP-34. Human KPP sequences have cytostatic,
CC antiarteriosclerotic, anticonvulsant, nootropic, neuroprotective,
CC cerebroprotective, anti-HIV, antiallergic, antiinflammatory and
CC thyromimetic activities, and can be used in gene therapy. The human KPP
CC polypeptides and polynucleotides of the invention are useful in
CC diagnosing, treating and preventing diseases or conditions associated
CC with the decreased expression or overexpression of KPP, such as cell
CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
CC disorders, or infections. They are also useful in assessing the effects
CC of exogenous compounds on the expression of nucleic acid and amino acid
CC sequences of KPP. The KPP sequences or their fragments are useful in
CC screening compounds for effectiveness as agonist or antagonist of the
CC polypeptides, or in altering the expression of the target polynucleotide
CC and compounds that specifically bind to or modulate the activity of the
CC polypeptide.
XX
SQ Sequence 436 AA;

Query Match 100.0%; Score 43; DB 8; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 274 QIAEGMAFI 282

RESULT 22
ABG79672
ID ABG79672 standard; protein; 437 AA.
XX
AC ABG79672;
XX
DT 15-NOV-2002 (first entry)
XX
DE Tumour involved gene (TIG) splice variant protein, NV-3.
XX
KW Human; splice variant; tumour-involved gene; TIG;
KW pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;
KW endothelial cell; cell differentiation; cell proliferation; apoptosis;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US2002086384-A1.
XX
PD 04-JUL-2002.
XX
PF 13-MAR-2001; 2001US-00805020.
XX
PR 14-MAR-2000; 2000IL-00135402.
PR 16-MAY-2000; 2000IL-00136154.
XX
PA (LEVI/) LEVINE Z.
PA (DAVI/) DAVID A.
PA (ROMA/) ROMANO C.
PA (BERN/) BERNSTEIN J.
XX
PI Levine Z, David A, Romano C, Bernstein J;
XX
DR WPI; 2002-635679/68.
DR N-PSDB; ABS65202.
XX
PT Novel nucleic acid sequence, which is an alternative splicing variant of
PT tumor involved genes, useful for detecting cancer, predisposition to
PT cancer, for evaluating cancer state and in gene therapy for treating
PT cancer.
XX
PS Claim 4; Page 68-69; 180pp; English.
XX
CC The invention discloses isolated human nucleic acid alternative splicing
CC variants that are all tumour-involved genes (TIGs). The nucleic acids and
CC polypeptides are useful for determining the level of a nucleic acid or
CC polypeptide in a biological sample, for detecting a variant nucleic acid
CC or polypeptide sequence in a biological sample, for determining the level
CC of variant nucleic acid or polypeptide sequences in a biological sample
CC and for determining the ratio between the level of variant sequence in a
CC first biological sample and the level of the original sequence from which
CC the variant has been varied by alternative splicing in a second
CC biological sample and for raising antibodies. A pharmaceutical
CC composition comprising a carrier and the nucleic acid, is useful for
CC treating diseases (e.g. cancer) that can be ameliorated or cured by
CC increasing or decreasing the level of the encoded protein. The nucleic
CC acids are also useful for diagnostic purposes, especially for detecting
CC cancer or a predisposition to cancer, for evaluating the state or
CC aggressiveness of cancer disease, in basic research, for understanding
CC the physiological function of the original TIG, in targeting or
CC developing pharmaceuticals, for distinguishing various stages in the life
CC cycle of the same type of cells which may be helpful for the development
CC of pharmaceuticals for various cancer stages in which cell cycle is non-
CC normal, for determining mutations in tumour-involved genes and in gene
CC therapy. The polypeptides are useful for identifying compounds capable of
CC binding to the variant product and modulating its activity and for
CC modulating endothelial differentiation and proliferation, as well as to
CC modulate apoptosis either ex vivo or in vivo. The sequences presented in
CC ABG796700-ABG79705 are the new variants (NV) 1-36 proteins of the TIGs
CC disclosed
XX
SQ Sequence 437 AA;

Query Match 100.0%; Score 43; DB 5; Length 437;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 347 QIAEGMAFI 355

```
RESULT 23
ADY52642
ID   ADY52642 standard; protein; 438 AA.
XX
AC   ADY52642;
XX
DT   19-MAY-2005  (first entry)
XX
DE   Human transcription factor TEL-Eco-RI-HCK kinase fusion protein 6.
XX
KW   oncogene; cancer; cytostatic; neoplasm; TEL; transcription factor;
KW   fusion protein; hck tyrosine kinase; enzyme.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   JP2005052018-A.
XX
PD   03-MAR-2005.
XX
PF   07-AUG-2003; 2003JP-00206534.
XX
PR   07-AUG-2003; 2003JP-00206534.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
DR   WPI; 2005-187380/20.
DR   N-PSDB; ADY52600.
XX
PT   Screening oncogene, by producing cDNA library having fusion DNA
PT   comprising cDNA encoding PNT region of TEL connected to downstream of
PT   promoter, introducing library into host cell, expressing fusion DNA and
PT   selecting transformed cells.
XX
PS   Disclosure; Page; 216pp; Japanese.
XX
CC   The invention relates to a novel method for screening an oncogene. The
CC   method comprises producing a cDNA library for a fusion DNA, comprising a
CC   cDNA encoding the PNT region of TEL connected downstream of a vector
CC   promoter, introducing the produced cDNA library into a host cell,
CC   expressing the fusion DNA, selecting the transformed cells and analyzing
CC   the base sequence of the fusion DNA in the transformed cell, and thus
CC   identifying the fusion DNA as an oncogene. TEL is a transcription factor
CC   which belongs to the Ets family and is known to form various genes and
CC   fusion genes via a chromosomal translocation in cancer cells, such as
CC   occurs in some cases of leukemia. The method of the invention may be
CC   useful for screening a substance which suppresses the proliferative
CC   property of a cancer cell, screening a substance which inhibits the
CC   activity of a kinase gene introduced into the cell and screening a
CC   substance for the treatment of cancer. The current sequence is that of
CC   the human transcription factor TEL-Eco-RI adapter-HCK kinase (residues 1-
CC   227) fusion protein of the invention.
XX
SQ   Sequence 438 AA;

  Query Match           100.0%;  Score 43;  DB 9;  Length 438;
  Best Local Similarity  100.0%;  Pred. No. 2.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        276 QIAEGMAFI 284


RESULT 24
ADC99048
ID   ADC99048 standard; protein; 458 AA.
XX
AC   ADC99048;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Human KPP protein - SEQ ID 1.
XX
KW   anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian;
KW   nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
KW   immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
KW   antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;
KW   osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;
KW   uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;
KW   virucide; protozoacide; fungicide; kinase; phosphatase; KPP;
KW   cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;
KW   cancer; developmental; mental retardation; neurological;
KW   Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;
KW   diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
KW   helminthic infection; transgenic; gene therapy; human; enzyme.
XX
OS   Homo sapiens.
XX
PN   WO2003033680-A2.
XX
PD   24-APR-2003.
XX
PF   17-OCT-2002; 2002WO-US033723.
XX
PR   19-OCT-2001; 2001US-0345474P.
PR   02-NOV-2001; 2001US-0343910P.
PR   13-NOV-2001; 2001US-0333098P.
PR   16-NOV-2001; 2001US-0332424P.
PR   30-NOV-2001; 2001US-0334288P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Bandman O,  Baughn MR,  Becha SD,  Borowsky ML,  Duggan BM;
PI   Emerling BM,  Forsythe IJ,  Gandhi AR,  Gorvad AE,  Griffin JA;
PI   Gururajan R,  Hafalia AJA,  Khan FA,  Lal PG,  Lee EA,  Lee SY;
PI   Lindquist EA,  Lu DAM,  Lu Y,  Marquis JP,  Nguyen DB,  Arvizu CS;
PI   Ramkumar J,  Recipon SA,  Richardson TW,  Swarnakar A,  Tang YT;
PI   Thornton MB,  Tran UK,  Chawla NK,  Warren BA,  Yang J,  Yao MG,  Yue H;
PI   Zebarjadian Y;
XX
DR   WPI; 2003-403214/38.
DR   N-PSDB; ADC99100.
XX
PT   New human kinases and phosphatases and polynucleotides, useful for
PT   diagnosing, treating or preventing autoimmune or inflammatory disorders
PT   (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
PT   cancer or hepatitis.
XX
PS   Claim 1; SEQ ID NO 1; 424pp; English.
XX
CC   The invention relates to a novel isolated polypeptide which is a human
CC   kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,
CC   agonists and antagonists are useful for diagnosing, treating or
CC   preventing cell proliferative disorders such as atherosclerosis,
CC   cirrhosis, hepatitis and cancer, developmental disorders e.g. mental
CC   retardation, neurological disorders including Alzheimer's disease and
CC   Parkinson's disease, autoimmune and inflammatory disorders such as
CC   Crohn's disease and diabetes mellitus and finally, viral, bacterial,
CC   fungal, parasitic, protozoan or helminthic infections. Furthermore, the
CC   polynucleotides encoding KPP may be useful for creating transgenic
CC   animals to model human disease, as well as during gene therapy
CC   procedures. The current sequence is that of the human KPP protein of the
CC   invention.
XX
SQ   Sequence 458 AA;

  Query Match           100.0%;  Score 43;  DB 7;  Length 458;
  Best Local Similarity  100.0%;  Pred. No. 2.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        296 QIAEGMAFI 304
```

```
RESULT 25
ADJ71657
ID   ADJ71657 standard; protein; 458 AA.
XX
AC   ADJ71657;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human NOV5a protein SEQ ID NO:58.
XX
KW   human; cytostatic; antidiabetic; anorectic; CNS; cardiovascular;
KW   antiinflammatory; gene therapy; antisense therapy; cancer; diabetes;
KW   obesity; endocrine disorder; inflammatory disorder.
XX
OS   Homo sapiens.
XX
PN   WO2004015076-A2.
XX
PD   19-FEB-2004.
XX
PF   07-AUG-2003; 2003WO-US024788.
XX
PR   07-AUG-2002; 2002US-0401597P.
PR   09-AUG-2002; 2002US-0402248P.
PR   12-AUG-2002; 2002US-0402815P.
PR   13-AUG-2002; 2002US-0403485P.
PR   14-AUG-2002; 2002US-0403574P.
PR   15-AUG-2002; 2002US-0403732P.
PR   20-AUG-2002; 2002US-0404829P.
PR   27-AUG-2002; 2002US-0406392P.
PR   06-AUG-2003; 2003US-00406392.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Anderson DW,  Berghs C,  Catterton E,  Edinger SR,  Gorman L,  Guo X;
PI   Herrmann JL,  Kekuda R,  Li L,  Rieger DK,  Zhong M;
XX
DR   WPI; 2004-180659/17.
DR   N-PSDB; ADJ71656.
XX
PT   Novel polypeptides (NOVX) and nucleic acid molecules useful for treating,
PT   preventing and diagnosing pathological conditions with NOVX-associated
PT   disorders, such as cancer, obesity, diabetes and inflammatory diseases.
XX
PS   Claim 2; SEQ ID NO 58; 267pp; English.
XX
CC   The invention relates to a novel isolated NOVX polypeptide. A polypeptide
CC   of the invention has cytostatic, antidiabetic, anorectic, CNS-gen.,
CC   cardiovascular-gen., and antiinflammatory activity. A polynucleotide
CC   encoding a polypeptide of the invention may have a use in gene therapy,
CC   and antisense therapy. The methods and compositions of the present
CC   invention are useful for the diagnosis and treatment of disorders
CC   associated with aberrant expression or activity of the NOVX polypeptide,
CC   such as cancer, diabetes, obesity, and endocrine, CNS, cardiovascular and
CC   inflammatory disorders. They can also be used in various detection and
CC   screening assays, chromosome mapping, tissue typing and predictive
CC   medicine. The present sequence represents a NOVX polypeptide of the
CC   invention.
XX
SQ   Sequence 458 AA;

  Query Match             100.0%;  Score 43;  DB 8;  Length 458;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        296 QIAEGMAFI 304


RESULT 26
ADY52641
ID   ADY52641 standard; protein; 465 AA.
XX
AC   ADY52641;
XX
DT   19-MAY-2005  (first entry)
XX
DE   Human transcription factor TEL-Eco-RI-HCK kinase fusion protein 5.
XX
KW   oncogene; cancer; cytostatic; neoplasm; TEL; transcription factor;
KW   fusion protein; hck tyrosine kinase; enzyme.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   JP2005052018-A.
XX
PD   03-MAR-2005.
XX
PF   07-AUG-2003; 2003JP-00206534.
XX
PR   07-AUG-2003; 2003JP-00206534.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
DR   WPI; 2005-187380/20.
DR   N-PSDB; ADY52599.
XX
PT   Screening oncogene, by producing cDNA library having fusion DNA
PT   comprising cDNA encoding PNT region of TEL connected to downstream of
PT   promoter, introducing library into host cell, expressing fusion DNA and
PT   selecting transformed cells.
XX
PS   Disclosure; Page; 216pp; Japanese.
XX
CC   The invention relates to a novel method for screening an oncogene. The
CC   method comprises producing a cDNA library for a fusion DNA, comprising a
CC   cDNA encoding the PNT region of TEL connected downstream of a vector
CC   promoter, introducing the produced cDNA library into a host cell,
CC   expressing the fusion DNA, selecting the transformed cells and analyzing
CC   the base sequence of the fusion DNA in the transformed cell, and thus
CC   identifying the fusion DNA as an oncogene. TEL is a transcription factor
CC   which belongs to the Ets family and is known to form various genes and
CC   fusion genes via a chromosomal translocation in cancer cells, such as
CC   occurs in some cases of leukemia. The method of the invention may be
CC   useful for screening a substance which suppresses the proliferative
CC   property of a cancer cell, screening a substance which inhibits the
CC   activity of a kinase gene introduced into the cell and screening a
CC   substance for the treatment of cancer. The current sequence is that of
CC   the human transcription factor TEL-Eco-RI adapter-HCK kinase (residues 1-
CC   200) fusion protein of the invention.
XX
SQ   Sequence 465 AA;

  Query Match             100.0%;  Score 43;  DB 9;  Length 465;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        303 QIAEGMAFI 311


RESULT 27
ADY52640
ID   ADY52640 standard; protein; 471 AA.
XX
AC   ADY52640;
XX
DT   19-MAY-2005  (first entry)
XX
DE   Human transcription factor TEL-Eco-RI-HCK kinase fusion protein 4.
XX
```

KW oncogene; cancer; cytostatic; neoplasm; TEL; transcription factor;
KW fusion protein; hck tyrosine kinase; enzyme.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN JP2005052018-A.
XX
PD 03-MAR-2005.
XX
PF 07-AUG-2003; 2003JP-00206534.
XX
PR 07-AUG-2003; 2003JP-00206534.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
DR WPI; 2005-187380/20.
DR N-PSDB; ADY52598.
XX
PT Screening oncogene, by producing cDNA library having fusion DNA
PT comprising cDNA encoding PNT region of TEL connected to downstream of
PT promoter, introducing library into host cell, expressing fusion DNA and
PT selecting transformed cells.
XX
PS Disclosure; Page; 216pp; Japanese.
XX
CC The invention relates to a novel method for screening an oncogene. The
CC method comprises producing a cDNA library for a fusion DNA, comprising a
CC cDNA encoding the PNT region of TEL connected downstream of a vector
CC promoter, introducing the produced cDNA library into a host cell,
CC expressing the fusion DNA, selecting the transformed cells and analyzing
CC the base sequence of the fusion DNA in the transformed cell, and thus
CC identifying the fusion DNA as an oncogene. TEL is a transcription factor
CC which belongs to the Ets family and is known to form various genes and
CC fusion genes via a chromosomal translocation in cancer cells, such as
CC occurs in some cases of leukemia. The method of the invention may be
CC useful for screening a substance which suppresses the proliferative
CC property of a cancer cell, screening a substance which inhibits the
CC activity of a kinase gene introduced into the cell and screening a
CC substance for the treatment of cancer. The current sequence is that of
CC the human transcription factor TEL-Eco-RI adapter-HCK kinase (residues 1-
CC 194) fusion protein of the invention.
XX
SQ Sequence 471 AA;

Query Match 100.0%; Score 43; DB 9; Length 471;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 309 QIAEGMAFI 317

RESULT 28
AEE05159
ID AEE05159 standard; protein; 504 AA.
XX
AC AEE05159;
XX
DT 26-JAN-2006 (first entry)
XX
DE Cancer-associated protein SEQ ID NO:477.
XX
KW cancer; microarray; hybridoma; monoclonal antibody; screening;
KW RNA interference; diagnosis; cytostatic; neoplasm; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2005107396-A2.
XX
PD 17-NOV-2005.
XX
PF 02-MAY-2005; 2005WO-US014965.
XX
PR 30-APR-2004; 2004US-00836956.
XX
PA (CHIR) CHIRON CORP.
XX
PI Morris DW, Malandro MS, Lai A, Tse C, Fattaey A;
XX
DR WPI; 2005-769640/78.
DR N-PSDB; AEE05158.
XX
PT New cancer-associated (CA) polynucleotide comprising at least 10
PT contiguous nucleotides, useful in preparing a composition for diagnosing
PT or treating cancer.
XX
PS Claim 18; SEQ ID NO 477; 148pp; English.
XX
CC The invention relates to new isolated cancer-associated nucleic acid and
CC polypeptide sequences. Also included are the following: a host cell
CC comprising the recombinant nucleic acid or expression vector; an
CC expression vector comprising the isolated nucleic acid; a microarray for
CC detecting a cancer associated (CA) nucleic acid comprising at least one
CC probe comprising at least 10 contiguous nucleotides of the sequence given
CC in the specification; an isolated polypeptide encoded within an open
CC reading frame of a CA sequence; an isolated antibody or its antigen
CC binding fragment that binds to the polypeptide; a hybridoma that produces
CC the monoclonal antibody; a kit for detecting cancer cells comprising the
CC antibody; a kit for diagnosing the presence of cancer in a test sample,
CC comprising at least one polynucleotide that selectively hybridizes to a
CC CA polynucleotide sequence; a method for detecting a presence or an
CC absence of cancer cells in an individual; an electronic library
CC comprising the polynucleotide or polypeptide or its fragment comprising
CC the CA polynucleotide or polypeptide sequence, or its complement; a
CC method of screening for anticancer activity; a method for detecting
CC cancer associated with expression of a polypeptide in a test cell sample;
CC a method for screening for a bioactive agent capable of modulating the
CC activity of a CA protein (CAP), where the CAP is encoded by the nucleic
CC acid sequence given in the specification; a method for diagnosing cancer;
CC a method for treating cancer; and a method for inhibiting expression of a
CC cancer associated (CA) gene in a cell. Inhibiting expression of a cancer
CC associated (CA) gene in a cell comprises contacting a cell expressing a
CC CA gene with a double stranded RNA comprising a sequence capable of
CC hybridizing to a cancer associated (CA) mRNA corresponding to the
CC polynucleotide sequences given in the specification, in an amount
CC sufficient to elicit RNA interference and inhibiting expression of the CA
CC gene in the cell. The double stranded RNA is provided by introducing a
CC short interfering RNA (siRNA) into the cell by transfection,
CC electroporation or microinjection. The double stranded RNA is provided by
CC introducing a short interfering RNA (siRNA) into the cell by an
CC expression vector. The polynucleotides are useful in preparing a
CC composition for diagnosing or treating cancer. The present sequence
CC represents a cancer-associated protein of the invention. Note: This
CC sequence is not shown in the specification but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences/17.11.2005/.
XX
SQ Sequence 504 AA;

Query Match 100.0%; Score 43; DB 9; Length 504;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 342 QIAEGMAFI 350

RESULT 29
AAB99332
ID AAB99332 standard; protein; 505 AA.
XX
AC AAB99332;
XX

DT 23-AUG-2001 (first entry)
XX
DE Human tyrosine kinase Hck protein sequence SEQ ID NO:11.
XX
KW Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck;
KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;
KW Hck signal transduction; human immunodeficiency virus; HIV infection;
KW anticancer.
XX
OS Homo sapiens.
XX
PN WO200132869-A1.
XX
PD 10-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-JP007500.
XX
PR 29-OCT-1999; 99JP-00309957.
XX
PA (SSSE) SSP CO LTD.
XX
PI Taniyama T, Narita T;
XX
DR WPI; 2001-316440/33.
XX
PT New proteins which bind to human tyrosine kinase Hck for promotion of
PT apoptosis and for the elucidation of the mechanism of Hck signal
PT transduction.
XX
PS Example 1; Page 33-35; 45pp; Japanese.
XX
CC The present invention describes a protein, designated HSB-1, which binds
CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids
CC encoding the protein and its derivatives; (2) recombinant vectors
CC containing the nucleic acids; and (3) host cells transformed by the
CC vectors and expressing the protein. HSB-1 has cytostatic activity, binds
CC tyrosine kinase, enhances tumour necrosis factor alpha and promotes
CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism
CC of Hck signal transduction and of the role of Hck in human
CC immunodeficiency virus (HIV) infection. They can be used for the
CC treatment of infections and other diseases with which Hck is associated.
CC They promote the anticancer activity of tumour necrosis factor alpha. The
CC present sequence represents the human tyrosine kinase Hck protein, which
CC is used in an example from the present invention
XX
SQ Sequence 505 AA;

Query Match 100.0%; Score 43; DB 4; Length 505;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 343 QIAEGMAFI 351

RESULT 30
ABW01407
ID ABW01407 standard; protein; 505 AA.
XX
AC ABW01407;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human haematopoietic cell tyrosine kinase protein.
XX
KW Haematopoietic cell; tyrosine kinase; hyperproliferative disorder;
KW cancer; therapy; inflammation; diabetes; viral infection; inflammation;
KW tumour; cytostatic; virucide; antisense therapy; human; enzyme.
XX
OS Homo sapiens.
XX
PN US2003125275-A1.
XX
PD 03-JUL-2003.
XX
PF 04-DEC-2001; 2001US-00007010.
XX
PR 04-DEC-2001; 2001US-00007010.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Borchers AH, Dobie KW;
XX
DR WPI; 2003-811000/76.
DR N-PSDB; AAD62155.
XX
PT New antisense oligonucleotides targeted to nucleic acids encoding
PT hematopoietic cell protein tyrosine kinase, useful for diagnosing or
PT treating cancer (e.g. leukemia), inflammation, diabetes or viral
PT infections.
XX
PS Disclosure; Page 28-30; 59pp; English.
XX
CC The invention relates to a compound targetted to a nucleic acid molecule
CC encoding haematopoietic cell protein tyrosine kinase. The compound
CC inhibits the expression of haematopoietic cell protein tyrosine kinase
CC and it specifically hybridises with the nucleic acid molecule encoding
CC the tyrosine kinase or with at least an 8-nucleobase portion of an active
CC site on the nucleic acid molecule encoding the tyrosine kinase. The
CC antisense compounds are useful for modulating the expression of
CC haematopoietic cell protein tyrosine kinase and treating diseases or
CC conditions associated with the expression of the tyrosine kinase, such as
CC hyperproliferative disorders (e.g. cancer), inflammation, diabetes or a
CC viral infection. The antisense compounds are also useful for diagnostics,
CC therapeutics, prophylaxis, e.g. to prevent or delay infection,
CC inflammation or tumour formation, as research reagents and kits and in
CC distinguishing between functions of various members of a biological
CC pathway. The present sequence is human haematopoietic cell tyrosine
CC kinase protein
XX
SQ Sequence 505 AA;

Query Match 100.0%; Score 43; DB 7; Length 505;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 343 QIAEGMAFI 351

Search completed: June 29, 2006, 09:13:00
Job time : 91.8313 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 09:13:45 ; Search time 13.3373 Seconds
(without alignments)
64.927 Million cell updates/sec

Title: US-10-062-257A-15
Perfect score: 43
Sequence: 1 QIAEGMAFI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	100.0	505	1	TVHUHC	protein-tyrosine k
2	43	100.0	507	1	A39939	protein-tyrosine k
3	43	100.0	509	1	I48845	protein-tyrosine k
4	43	100.0	509	1	OKHULK	protein-tyrosine k
5	40	93.0	503	1	JQ1321	protein-tyrosine k
6	40	93.0	503	1	TVMSHC	protein-tyrosine k
7	40	93.0	505	2	I37206	protein-tyrosine k
8	40	93.0	512	1	A39719	protein-tyrosine k
9	40	93.0	512	1	I56160	protein-tyrosine k
10	40	93.0	512	1	TVHULY	protein-tyrosine k
11	40	93.0	544	2	I51593	protein-tyrosine k
12	39	90.7	499	1	A40092	protein-tyrosine k
13	37	86.0	528	1	TVFVG9	protein-tyrosine k
14	37	86.0	537	1	A45501	protein-tyrosine k
15	37	86.0	541	1	TVCHYS	protein-tyrosine k
16	37	86.0	541	2	S31645	protein-tyrosine k
17	37	86.0	543	1	TVHUYS	protein-tyrosine k
18	37	86.0	941	1	TVMVMD	protein-tyrosine k
19	37	86.0	972	1	TVHUMD	macrophage colony-
20	37	86.0	976	1	TVMSMD	macrophage colony-
21	37	86.0	978	2	S16385	macrophage colony-
22	37	86.0	980	1	TVCTMD	macrophage colony-
23	36	83.7	392	2	S04205	protein-tyrosine k
24	36	83.7	517	2	A43807	protein-tyrosine k
25	36	83.7	517	2	S24547	protein-tyrosine k
26	36	83.7	529	1	TVHUFR	protein-tyrosine k
27	36	83.7	663	1	TVMVRR	protein-tyrosine k
28	36	83.7	790	1	FOMVHZ	gag-kit polyprotei
29	36	83.7	976	1	TVHUKT	protein-tyrosine k
30	36	83.7	977	2	I45877	protein-tyrosine k
31	36	83.7	978	1	A49814	protein-tyrosine k
32	35	81.4	509	1	TVHAST	protein-tyrosine k
33	34	79.1	100	2	I51118	protein-tyrosine k
34	34	79.1	102	2	I51719	protein-tyrosine k
35	34	79.1	103	2	I51725	protein-tyrosine k
36	34	79.1	103	2	I51595	protein-tyrosine k
37	34	79.1	103	2	I51389	protein-tyrosine k
38	34	79.1	103	2	I51399	protein-tyrosine k
39	34	79.1	103	2	I51590	protein-tyrosine k
40	34	79.1	103	2	I51591	protein-tyrosine k
41	34	79.1	103	2	I51715	protein-tyrosine k
42	34	79.1	103	2	I51716	protein-tyrosine k
43	34	79.1	103	2	I51717	protein-tyrosine k
44	34	79.1	103	2	I51718	protein-tyrosine k
45	34	79.1	103	2	I51721	protein-tyrosine k
46	34	79.1	103	2	I51727	protein-tyrosine k
47	34	79.1	103	2	I51102	protein-tyrosine k
48	34	79.1	104	2	I50010	protein-tyrosine k
49	34	79.1	104	2	I51108	protein-tyrosine k
50	34	79.1	104	2	I51115	protein-tyrosine k
51	34	79.1	104	2	I51390	protein-tyrosine k
52	34	79.1	104	2	I51393	protein-tyrosine k
53	34	79.1	104	2	I51394	protein-tyrosine k
54	34	79.1	104	2	I51397	protein-tyrosine k
55	34	79.1	104	2	I51398	protein-tyrosine k
56	34	79.1	104	2	I51722	protein-tyrosine k
57	34	79.1	104	2	I51724	protein-tyrosine k
58	34	79.1	104	2	I51710	protein-tyrosine k
59	34	79.1	104	2	I51594	protein-tyrosine k
60	34	79.1	104	2	I51728	protein-tyrosine k
61	34	79.1	446	2	T34782	probable signal pe
62	34	79.1	484	2	AG1327	L-aspartate oxidas
63	34	79.1	496	2	A56040	protein-tyrosine k
64	34	79.1	523	1	TVFVMT	protein-tyrosine k
65	34	79.1	526	1	OKFVYR	protein-tyrosine k
66	34	79.1	526	1	TVFV60	protein-tyrosine k
67	34	79.1	526	1	TVFVR	protein-tyrosine k
68	34	79.1	526	2	S15582	protein-tyrosine k
69	34	79.1	526	2	S20808	protein-tyrosine k
70	34	79.1	526	2	S26420	protein-tyrosine k
71	34	79.1	532	1	B34104	protein-tyrosine k
72	34	79.1	532	1	A34104	protein-tyrosine k
73	34	79.1	533	1	TVCHS	protein-tyrosine k
74	34	79.1	536	2	S33569	protein-tyrosine k
75	34	79.1	537	1	A43806	protein-tyrosine k
76	34	79.1	539	2	B49114	protein-tyrosine k
77	34	79.1	541	1	A43610	protein-tyrosine k
78	34	79.1	542	1	TVHUSC	protein-tyrosine k
79	34	79.1	545	2	S52313	protein-tyrosine k
80	34	79.1	546	2	S52314	protein-tyrosine k
81	34	79.1	557	1	TVFVS2	protein-tyrosine k
82	34	79.1	568	1	TVFVS1	protein-tyrosine k
83	34	79.1	587	1	TVFVPR	protein-tyrosine k
84	34	79.1	1187	1	TVHUY2	protein-tyrosine k
85	33	76.7	105	2	B54864	mannose/glucose-sp
86	33	76.7	319	2	G97660	probable kinase (A
87	33	76.7	319	2	AB2885	sugar kinase [impo
88	33	76.7	451	1	S49016	protein-tyrosine k
89	33	76.7	484	2	C88264	protein kin-15 [im
90	33	76.7	488	2	I44330	protein-tyrosine k
91	33	76.7	534	1	A44991	protein-tyrosine k
92	33	76.7	534	1	S33568	protein-tyrosine k
93	33	76.7	537	1	TVHUSY	protein-tyrosine k
94	33	76.7	537	2	I51592	protein-tyrosine k
95	33	76.7	542	2	A49114	protein-tyrosine k
96	33	76.7	570	2	T48485	hypothetical prote
97	33	76.7	592	2	T35160	glucose-6-phosphat
98	33	76.7	960	1	JN0677	protein-tyrosine k
99	33	76.7	1091	2	S33596	protein-tyrosine k
100	32	74.4	142	2	JQ1032	insulin-like growt

ALIGNMENTS

RESULT 1
TVHUHC
protein-tyrosine kinase (EC 2.7.1.112) hck - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 10-Nov-1995 #text_change 05-Oct-2004
C;Accession: A27811; A27812; JC1149; C38268; S31103
R;Quintrell, N.; Lebo, R.; Varmus, H.; Bishop, J.M.; Pettenati, M.J.; Le Beau, M.M.; Dia
Mol. Cell. Biol. 7, 2267-2275, 1987
A;Title: Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and
A;Reference number: A27811; MUID:87257942; PMID:3496523
A;Accession: A27811
A;Molecule type: mRNA
A;Residues: 1-505 <QUI>
A;Cross-references: UNIPROT:P08631; UNIPARC:UPI000015C528; GB:M16591
A;Note: the codon given for 3-Cys (TCG) is inconsistent with the authors' translation
R;Ziegler, S.F.; Marth, J.D.; Lewis, D.B.; Perlmutter, R.M.
Mol. Cell. Biol. 7, 2276-2285, 1987
A;Title: Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of h
A;Reference number: A27812; MUID:87257943; PMID:3453117
A;Accession: A27812
A;Molecule type: mRNA
A;Residues: 1-505 <ZIE>
A;Cross-references: UNIPARC:UPI000015C528; GB:M16592; NID:g183913; PIDN:AAA52644.1; PID:
R;Hradetzky, D.; Strebhardt, K.; Ruebsamen-Waigmann, H.
Gene 113, 275-280, 1992
A;Title: The genomic locus of the human hemopoietic-specific cell protein tyrosine kinas
A;Reference number: JC1149; MUID:92241680; PMID:1572549
A;Accession: JC1149
A;Molecule type: DNA
A;Residues: 157-505 <HRA>
A;Cross-references: UNIPARC:UPI0000172589; EMBL:X59741
R;Partanen, J.; Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A;Reference number: A38268; MUID:91062389; PMID:2247464
A;Accession: C38268
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 362-417 <PAR>
A;Cross-references: UNIPARC:UPI000017258A
C;Genetics:
A;Gene: GDB:HCK
A;Cross-references: GDB:119303; OMIM:142370
A;Map position: 20q11-20q12
A;Introns: 207/1; 258/1; 318/1; 343/3; 395/1; 439/1
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;2-505/Product: protein-tyrosine kinase hck #status predicted <MAT>
F;64-112/Domain: SH3 homology <SH3>
F;123-220/Domain: SH2 homology <SH2>
F;239-497/Domain: protein kinase homology <KIN>
F;247-255/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;269/Active site: Lys #status predicted
F;390/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match 100.0%; Score 43; DB 1; Length 505;
  Best Local Similarity 100.0%; Pred. No. 0.58;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 343 QIAEGMAFI 351

RESULT 2
A39939
protein-tyrosine kinase (EC 2.7.1.112) tkl [similarity] - chicken
N;Alternate names: kinase-related transforming protein (tkl); T-cell surface antigen ass
C;Species: Gallus gallus (chicken)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C;Accession: A42126; A39939
R;Chow, L.M.; Ratcliffe, M.J.; Veillette, A.
Mol. Cell. Biol. 12, 1226-1233, 1992
A;Title: tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene.
A;Reference number: A42126; MUID:92186854; PMID:1545804
A;Accession: A42126
A;Molecule type: mRNA
A;Residues: 1-88 <CHO>
A;Cross-references: UNIPARC:UPI0000172587; GB:M85043
A;Experimental source: thymus, spleen
A;Note: sequence extracted from NCBI backbone (NCBIN:88831, NCBIP:88833)
R;Strebhardt, K.; Mullins, J.I.; Bruck, C.; Ruebsamen-Waigmann, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987
A;Title: Additional member of the protein-tyrosine kinase family: the src-and lck-relate
A;Reference number: A39939; MUID:88097370; PMID:3321053
A;Accession: A39939
A;Molecule type: mRNA
A;Residues: 52-507 <STR>
A;Cross-references: UNIPARC:UPI00001713B3; GB:J03579; NID:g212712; PIDN:AAA49081.1; PID:
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;66-114/Domain: SH3 homology <SH3>
F;125-222/Domain: SH2 homology <SH2>
F;241-499/Domain: protein kinase homology <KIN>
F;249-257/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match 100.0%; Score 43; DB 1; Length 507;
  Best Local Similarity 100.0%; Pred. No. 0.58;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 345 QIAEGMAFI 353

RESULT 3
I48845
protein-tyrosine kinase (EC 2.7.1.112) lck, lymphocyte - mouse
N;Alternate names: p56; protein-tyrosine kinase tck
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: I48845; A23639; I57629; I77452
R;Voronova, A.F.; Sefton, B.M.
Nature 319, 682-685, 1986
A;Title: Expression of a new tyrosine protein kinase is stimulated by retrovirus promote
A;Reference number: I48845; MUID:86146842; PMID:3081813
A;Accession: I48845
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-509 <VOR1>
A;Cross-references: UNIPROT:Q91X65; UNIPARC:UPI000000418D; EMBL:X03533; NID:g54813; PIDN
R;Marth, J.D.; Peet, R.; Krebs, E.G.; Perimutter, R.M.
Cell 43, 393-404, 1985
A;Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpres
A;Reference number: A23639; MUID:86079521; PMID:2416464
A;Accession: A23639
A;Molecule type: mRNA
A;Residues: 1-282,'VP',285-509 <MAR>
A;Cross-references: UNIPARC:UPI0000172586; GB:M12056; NID:g198763
A;Note: the sequence is revised in GenBank entry MUSLCK, release 116.0, (PIDN:AAB59674.1
R;Voronova, A.F.; Adler, H.T.; Sefton, B.M.
Mol. Cell. Biol. 7, 4407-4413, 1987
A;Title: Two lck transcripts containing different 5' untranslated regions are present in
A;Reference number: I57629; MUID:88142832; PMID:3501824
A;Accession: I57629
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

A;Residues: 1-11 <VOR>
A;Cross-references: UNIPARC:UPI000016CE9D; GB:M18098; NID:g198766; PIDN:AAA39421.1; PID:
R;Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
Mol. Cell. Biol. 8, 3058-3064, 1988
A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel
A;Reference number: I57636; MUID:89096891; PMID:2850479
A;Accession: I77452
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-35,'VR' <GAR>
A;Cross-references: UNIPARC:UPI000016CE9E; GB:M21511; NID:g198768; PIDN:AAA39422.1; PID:
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming prc
F;68-116/Domain: SH3 homology <SH3>
F;127-224/Domain: SH2 homology <SH2>
F;243-501/Domain: protein kinase homology <KIN>
F;251-259/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;273/Active site: Lys #status predicted
F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 100.0%; Score 43; DB 1; Length 509;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 347 QIAEGMAFI 355

RESULT 4
OKHULK
protein-tyrosine kinase (EC 2.7.1.112) lck - human
N;Alternate names: kinase-related transforming protein (lck)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 05-Oct-2004
C;Accession: JQ0152; S07822; S07200; S01879; S07143; A32797; I57636
R;Rouer, E.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R.
Gene 84, 105-113, 1989
A;Title: Structure of the human lck gene: differences in genomic organisation within src
A;Reference number: JQ0152; MUID:90108697; PMID:2558056
A;Accession: JQ0152
A;Molecule type: DNA
A;Residues: 1-509 <ROU>
A;Cross-references: UNIPROT:P06239; UNIPARC:UPI0000151F17; EMBL:X14053
R;Perlmutter, R.M.; Marth, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, C.B.
J. Cell. Biochem. 38, 117-126, 1988
A;Title: Structure and expression of lck transcripts in human lymphoid cells.
A;Reference number: S07822; MUID:89123626; PMID:3265417
A;Accession: S07822
A;Molecule type: mRNA
A;Residues: 1-86,'P',88-509 <PER>
A;Cross-references: UNIPARC:UPI0000163BD5; EMBL:X13529; NID:g34294; PIDN:CAA31884.1; PID
R;Koga, Y.; Caccia, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikai, Y.; Mak, T.W.
Eur. J. Immunol. 16, 1643-1646, 1986
A;Title: A human T cell-specific cDNA clone (YT16) encodes a protein with extensive homc
A;Reference number: S07200; MUID:87133831; PMID:3493153
A;Accession: S07200
A;Molecule type: mRNA
A;Residues: 1-205,'ASAITPI',212-257,'RCGW',262,'TTT',266,'T',268-281,'AGRLP',287-503,'ST
A;Cross-references: UNIPARC:UPI000016B09E; EMBL:X05027; NID:g36807; PIDN:CAA28691.1; PID
R;Veillette, A.; Foss, F.M.; Sausville, E.A.; Bolen, J.B.; Rosen, N.
Oncogene Res. 1, 357-374, 1987
A;Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other n
A;Reference number: S01879; MUID:88217332; PMID:2835736
A;Accession: S01879
A;Molecule type: mRNA
A;Residues: 368-471,'H',473-509 <VEI>
A;Cross-references: UNIPARC:UPI000016ABFC; EMBL:X06369; NID:g34288; PIDN:CAA29667.1; PID
R;Trevillyan, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Linna, T.J.
Biochim. Biophys. Acta 888, 286-295, 1986
A;Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56(LSTRA).
A;Reference number: S07143; MUID:87000726; PMID:3489486
A;Accession: S07143
A;Molecule type: mRNA
A;Residues: 'A',376-509 <TRE>
A;Cross-references: UNIPARC:UPI000016AF39; EMBL:X04476; NID:g35779; PIDN:CAA28165.1; PII
R;Takadera, T.; Leung, S.; Gernone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.W
Mol. Cell. Biol. 9, 2173-2180, 1989
A;Title: Structure of the two promoters of the human lck gene: differential accumulation
A;Reference number: A32797; MUID:89313764; PMID:2787474
A;Accession: A32797
A;Molecule type: DNA
A;Residues: 1-35 <TAK>
A;Cross-references: UNIPARC:UPI000016ABFF; GB:M26692; NID:g341523; PIDN:AAA59503.1; PID:
R;Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
Mol. Cell. Biol. 8, 3058-3064, 1988
A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel
A;Reference number: I57636; MUID:89096891; PMID:2850479
A;Accession: I57636
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-35,'VR' <RES>
A;Cross-references: UNIPARC:UPI000016ABFD; GB:M21510; NID:g187031; PIDN:AAA59501.1; PID:
C;Comment: Protein tyrosine kinases play important roles in the control of cell growth a
C;Genetics:
A;Gene: GDB:LCK
A;Cross-references: GDB:119360; OMIM:153390
A;Map position: 1p35-1p34.3
A;Introns: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;2-509/Product: protein-tyrosine kinase lck #status predicted <MAT>
F;68-116/Domain: SH3 homology <SH3>
F;127-224/Domain: SH2 homology <SH2>
F;243-501/Domain: protein kinase homology <KIN>
F;251-259/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3,5/Binding site: palmitate (Cys) (covalent) #status predicted
F;273/Active site: Lys #status predicted
F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 100.0%; Score 43; DB 1; Length 509;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 347 QIAEGMAFI 355

RESULT 5
JQ1321
protein-tyrosine kinase (EC 2.7.1.112) hck - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: JQ1321; S18974
R;Okano, Y.; Sugimoto, Y.; Fukuoka, M.; Matsui, A.; Nagata, K.; Nozawa, Y.
Biochem. Biophys. Res. Commun. 181, 1137-1144, 1991
A;Title: Identification of rat cDNA encoding hck tyrosine kinase from megakaryocytes.
A;Reference number: JQ1321; MUID:92109719; PMID:1764064
A;Accession: JQ1321
A;Molecule type: mRNA
A;Residues: 1-503 <OKA>
A;Cross-references: UNIPROT:P50545; UNIPARC:UPI000012C350; GB:S74141; NID:g241436; PIDN:
A;Experimental source: megakaryocyte
R;Rema, V.; Swarup, G.
submitted to the EMBL Data Library, December 1991
A;Reference number: S18974
A;Accession: S18974
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-50,'V',52-204,'R',206-305,'T',307-503 <REM>
A;Cross-references: UNIPARC:UPI0000170BD7; EMBL:X62345; NID:g57581; PIDN:CAA44218.1; PID

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C;Genetics:
A;Gene: hck
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming prc
n kinase
F;62-110/Domain: SH3 homology <SH3>
F;121-218/Domain: SH2 homology <SH2>
F;237-495/Domain: protein kinase homology <KIN>
F;245-253/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;267/Active site: Lys #status predicted
F;388/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             93.0%;  Score 40;  DB 1;  Length 503;
  Best Local Similarity   88.9%;  Pred. No. 2.4;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              ||:||||||
Db        341 QISEGMAFI 349


RESULT 6
TVMSHC
protein-tyrosine kinase (EC 2.7.1.112) hck - mouse
N;Alternate names: kinase-related transforming protein (bmk)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C;Accession: A27282; A39973
R;Klemsz, M.J.; McKercher, S.R.; Maki, R.A.
Nucleic Acids Res. 15, 9600, 1987
A;Title: Nucleotide sequence of the mouse hck gene.
A;Reference number: A27282; MUID:88067781; PMID:3684607
A;Accession: A27282
A;Molecule type: mRNA
A;Residues: 1-503 <KLE>
A;Cross-references: UNIPROT:P08103; UNIPARC:UPI00000018DD; GB:Y00487; NID:g51209; PIDN:C
R;Holtzman, D.A.; Cook, W.D.; Dunn, A.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 8325-8329, 1987
A;Title: Isolation and sequence of a cDNA corresponding to a src-related gene expressed
A;Reference number: A39973; MUID:88068587; PMID:3317404
A;Accession: A39973
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-503 <HOL>
A;Cross-references: UNIPARC:UPI00000018DD; GB:J03023; NID:g192212; PIDN:AAA37305.1; PID:
C;Genetics:
A;Gene: hck
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phc
F;62-110/Domain: SH3 homology <SH3>
F;121-218/Domain: SH2 homology <SH2>
F;237-495/Domain: protein kinase homology <KIN>
F;245-253/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;267/Active site: Lys #status predicted
F;388,499/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             93.0%;  Score 40;  DB 1;  Length 503;
  Best Local Similarity   88.9%;  Pred. No. 2.4;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              ||:||||||
Db        341 QISEGMAFI 349


RESULT 7
I37206
protein-tyrosine kinase (EC 2.7.1.112) blk - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Oct-2004
C;Accession: I37206; S51647
R;Islam, K.B.; Rabbani, H.; Larsson, C.; Sanders, R.; Smith, C.I.
J. Immunol. 154, 1265-1272, 1995
A;Title: Molecular cloning, characterization, and chromosomal localization of a human ly
A;Reference number: I37206; MUID:95123078; PMID:7822795
A;Accession: I37206
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-505 <RES>
A;Cross-references: UNIPROT:P51451; UNIPARC:UPI0000163B22; EMBL:Z33998; NID:g601951; PID
C;Genetics:
A;Gene: GDB:BLK
A;Cross-references: GDB:454114; OMIM:191305
A;Map position: 8p23-8p22
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; tyro
F;65-113/Domain: SH3 homology <SH3>
F;124-220/Domain: SH2 homology <SH2>
F;239-497/Domain: protein kinase homology <KIN>
F;247-255/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;269/Active site: Lys #status predicted

  Query Match             93.0%;  Score 40;  DB 2;  Length 505;
  Best Local Similarity   88.9%;  Pred. No. 2.4;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||:|
Db        343 QIAEGMAYI 351


RESULT 8
A39719
protein-tyrosine kinase (EC 2.7.1.112) lyn, long splice form - mouse
N;Contains: protein-tyrosine kinase lyn, short splice form
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: A39719; B39719; A39750; B39750
R;Stanley, E.; Ralph, S.; McEwen, S.; Boulet, I.; Holtzman, D.A.; Lock, P.; Dunn, A.R.
Mol. Cell. Biol. 11, 3399-3406, 1991
A;Title: Alternatively spliced murine lyn mRNAs encode distinct proteins.
A;Reference number: A39719; MUID:91260683; PMID:1710766
A;Accession: A39719
A;Molecule type: mRNA
A;Residues: 1-512 <STA1>
A;Cross-references: UNIPROT:P25911; UNIPARC:UPI000016CEBE; GB:M64608; NID:g198938; PIDN:
A;Accession: B39719
A;Molecule type: mRNA
A;Residues: 1-24,46-512 <STA2>
A;Cross-references: UNIPARC:UPI0000172584; GB:M64608
R;Yi, T.; Bolen, J.B.; Ihle, J.N.
Mol. Cell. Biol. 11, 2391-2398, 1991
A;Title: Hematopoietic cells express two forms of lyn kinase differing by 21 amino acids
A;Reference number: A39750; MUID:91203857; PMID:2017160
A;Accession: A39750
A;Molecule type: mRNA
A;Residues: 1-76,'F',78-160,'I',162-278,'L',280-390,'I',392-424,'D',426-512 <YI1>
A;Cross-references: UNIPARC:UPI000016CEBF; GB:M57696; NID:g198940; PIDN:AAA39471.1; PID:
A;Accession: B39750
A;Molecule type: mRNA
A;Residues: 1-24,46-76,'F',78-160,'I',162-278,'L',280-390,'I',392-424,'D',426-512 <YI2>
A;Cross-references: UNIPARC:UPI000016CEC0; GB:M57697; NID:g198942; PIDN:AAA39472.1; PID:
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
F;1-512/Product: protein-tyrosine kinase lyn, long splice form #status predicted <MATL>
F;1-24,46-512/Product: protein-tyrosine kinase lyn, short splice form #status predicted
F;70-118/Domain: SH3 homology <SH3>
F;129-226/Domain: SH2 homology <SH2>
F;245-504/Domain: protein kinase homology <KIN>
F;253-261/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
```

```
F;275/Active site: Lys #status predicted
F;397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match            93.0%;  Score 40;  DB 1;  Length 512;
  Best Local Similarity  88.9%;  Pred. No. 2.4;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||:|
Db        350 QIAEGMAYI 358


RESULT 9
I56160
protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - rat
N;Contains: protein-tyrosine kinase lyn, splice form B
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: I56160; I67811; I67812
R;Minoguchi, K.; Nishikata, H.; Siraganian, R.P.
J. Immunol. 150, 222, 1993
A;Title: Bacterially expressed rat p56lyn binds several proteins in rat basophilic leuke
A;Reference number: I56160
A;Accession: I56160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-512 <MIN>
A;Cross-references: UNIPROT:Q07014; UNIPARC:UPI0000167AC2; GB:L14951; NID:g294582; PIDN:
R;Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.
Gene 138, 219-222, 1994
A;Title: The cDNAs encoding two forms of the LYN protein tyrosine kinase are expressed i
A;Reference number: I53715; MUID:94171041; PMID:8125304
A;Accession: I67811
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-230,'L',232-307,'A',309-418,'Y',420-512 <RID1>
A;Cross-references: UNIPARC:UPI0000170BE3; GB:L14782; NID:g294578; PIDN:AAA20944.1; PID:
A;Note: in Genbank entry RATLYNATYR, release 116.0, PIDN:AAA20944.1, the source is desig
A;Accession: I67812
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-24,46-230,'L',232-307,'A',309-418,'Y',420-512 <RID2>
A;Cross-references: UNIPARC:UPI0000170BE2; GB:L14823; NID:g294580; PIDN:AAA20945.1; PID:
A;Note: in Genbank entry RATLYNBTYR, release 116.0, PIDN:AAA20945.1, the source is desig
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
F;2-512/Product: protein-tyrosine kinase lyn, splice form A #status predicted <MATA>
F;2-24,46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <MAT
F;70-118/Domain: SH3 homology <SH3>
F;129-226/Domain: SH2 homology <SH2>
F;245-504/Domain: protein kinase homology <KIN>
F;253-261/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;275/Active site: Lys #status predicted
F;397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match            93.0%;  Score 40;  DB 1;  Length 512;
  Best Local Similarity  88.9%;  Pred. No. 2.4;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||:|
Db        350 QIAEGMAYI 358


RESULT 10
TVHULY
protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - human
N;Contains: protein-tyrosine kinase lyn, splice form B
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 05-Oct-2004
C;Accession: A26719; D38268; PH0949; I53715
R;Yamanashi, Y.; Fukushige, S.I.; Semba, K.; Sukegawa, J.; Miyajima, N.; Matsubara, K.;
Mol. Cell. Biol. 7, 237-243, 1987
A;Title: The yes-related cellular gene lyn encodes a possible tyrosine kinase similar t
A;Reference number: A26719; MUID:87172710; PMID:3561390
A;Accession: A26719
A;Molecule type: mRNA
A;Residues: 1-512 <YAM>
A;Cross-references: UNIPROT:P07948; UNIPARC:UPI000013DACD; GB:M16038; NID:g187268; PIDN
R;Partanen, J.; Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A;Reference number: A38268; MUID:91062389; PMID:2247464
A;Accession: D38268
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 369-424 <PAR>
A;Cross-references: UNIPARC:UPI0000172583
R;Bielke, W.; Ziemieki, A.; Kappos, L.; Miescher, G.C.
Biochem. Biophys. Res. Commun. 186, 1403-1409, 1992
A;Title: Expression of the B cell-associated tyrosine kinase gene lyn in primary neurobl
A;Reference number: PH0949; MUID:92378604; PMID:1510669
A;Accession: PH0949
A;Molecule type: mRNA
A;Residues: 369-424 <BIE>
A;Cross-references: UNIPARC:UPI0000172583
A;Experimental source: neuroblastoma SK-IN cell
R;Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.
Gene 138, 219-222, 1994
A;Title: The cDNAs encoding two forms of the LYN protein tyrosine kinase are expressed i
A;Reference number: I53715; MUID:94171041; PMID:8125304
A;Accession: I53715
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-24,46-512 <RID>
A;Cross-references: UNIPARC:UPI000016AC37; GB:M79321; NID:g187270; PIDN:AAB50019.1; PID:
A;Experimental source: splice form B
C;Genetics:
A;Gene: GDB:LYN
A;Cross-references: GDB:120159; OMIM:165120
A;Map position: 8q13-8qter
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
yrosine-specific protein kinase
F;2-512/Product: protein-tyrosine kinase lyn, splice form A #status predicted <MATA>
F;2-24,46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <MAT
F;70-118/Domain: SH3 homology <SH3>
F;129-226/Domain: SH2 homology <SH2>
F;245-504/Domain: protein kinase homology <KIN>
F;253-261/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;275/Active site: Lys #status predicted
F;397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match            93.0%;  Score 40;  DB 1;  Length 512;
  Best Local Similarity  88.9%;  Pred. No. 2.4;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||:|
Db        350 QIAEGMAYI 358


RESULT 11
I51593
protein-tyrosine kinase (EC 2.7.1.112) yes - Xiphophorus helleri
C;Species: Xiphophorus helleri
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 05-Oct-2004
C;Accession: I51593
R;Hannig, G.; Ottilie, S.; Schartl, M.
Oncogene 6, 361-369, 1991
A;Title: Conservation of structure and expression of the c-yes and fyn genes in lower ve
```

A;Reference number: I51592; MUID:91187435; PMID:1707152
A;Accession: I51593
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-544 <HAN>
A;Cross-references: UNIPROT:P27447; UNIPARC:UPI000013ACBA; EMBL:X54970; NID:g64483; PIDN
C;Genetics:
A;Gene: Xyes
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;99-148/Domain: SH3 homology <SH3>
F;159-256/Domain: SH2 homology <SH2>
F;276-534/Domain: protein kinase homology <KIN>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;306/Active site: Lys #status predicted
F;427,538/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 93.0%; Score 40; DB 2; Length 544;
Best Local Similarity 88.9%; Pred. No. 2.6;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||:|||||
Db 380 QIADGMAFI 388

RESULT 12
A40092
protein-tyrosine kinase (EC 2.7.1.112) blk [validated] - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C;Accession: A40092
R;Dymecki, S.M.; Niederhuber, J.E.; Desiderio, S.V.
Science 247, 332-336, 1990
A;Title: Specific expression of a tyrosine kinase gene, blk, in B lymphoid cells.
A;Reference number: A40092; MUID:90117147; PMID:2404338
A;Accession: A40092
A;Molecule type: mRNA
A;Residues: 1-499 <DYM>
A;Cross-references: UNIPROT:P16277; UNIPARC:UPI0000151F18; GB:M30903; NID:g202076; PIDN:
C;Genetics:
A;Gene: MGI:Blk
A;Cross-references: MGI:88169
A;Map position: 14:28.0
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;59-107/Domain: SH3 homology <SH3>
F;118-214/Domain: SH2 homology <SH2>
F;233-491/Domain: protein kinase homology <KIN>
F;241-249/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;263/Active site: Lys #status predicted

Query Match 90.7%; Score 39; DB 1; Length 499;
Best Local Similarity 77.8%; Pred. No. 3.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|:|||||:|
Db 337 QVAEGMAYI 345

RESULT 13
TVFVG9
protein-tyrosine kinase (EC 2.7.1.112) yes - avian sarcoma virus Y73
C;Species: avian sarcoma virus Y73
A;Note: host Gallus gallus (chicken)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 05-Oct-2004
C;Accession: A00633
R;Kitamura, N.; Kitamura, A.; Toyoshima, K.; Hirayama, Y.; Yoshida, M.
Nature 297, 205-208, 1982
A;Title: Avian sarcoma virus Y73 genome sequence and structural similarity of its transf
A;Reference number: A00633; MUID:82195528; PMID:6281656
A;Accession: A00633
A;Molecule type: genomic RNA
A;Residues: 1-528 <KIT>
A;Cross-references: UNIPARC:UPI000017258B
C;Comment: This protein is synthesized as a gag-yes polyprotein.
C;Genetics:
A;Gene: yes
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; tran
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match 86.0%; Score 37; DB 1; Length 528;
Best Local Similarity 77.8%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||:|||:|
Db 369 QIADGMAYI 377

RESULT 14
A45501
protein-tyrosine kinase (EC 2.7.1.112) yes [similarity] - African clawed frog
N;Alternate names: kinase-related transforming protein (yes)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C;Accession: A45501; S08517
R;Steele, R.E.; Irwin, M.Y.; Knudsen, C.L.; Collett, J.W.; Fero, J.B.
Oncogene Res. 1, 223-233, 1989
A;Title: The yes proto-oncogene is present in amphibians and contributes to the maternal
A;Reference number: A45501
A;Accession: A45501
A;Molecule type: mRNA
A;Residues: 1-537 <STE>
A;Cross-references: UNIPROT:P10936; UNIPARC:UPI0000172588; GB:X14377
R;Steele, R.E.; Irwin, M.Y.; Knudsen, C.L.; Collett, J.W.; Fero, J.B.
submitted to the EMBL Data Library, February 1989
A;Reference number: S08517
A;Accession: S08517
A;Molecule type: mRNA
A;Residues: 1-250,'S',252-537 <ST2>
A;Cross-references: UNIPARC:UPI000013ACB9; EMBL:X14377; NID:g65272; PIDN:CAA32551.1; PID
C;Genetics:
A;Gene: yes
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro
F;92-141/Domain: SH3 homology <SH3>
F;152-249/Domain: SH2 homology <SH2>
F;269-527/Domain: protein kinase homology <KIN>
F;277-285/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;299/Active site: Lys #status predicted
F;420,531/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 86.0%; Score 37; DB 1; Length 537;
Best Local Similarity 77.8%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||:|||:|
Db 373 QIADGMAYI 381

RESULT 15
TVCHYS
protein-tyrosine kinase (EC 2.7.1.112) yes - chicken
N;Alternate names: kinase-related transforming protein yes
C;Species: Gallus gallus (chicken)

```
C;Date: 30-Jun-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004
C;Accession: S03324; S05283; S01689
R;Zheng, X.; Podell, S.; Sefton, B.M.; Kaplan, P.L.
Oncogene 4, 99-104, 1989
A;Title: The sequence of chicken c-yes and p61(c-yes).
A;Reference number: S03324; MUID:89128204; PMID:2464785
A;Accession: S03324
A;Molecule type: mRNA
A;Residues: 1-541 <ZHE>
A;Cross-references: UNIPROT:P09324; UNIPARC:UPI0000047A82; EMBL:X13207
R;Kaplan, P.L.
submitted to the EMBL Data Library, October 1988
A;Reference number: S05283
A;Accession: S05283
A;Molecule type: mRNA
A;Residues: 1-66,'IHPLR',72-81,'Q',83-541 <KAP>
A;Cross-references: UNIPARC:UPI0000171303; EMBL:X13207; NID:g63362; PIDN:CAA31595.1; PID
R;Sudol, M.; Kieswetter, C.; Zhao, Y.H.; Dorai, T.; Wang, L.H.; Hanafusa, H.
Nucleic Acids Res. 16, 9876, 1988
A;Title: Nucleotide sequence of a cDNA for the chick yes proto-oncogene: comparison with
A;Reference number: S01689; MUID:89041591; PMID:3054816
A;Accession: S01689
A;Molecule type: mRNA
A;Residues: 1-237,'S',239-541 <SUD>
A;Cross-references: UNIPARC:UPI000017258C; EMBL:X12461
C;Genetics:
A;Gene: yes
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;2-541/Product: protein-tyrosine kinase yes #status predicted <MAT>
F;96-145/Domain: SH3 homology <SH3>
F;156-253/Domain: SH2 homology <SH2>
F;273-531/Domain: protein kinase homology <KIN>
F;281-289/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;303/Active site: Lys #status predicted
F;424,535/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             86.0%;  Score 37;  DB 1;  Length 541;
  Best Local Similarity   77.8%;  Pred. No. 10;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||:|||:|
Db        377 QIADGMAYI 385


RESULT 16
S31645
protein-tyrosine kinase (EC 2.7.1.112) yes - mouse
N;Alternate names: gene c-yes protein
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1994 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C;Accession: I48318; S31645
R;Klages, S.; Adam, D.; Eiseman, E.; Fargnoli, J.; Dymecki, S.M.; Desiderio, S.V.; Bolen
Oncogene 8, 713-719, 1993
A;Title: Molecular cloning and analysis of cDNA encoding the murine c-yes tyrosine prote
A;Reference number: I48318; MUID:93173515; PMID:8437854
A;Accession: I48318
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-541 <RES>
A;Cross-references: UNIPROT:Q04736; UNIPARC:UPI00000018E2; EMBL:X67677; NID:g50623; PIDN
C;Genetics:
A;Gene: c-yes
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;96-145/Domain: SH3 homology <SH3>
F;156-253/Domain: SH2 homology <SH2>
F;273-531/Domain: protein kinase homology <KIN>
F;281-289/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;303/Active site: Lys #status predicted
F;424,535/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             86.0%;  Score 37;  DB 2;  Length 541;
  Best Local Similarity   77.8%;  Pred. No. 10;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||:|||:|
Db        377 QIADGMAYI 385


RESULT 17
TVHUYS
protein-tyrosine kinase (EC 2.7.1.112) yes-1 - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Oct-2004
C;Accession: A26714
R;Sukegawa, J.; Semba, K.; Yamanashi, Y.; Nishizawa, M.; Miyajima, N.; Yamamoto, T.; Toy
Mol. Cell. Biol. 7, 41-47, 1987
A;Title: Characterization of cDNA clones for the human c-yes gene.
A;Reference number: A26714; MUID:87172733; PMID:2436037
A;Accession: A26714
A;Molecule type: mRNA
A;Residues: 1-543 <SUK>
A;Cross-references: UNIPROT:P07947; UNIPARC:UPI0000062316; GB:M15990; NID:g181267; PIDN:
C;Genetics:
A;Gene: GDB:YES1
A;Cross-references: GDB:119637; OMIM:164880
A;Map position: 18p11.31-18p11.22
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
in kinase
F;2-543/Product: protein-tyrosine kinase yes-1 #status predicted <MAT>
F;98-147/Domain: SH3 homology <SH3>
F;158-255/Domain: SH2 homology <SH2>
F;275-533/Domain: protein kinase homology <KIN>
F;283-291/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;305/Active site: Lys #status predicted
F;426/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             86.0%;  Score 37;  DB 1;  Length 543;
  Best Local Similarity   77.8%;  Pred. No. 10;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||:|||:|
Db        379 QIADGMAYI 387


RESULT 18
TVMVMD
protein-tyrosine kinase (EC 2.7.1.112) fms precursor - feline sarcoma virus (strain McDo
C;Species: feline sarcoma virus
A;Note: host Felis sp. (cat)
C;Date: 27-Nov-1985 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004
C;Accession: A00654
R;Hampe, A.; Gobet, M.; Sherr, C.J.; Galibert, F.
Proc. Natl. Acad. Sci. U.S.A. 81, 85-89, 1984
A;Title: Nucleotide sequence of the feline retroviral oncogene v-fms shows unexpected ho
A;Reference number: A00654; MUID:84119469; PMID:6582485
A;Accession: A00654
A;Molecule type: DNA
A;Residues: 1-941 <HAM>
A;Cross-references: UNIPROT:P00545; UNIPARC:UPI00001725B1
C;Comment: This protein is synthesized as a gag-fms polyprotein.
C;Genetics:
A;Gene: fms
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
```

C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein; otein kinase
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-941/Product: protein-tyrosine kinase fms #status predicted <MAT>
F;24-509/Domain: extracellular #status predicted <EXT>
F;35-86/Domain: immunoglobulin homology <IMM1>
F;120-179/Domain: immunoglobulin homology <IMM2>
F;217-280/Domain: immunoglobulin homology <IMM3>
F;316-381/Domain: immunoglobulin homology <IMM4>
F;410-484/Domain: immunoglobulin homology <IMM5>
F;510-534/Domain: transmembrane #status predicted <TMM>
F;535-941/Domain: intracellular #status predicted <INT>
F;577-915/Domain: protein kinase homology <KIN>
F;585-593/Region: protein kinase ATP-binding motif
F;42-84,127-177,224-278,417-482/Disulfide bonds: #status predicted
F;45,73,94,153,275,286,302,335,410,477,490/Binding site: carbohydrate (Asn) (covalent) #
F;613,630,776/Active site: Lys, Glu, Asp #status predicted
F;781,794/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 86.0%; Score 37; DB 1; Length 941;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|:|:||||:
Db 759 QVAQGMAFL 767

RESULT 19
TVHUMD
macrophage colony-stimulating factor 1 receptor precursor - human
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) csf1r/fms
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
C;Accession: S08123; A24533; I56672; I57648; I59083; I52772
R;Hampe, A.; Shamoon, B.M.; Gobet, M.; Sherr, C.J.; Galibert, F.
Oncogene Res. 4, 9-17, 1989
A;Title: Nucleotide sequence and structural organization of the human FMS proto-oncogene
A;Reference number: S08123; MUID:89239490; PMID:2524025
A;Accession: S08123
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-972 <HAM>
A;Cross-references: UNIPROT:P07333; UNIPARC:UPI000004984A; GB:U63963; EMBL:X14720; NID:g
A;Note: this sequence was submitted to the EMBL Data Library, March 1989
R;Coussens, L.; Van Beveren, C.; Smith, D.; Chen, E.; Mitchell, R.L.; Isacke, C.M.; Verm
Nature 320, 277-280, 1986
A;Title: Structural alteration of viral homologue of receptor proto-oncogene fms at carb
A;Reference number: A24533; MUID:86175013; PMID:2421165
A;Accession: A24533
A;Molecule type: mRNA
A;Residues: 1-53,'A',55-972 <COU>
A;Cross-references: UNIPARC:UPI000016A6AB; GB:J03149
A;Note: the authors translated the codon GCA for residue 54 as Pro
R;Wheeler, E.F.; Roussel, M.F.; Hampe, A.; Walker, M.H.; Fried, V.A.; Look, A.T.; Retter
J. Virol. 59, 224-233, 1986
A;Title: The amino-terminal domain of the v-fms oncogene product includes a functional s
sequences.
A;Reference number: I56672; MUID:86281820; PMID:3525854
A;Accession: I56672
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-16 <RES>
A;Cross-references: UNIPARC:UPI000000060C; GB:M14002; NID:g182676; PIDN:AAA35849.1; PID:
R;Visvader, J.; Verma, I.M.
Mol. Cell. Biol. 9, 1336-1341, 1989
A;Title: Differential transcription of exon 1 of the human c-fms gene in placental troph
A;Reference number: I57648; MUID:89261741; PMID:2524648
A;Accession: I57648
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-16 <RE2>
A;Cross-references: UNIPARC:UPI000000060C; GB:M25786; NID:g349454; PIDN:AAA58421.1; PID:
R;Browning, P.J.; Bunn, H.F.; Cline, A.; Shuman, M.; Nienhuis, A.W.
Proc. Natl. Acad. Sci. U.S.A. 83, 7800-7804, 1986
A;Title: Replacement' of COOH-terminal truncation of v-fms with c-fms sequences markedly
A;Reference number: I59083; MUID:87017034; PMID:3532121
A;Accession: I59083
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 874-972 <RE3>
A;Cross-references: UNIPARC:UPI0000000418; GB:M14193; NID:g182521; PIDN:AAA35834.1; PID:
R;Nienhuis, A.W.; Bunn, H.F.; Turner, P.H.; Gopal, T.V.; Nash, W.G.; O'Brien, S.
Cell 42, 421-428, 1985
A;Title: Expression of the human c-fms proto-oncogene in hematopoietic cells and its del
A;Reference number: I52772; MUID:85282599; PMID:4028159
A;Accession: I52772
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 244-295 <RE4>
A;Cross-references: UNIPARC:UPI0000000409; GB:M11067; NID:g182674; PIDN:AAA35848.1; PID:
C;Genetics:
A;Gene: GDB:CSF1R; FMS
A;Cross-references: GDB:120600; OMIM:164770
A;Map position: 5q33.2-5q33.3
A;Introns: 17/1; 103/1; 198/1; 243/3; 297/1; 361/2; 400/1; 440/2; 504/1; 542/3; 585/1; 6
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
fic protein kinase
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-972/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MAT
F;24-512/Domain: extracellular #status predicted <EXT>
F;35-86/Domain: immunoglobulin homology <IMM1>
F;120-179/Domain: immunoglobulin homology <IMM2>
F;217-280/Domain: immunoglobulin homology <IMM3>
F;316-383/Domain: immunoglobulin homology <IMM4>
F;412-487/Domain: immunoglobulin homology <IMM5>
F;513-537/Domain: transmembrane #status predicted <TMM>
F;538-972/Domain: intracellular #status predicted <INT>
F;580-917/Domain: protein kinase homology <KIN>
F;588-596/Region: protein kinase ATP-binding motif
F;42-84,127-177,224-278,419-485/Disulfide bonds: #status predicted
F;45,73,153,240,275,302,335,353,412,428,480/Binding site: carbohydrate (Asn) (covalent)
F;616,633,778/Active site: Lys, Glu, Asp #status predicted
F;783,796/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 86.0%; Score 37; DB 1; Length 972;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|:|:||||:
Db 761 QVAQGMAFL 769

RESULT 20
TVMSMD
macrophage colony-stimulating factor 1 receptor precursor - mouse
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) csf1r/fms
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
C;Accession: S01880
R;Rothwell, V.M.; Rohrschneider, L.R.
Oncogene Res. 1, 311-324, 1987
A;Title: Murine c-fms cDNA: cloning, sequence analysis and retroviral expression.
A;Reference number: S01880; MUID:88217329; PMID:2966922
A;Accession: S01880
A;Molecule type: mRNA
A;Residues: 1-976 <ROT>
A;Cross-references: UNIPARC:UPI00001725B2; EMBL:X06368
C;Genetics:
A;Gene: fms
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
fic protein kinase
F;1-19/Domain: signal sequence #status predicted <SIG>

```
F;20-976/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MAT
F;20-515/Domain: extracellular #status predicted <EXT>
F;35-86/Domain: immunoglobulin homology <IMM1>
F;120-179/Domain: immunoglobulin homology <IMM2>
F;217-280/Domain: immunoglobulin homology <IMM3>
F;316-381/Domain: immunoglobulin homology <IMM4>
F;410-485/Domain: immunoglobulin homology <IMM5>
F;516-535/Domain: transmembrane #status predicted <TMM>
F;536-976/Domain: intracellular #status predicted <INT>
F;578-914/Domain: protein kinase homology <KIN>
F;586-594/Region: protein kinase ATP-binding motif
F;42-84,127-177,224-278,417-483/Disulfide bonds: #status predicted
F;45,73,302,335,389,410,449,478,491/Binding site: carbohydrate (Asn) (covalent) #status
F;614,631,776/Active site: Lys, Glu, Asp #status predicted
F;781,794/Binding site: magnesium (Asn, Asp) #status predicted

  Query Match             86.0%;  Score 37;  DB 1;  Length 976;
  Best Local Similarity   66.7%;  Pred. No. 19;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |:|:||||:
Db        759 QVAQGMAFL 767


RESULT 21
S16385
macrophage colony-stimulating factor 1 receptor precursor - rat
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) CSF-1R
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004
C;Accession: I60321; S16385
R;Borycki, A.G.; Guillier, M.; Leibovitch, M.P.; Leibovitch, S.A.
Growth Factors 6, 209-218, 1992
A;Title: Molecular cloning of CSF-1 receptor from rat myoblasts. Sequence analysis and r
A;Reference number: I60321; MUID:93001225; PMID:1389227
A;Accession: I60321
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-978 <RES>
A;Cross-references: UNIPROT:Q00495; UNIPARC:UPI000012DDBB; EMBL:X61479; NID:g57543; PIDN
A;Note: in Genbank entry RRCSF1, release 113.0, the source is designated as Rattus rattu
A;Note: submitted to the EMBL Data Library, August 1991
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; kinase-relat
 protein; tyrosine-specific protein kinase
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-978/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MAT
F;20-515/Domain: extracellular #status predicted <EXT>
F;35-86/Domain: immunoglobulin homology <IMM1>
F;120-179/Domain: immunoglobulin homology <IMM2>
F;217-280/Domain: immunoglobulin homology <IMM3>
F;316-381/Domain: immunoglobulin homology <IMM4>
F;410-485/Domain: immunoglobulin homology <IMM5>
F;516-535/Domain: transmembrane #status predicted <TMM>
F;536-978/Domain: intracellular #status predicted <INT>
F;578-915/Domain: protein kinase homology <KIN>
F;586-594/Region: protein kinase ATP-binding motif
F;42-84,127-177,224-278,417-483/Disulfide bonds: #status predicted
F;45,73,302,335,389,410,449,478,491/Binding site: carbohydrate (Asn) (covalent) #status
F;614,631,776/Active site: Lys, Glu, Asp #status predicted
F;781,794/Binding site: magnesium (Asn, Asp) #status predicted

  Query Match             86.0%;  Score 37;  DB 2;  Length 978;
  Best Local Similarity   66.7%;  Pred. No. 19;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |:|:||||:
Db        759 QVAQGMAFL 767


RESULT 22
TVCTMD
macrophage colony-stimulating factor 1 receptor precursor - cat
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) csf1r/fms
C;Species: Felis silvestris catus (domestic cat)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C;Accession: A31636
R;Woolford, J.; McAuliffe, A.; Rohrschneider, L.R.
Cell 55, 965-977, 1988
A;Title: Activation of the feline c-fms proto-oncogene: multiple alterations are require
A;Reference number: A31636; MUID:89077553; PMID:2849512
A;Accession: A31636
A;Molecule type: mRNA
A;Residues: 1-980 <WOO>
A;Cross-references: UNIPROT:P13369; UNIPARC:UPI000012DDB9; EMBL:X03663
C;Genetics:
A;Gene: fms
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
fic protein kinase
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-980/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MAT
F;24-509/Domain: extracellular #status predicted <EXT>
F;35-86/Domain: immunoglobulin homology <IMM1>
F;120-179/Domain: immunoglobulin homology <IMM2>
F;217-280/Domain: immunoglobulin homology <IMM3>
F;316-381/Domain: immunoglobulin homology <IMM4>
F;410-484/Domain: immunoglobulin homology <IMM5>
F;510-534/Domain: transmembrane #status predicted <TMM>
F;535-980/Domain: intracellular #status predicted <INT>
F;577-915/Domain: protein kinase homology <KIN>
F;585-593/Region: protein kinase ATP-binding motif
F;42-84,127-177,224-278,417-482/Disulfide bonds: #status predicted
F;45,73,94,153,275,302,335,410,477,490/Binding site: carbohydrate (Asn) (covalent) #stat
F;613,630,776/Active site: Lys, Glu, Asp #status predicted
F;781,794/Binding site: magnesium (Asn, Asp) #status predicted

  Query Match             86.0%;  Score 37;  DB 1;  Length 980;
  Best Local Similarity   66.7%;  Pred. No. 19;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |:|:||||:
Db        759 QVAQGMAFL 767


RESULT 23
S04205
protein-tyrosine kinase (EC 2.7.1.112) - feline sarcoma virus (fragment)
N;Alternate names: gag-onc fusion protein
C;Species: feline sarcoma virus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S04205
R;Kappes, B.; Ziemiecki, A.; Mueller, R.G.; Theilen, G.H.; Bauer, H.; Barnekow, A.
Oncogene 4, 363-372, 1989
A;Title: The TP1 isolate of feline sarcoma virus encodes a fgr-related oncogene lacking
A;Reference number: S04205; MUID:89201884; PMID:2539576
A;Accession: S04205
A;Molecule type: DNA
A;Residues: 1-392 <KAP>
A;Cross-references: UNIPROT:Q28414; UNIPARC:UPI00001046DB; EMBL:X14842; NID:g1089; PIDN:
C;Superfamily: feline sarcoma virus protein-tyrosine kinase fgr; protein kinase homology
C;Keywords: ATP; autophosphorylation; myristylation; oncogene; phosphoprotein; phosphotr
F;7-104/Domain: SH2 homology <SH2>
F;124-382/Domain: protein kinase homology <KIN>
F;132-140/Region: protein kinase ATP-binding motif
F;154/Active site: Lys #status predicted
F;275,386/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             83.7%;  Score 36;  DB 2;  Length 392;
  Best Local Similarity   66.7%;  Pred. No. 12;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
```

```
              |:|||||::
Db        228 QVAEGMAYM 236


RESULT 24
A43807
protein-tyrosine kinase (EC 2.7.1.112) fgr - mouse
N;Alternate names: kinase-related transforming protein (fgr)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 05-Oct-2004
C;Accession: A43807; S10072; A33127
R;King, F.J.; Cole, M.D.
Oncogene 5, 337-344, 1990
A;Title: Molecular cloning and sequencing of the murine c-fgr gene.
A;Reference number: A43807; MUID:90191719; PMID:2179817
A;Accession: A43807
A;Molecule type: mRNA
A;Residues: 1-517 <KIN>
A;Cross-references: UNIPROT:P14234; UNIPARC:UPI00000041D4; GB:X52191; NID:g50395; PIDN:C
A;Experimental source: monocyte tumor cell line from strain Balb/c
R;Yi, T.L.; Willman, C.L.
Oncogene 4, 1081-1087, 1989
A;Title: Cloning of the murine c-fgr proto-oncogene cDNA and induction of c-fgr expressi
A;Reference number: S10072; MUID:89385605; PMID:2674853
A;Accession: S10072
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-40,'N',42-211,'Q',213-517 <YIA>
A;Cross-references: UNIPARC:UPI0000028C67; EMBL:X16440; NID:g50393; PIDN:CAA34463.1; PID
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;72-121/Domain: SH3 homology <SH3>
F;132-229/Domain: SH2 homology <SH2>
F;249-507/Domain: protein kinase homology <KIXX>
F;257-265/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;279/Active site: Lys #status predicted
F;511/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             83.7%;  Score 36;  DB 2;  Length 517;
  Best Local Similarity   66.7%;  Pred. No. 16;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |:|||||::
Db        353 QVAEGMAYM 361


RESULT 25
S24547
protein-tyrosine kinase (EC 2.7.1.112) fgr - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C;Accession: S24547; PT0200
R;Yue, C.C.
submitted to the EMBL Data Library, December 1990
A;Reference number: S24547
A;Accession: S24547
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-517 <YUE>
A;Cross-references: UNIPROT:Q63206; UNIPARC:UPI00000E7676; EMBL:X57018; NID:g56145; PIDN
R;Yue, C.C.
Mol. Immunol. 28, 399-408, 1991
A;Title: Novel putative protein kinase clones from a rat large granular lymphocyte tumor
A;Reference number: PT0196; MUID:91287726; PMID:2062320
A;Accession: PT0200
A;Molecule type: mRNA
A;Residues: 371-427 <YU2>
A;Cross-references: UNIPARC:UPI00001755F4
A;Experimental source: lymphocyte cell line
C;Genetics:
A;Gene: FGR
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;72-121/Domain: SH3 homology <SH3>
F;132-229/Domain: SH2 homology <SH2>
F;249-507/Domain: protein kinase homology <KIN>
F;257-265/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;279/Active site: Lys #status predicted
F;511/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             83.7%;  Score 36;  DB 2;  Length 517;
  Best Local Similarity   66.7%;  Pred. No. 16;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |:|||||::
Db        353 QVAEGMAYM 361


RESULT 26
TVHUFR
protein-tyrosine kinase (EC 2.7.1.112) fgr - human
N;Alternate names: kinase-related transforming protein (fgr)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 30-Sep-1989 #text_change 05-Oct-2004
C;Accession: A27676; A28353; A24842; A45930; S24306
R;Katamine, S.; Notario, V.; Rao, C.D.; Miki, T.; Cheah, M.S.C.; Tronick, S.R.; Robbins,
Mol. Cell. Biol. 8, 259-266, 1988
A;Title: Primary structure of the human fgr proto-oncogene product p55(c-fgr).
A;Reference number: A27676; MUID:88094395; PMID:3275868
A;Accession: A27676
A;Molecule type: mRNA
A;Residues: 1-529 <REA>
A;Cross-references: UNIPROT:P09769; UNIPARC:UPI000012A72F; GB:M19722; GB:J03429; NID:g18
R;Inoue, K.; Ikawa, S.; Semba, K.; Sukegawa, J.; Yamamoto, T.; Toyoshima, K.
Oncogene 1, 301-304, 1987
A;Title: Isolation and sequencing of cDNA clones homologous to the v-fgr oncogene from a
A;Reference number: A28353; MUID:88262220; PMID:3330776
A;Accession: A28353
A;Molecule type: mRNA
A;Residues: 1-143 <INO>
A;Cross-references: UNIPARC:UPI000017258D
R;Nishizawa, M.; Semba, K.; Yoshida, M.C.; Yamamoto, T.; Sasaki, M.; Toyoshima, K.
Mol. Cell. Biol. 6, 511-517, 1986
A;Title: Structure, expression, and chromosomal location of the human c-fgr gene.
A;Reference number: A24842; MUID:87064334; PMID:3023853
A;Accession: A24842
A;Molecule type: DNA
A;Residues: 111-416 <REB>
A;Cross-references: UNIPARC:UPI000016A8FC; GB:M12724; NID:g182581; PIDN:AAA52762.1; PID:
R;Brickell, P.M.; Patel, M.
Br. J. Cancer 58, 704-709, 1988
A;Title: Structure and expression of c-fgr protooncogene mRNA in Epstein-Barr virus conv
A;Reference number: A45930; MUID:89134667; PMID:2852026
A;Accession: A45930
A;Molecule type: mRNA
A;Residues: 1-177;524-529 <BRI>
A;Cross-references: UNIPARC:UPI000006D52E; UNIPARC:UPI000017258E; GB:M27454
R;Patel, M.; Leevers, S.J.; Brickell, P.M.
Oncogene 5, 201-206, 1990
A;Title: Structure of the complete human c-fgr proto-oncogene and identification of mult
A;Reference number: S24306; MUID:90206622; PMID:1690869
A;Accession: S24306
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-142 <PAT>
A;Cross-references: UNIPARC:UPI0000070DB5; EMBL:X52207; NID:g29893; PIDN:CAA36457.2; PID
C;Genetics:
A;Gene: GDB:FGR
A;Cross-references: GDB:120615; OMIM:164940
A;Map position: 1p36.2-1p36.1
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
```

C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
in kinase
F;84-133/Domain: SH3 homology <SH3>
F;144-241/Domain: SH2 homology <SH2>
F;261-519/Domain: protein kinase homology <KIN>
F;269-277/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3,6/Binding site: palmitate (Cys) (covalent) #status predicted
F;291/Active site: Lys #status predicted
F;523/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match 83.7%; Score 36; DB 1; Length 529;
  Best Local Similarity 66.7%; Pred. No. 16;
  Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
Db 365 QVAEGMAYM 373

RESULT 27
TVMVRR
protein-tyrosine kinase (EC 2.7.1.112) fgr - feline sarcoma virus (strain Gardner-Rashee
C;Species: feline sarcoma virus
A;Note: host Felis sp. (cat)
C;Date: 27-Nov-1985 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: A00653; A03937
R;Naharro, G.; Robbins, K.C.; Reddy, E.P.
Science 223, 63-66, 1984
A;Title: Gene product of v-fgr onc: hybrid protein containing a portion of actin and a t
A;Reference number: A00653; MUID:84097512; PMID:6318314
A;Accession: A00653
A;Molecule type: DNA
A;Residues: 1-663 <NAH>
A;Cross-references: UNIPROT:P00544; UNIPARC:UPI000017101E; GB:X00255; GB:K01487; NID:g61
A;Note: the authors translated the codon GAT for residue 14 as Glu
C;Comment: This protein is synthesized as a gag-fgr polyprotein.
C;Genetics:
A;Gene: fgr
C;Superfamily: feline sarcoma virus protein-tyrosine kinase fgr; protein kinase homology
C;Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; poly
F;1-118/Region: gag polyprotein similarity
F;141-268/Region: actin similarity
F;285-382/Domain: SH2 homology <SH2>
F;402-660/Domain: protein kinase homology <KIN>
F;410-418/Region: protein kinase ATP-binding motif
F;432/Active site: Lys #status predicted

  Query Match 83.7%; Score 36; DB 1; Length 663;
  Best Local Similarity 66.7%; Pred. No. 21;
  Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
Db 506 QVAEGMAYM 514

RESULT 28
FOMVHZ
gag-kit polyprotein precursor - feline sarcoma virus (strain Hardy-Zuckerman 4)
N;Contains: amino end of core protein p30; core protein p12; core protein p15; protein-t
C;Species: feline sarcoma virus
A;Note: host Felis sp. (cat)
C;Date: 04-Dec-1986 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C;Accession: A03936; A00655
R;Besmer, P.; Murphy, J.E.; George, P.C.; Qiu, F.; Bergold, P.J.; Lederman, L.; Snyder J
Nature 320, 415-421, 1986
A;Title: A new acute transforming feline retrovirus and relationship of its oncogene v-k
A;Reference number: A00655; MUID:86175044; PMID:3007997
A;Accession: A03936
A;Molecule type: DNA
A;Residues: 1-790 <BES>
A;Cross-references: UNIPROT:P04322; UNIPARC:UPI000017101D; GB:X03711; NID:g61535; PIDN:C
C;Genetics:
A;Gene: gag-kit
C;Superfamily: feline sarcoma virus gag-kit polyprotein; protein kinase homology
C;Keywords: ATP; core protein; oncogene; phosphotransferase; polyprotein; transforming p
F;1-74/Domain: leader peptide #status predicted <LDP>
F;75-781/Product: gag-kit polyprotein #status predicted <MAT>
F;75-201/Product: core protein p15 #status predicted <C15>
F;202-271/Product: core protein p12 #status predicted <C12>
F;272-414/Product: core protein p30 (fragment) #status predicted <P30>
F;439-783/Domain: protein kinase homology <KIN>
F;447-455/Region: protein kinase ATP-binding motif
F;475/Active site: Lys #status predicted

  Query Match 83.7%; Score 36; DB 1; Length 790;
  Best Local Similarity 66.7%; Pred. No. 24;
  Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
Db 627 QVAKGMAFL 635

RESULT 29
TVHUKT
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - human
N;Alternate names: mast/stem cell growth factor receptor; tyrosine kinase receptor c-kit
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 05-Oct-2004
C;Accession: S01426; PC1015; A41815; B41815; C41815; I37948; I56954; I54336
R;Yarden, Y.; Kuang, W.J.; Yang-Feng, T.; Coussens, L.; Munemitsu, S.; Dull, T.J.; Chen,
EMBO J. 6, 3341-3351, 1987
A;Title: Human proto-oncogene c-kit: a new cell surface receptor tyrosine kinase for an
A;Reference number: S01426; MUID:88111521; PMID:2448137
A;Accession: S01426
A;Molecule type: mRNA
A;Residues: 1-976 <YAR>
A;Cross-references: UNIPROT:P10721; UNIPARC:UPI000003F17D; GB:X06182; NID:g34084; PIDN:C
R;Hu, W.X.; Cornu, F.; Andre, C.; Galibert, F.
Chinese Biochem. J. 7, 618-629, 1991
A;Title: Nucleotide sequece of two neighbouring fragments of human c-kit proto-oncogene
A;Reference number: PC1015
A;Accession: PC1015
A;Molecule type: DNA
A;Residues: 412-713 <HUW>
A;Cross-references: UNIPARC:UPI00001725B3
A;Note: article in Chinese with English abstract
R;Spritz, R.A.; Giebel, L.B.; Holmes, S.A.
Am. J. Hum. Genet. 50, 261-269, 1992
A;Title: Dominant negative and loss of function mutations of the c-kit (mast/stem cell g
A;Reference number: A41815; MUID:92133600; PMID:1370874
A;Accession: A41815
A;Molecule type: DNA
A;Residues: 579-583,'L',585-589 <SPR>
A;Cross-references: UNIPARC:UPI000011F7BF; GB:S78839; NID:g244084; PIDN:AAB21234.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:78839, NCBIP:78842)
A;Note: disease-related mutant from patient with piebaldism
A;Accession: B41815
A;Molecule type: DNA
A;Residues: 637-641,'SPELPW' <SP2>
A;Cross-references: UNIPARC:UPI000011F7C0; GB:S78843; NID:g244086; PIDN:AAB21235.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:78843, NCBIP:78844)
A;Note: disease-related mutant from patient with piebaldism
A;Accession: C41815
A;Molecule type: DNA
A;Residues: 556-560,'GGDKWK' <SP3>
A;Cross-references: UNIPARC:UPI000011F7C1; GB:S78845; NID:g244088; PIDN:AAB21236.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:78845, NCBIP:78846)
A;Note: disease-related mutant from patient with piebaldism
R;Giebel, L.B.; Strunk, K.M.; Holmes, S.A.; Spritz, R.A.
Oncogene 7, 2207-2217, 1992
A;Title: Organization and nucleotide sequence of the human KIT (mast/stem cell growth fa
A;Reference number: I37948; MUID:93064697; PMID:1279499

A;Accession: I37948
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-976 <RES>
A;Cross-references: UNIPARC:UPI000003F17D; EMBL:X69301; NID:g34089; PIDN:CAA49159.1; PID
A;Note: an alternative splice form omitting residues 510-513 is described
R;Yamamoto, K.; Tojo, A.; Aoki, N.; Shibuya, M.
Jpn. J. Cancer Res. 84, 1136-1144, 1993
A;Title: Characterization of the promoter region of the human c-kit proto-oncogene.
A;Reference number: I56954; MUID:94103107; PMID:7506248
A;Accession: I56954
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-22 <RE2>
A;Cross-references: UNIPARC:UPI00000737F3; GB:S67773; NID:g459358; PIDN:AAB29529.1; PID:
R;Spritz, R.A.; Holmes, S.A.; Berg, S.Z.; Nordlund, J.J.; Fukai, K.
Hum. Mol. Genet. 2, 1499-1500, 1993
A;Title: A recurrent deletion in the KIT (mast/stem cell growth factor receptor) proto-c
A;Reference number: I54336; MUID:94061059; PMID:7694728
A;Accession: I54336
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 242-250 <RE3>
A;Cross-references: UNIPARC:UPI0000072C21; GB:S67686; NID:g460545; PIDN:AAD13996.1; PID:
C;Genetics:
A;Gene: GDB:KIT
A;Cross-references: GDB:120117; OMIM:164920
A;Map position: 4q12-4q12
A;Introns: 23/1; 113/1; 207/1; 252/3; 309/1; 372/2; 411/1; 449/2; 514/1; 549/3; 592/1; 6
A;Note: defects in this gene may result in piebaldism
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; kinase-related
rotein; tyrosine-specific protein kinase
F;1-976/Product: protein-tyrosine kinase kit precursor, long form #status predicted <MAT
F;1-509,514-976/Product: protein-tyrosine kinase kit precursor, short form #status predi
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-976/Product: protein-tyrosine kinase kit #status predicted <MAT>
F;23-520/Domain: extracellular #status predicted <EXT>
F;51-99/Domain: immunoglobulin homology <IMM1>
F;129-188/Domain: immunoglobulin homology <IMM2>
F;226-292/Domain: immunoglobulin homology <IMM3>
F;328-394/Domain: immunoglobulin homology <IMM4>
F;423-493/Domain: immunoglobulin homology <IMM5>
F;521-543/Domain: transmembrane #status predicted <TMM>
F;544-976/Domain: intracellular #status predicted <INT>
F;587-931/Domain: protein kinase homology <KIN>
F;595-603/Region: protein kinase ATP-binding motif
F;58-97,136-186,233-290,428-491/Disulfide bonds: #status predicted
F;130,145,283,293,300,320,352,367,463,486/Binding site: carbohydrate (Asn) (covalent) #s
F;623,640,792/Active site: Lys, Glu, Asp #status predicted
F;797,810/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 83.7%; Score 36; DB 1; Length 976;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|:|:||||:
Db 775 QVAKGMAFL 783

RESULT 30
I45877
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - aurochs
C;Species: Bos primigenius (aurochs)
C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 05-Oct-2004
C;Accession: I45877
R;Kubota, T.; Hikono, H.; Sasaki, E.; Sakurai, M.
Gene 141, 305-306, 1994
A;Title: Sequence of a bovine c-kit proto-oncogene cDNA.
A;Reference number: I45877; MUID:94215924; PMID:7512939

A;Accession: I45877
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-977 <KUB>
A;Cross-references: UNIPARC:UPI000012DEB2; GB:D16680; NID:g516659; PIDN:BAA04084.1; PID:
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;329-395/Domain: immunoglobulin homology <IMM>
F;588-932/Domain: protein kinase homology <KIN>

Query Match 83.7%; Score 36; DB 2; Length 977;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|:|:||||:
Db 776 QVAKGMAFL 784

Search completed: June 29, 2006, 09:31:29
Job time : 14.3373 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:39 ; Search time 105.831 Seconds
(without alignments)
78.664 Million cell updates/sec

Title: US-10-062-257A-15
Perfect score: 43
Sequence: 1 QIAEGMAFI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	100.0	249	2	Q9U8V6_EPTBU	Q9u8v6 eptatretus
2	43	100.0	368	2	Q3TLX4_MOUSE	Q3tlx4 mus musculu
3	43	100.0	379	2	Q4FZR6_RAT	Q4fzr6 rattus norv
4	43	100.0	503	1	HCK_MACFA	Q95m30 macaca fasc
5	43	100.0	507	1	LCK_CHICK	P42683 gallus gall
6	43	100.0	508	1	LCK_AOTNA	Q5pxs1 aotus nancy
7	43	100.0	508	1	LCK_HUMAN	P06239 homo sapien
8	43	100.0	508	1	LCK_MOUSE	P06240 mus musculu
9	43	100.0	509	2	Q7RTZ3_HUMAN	Q7rtz3 homo sapien
10	43	100.0	509	2	Q95M32_9PRIM	Q95m32 hylobates s
11	43	100.0	509	2	Q3ZCM0_BOVIN	Q3zcm0 bos taurus
12	43	100.0	516	2	Q573B4_HUMAN	Q573b4 homo sapien
13	43	100.0	525	1	HCK_HUMAN	P08631 homo sapien
14	43	100.0	570	2	Q504R5_HUMAN	Q504r5 homo sapien
15	43	100.0	580	2	Q2VPE2_HUMAN	Q2vpe2 homo sapien
16	42	97.7	249	2	Q9PVV0_LAMRE	Q9pvv0 lampetra re
17	40	93.0	322	2	Q4RR72_TETNG	Q4rr72 tetraodon n
18	40	93.0	485	2	Q5TYU7_BRARE	Q5tyu7 brachydanio
19	40	93.0	488	2	O13064_XENLA	O13064 xenopus lae
20	40	93.0	491	2	Q3U6Q5_MOUSE	Q3u6q5 mus musculu
21	40	93.0	491	2	Q8CEI0_MOUSE	Q8cei0 mus musculu
22	40	93.0	492	2	Q5ZMB9_CHICK	Q5zmb9 gallus gall
23	40	93.0	502	1	HCK_RAT	P50545 rattus norv
24	40	93.0	502	2	Q9DDK6_SALSA	Q9ddk6 salmo salar
25	40	93.0	503	2	Q3UD17_MOUSE	Q3ud17 m bone marr
26	40	93.0	503	2	Q6AYV7_RAT	Q6ayv7 rattus norv
27	40	93.0	504	1	BLK_HUMAN	P51451 homo sapien
28	40	93.0	505	2	Q96IN1_HUMAN	Q96in1 homo sapien
29	40	93.0	510	2	Q66I04_BRARE	Q66i04 brachydanio
30	40	93.0	511	1	LYN_HUMAN	P07948 homo sapien
31	40	93.0	511	1	LYN_MOUSE	P25911 mus musculu
32	40	93.0	511	1	LYN_RAT	Q07014 rattus norv
33	40	93.0	511	2	Q4RL31_TETNG	Q4rl31 tetraodon n
34	40	93.0	512	2	Q3TCS3_MOUSE	Q3tcs3 m nod-deriv
35	40	93.0	523	1	HCK_MOUSE	P08103 mus musculu
36	40	93.0	543	1	YES_XIPHE	P27447 xiphophorus
37	40	93.0	546	2	Q6EWH1_BRARE	Q6ewh1 brachydanio
38	40	93.0	563	2	Q4RN20_TETNG	Q4rn20 tetraodon n
39	40	93.0	582	2	Q6NUK7_HUMAN	Q6nuk7 homo sapien
40	39	90.7	498	1	BLK_MOUSE	P16277 mus musculu
41	39	90.7	499	2	Q3TAT8_MOUSE	Q3tat8 mus musculu
42	39	90.7	499	2	Q4KM97_RAT	Q4km97 rattus norv
43	39	90.7	499	2	Q8K2M8_MOUSE	Q8k2m8 mus musculu
44	38	88.4	503	2	Q6TPQ4_BRARE	Q6tpq4 brachydanio
45	38	88.4	516	2	Q4TEC2_TETNG	Q4tec2 tetraodon n
46	38	88.4	1116	2	Q4TEC1_TETNG	Q4tec1 tetraodon n
47	37	86.0	308	2	Q9U8V0_EPTBU	Q9u8v0 eptatretus
48	37	86.0	489	2	Q6AXQ3_RAT	Q6axq3 rattus norv
49	37	86.0	508	1	LCK_SAISC	Q95kr7 saimiri sci
50	37	86.0	528	1	YES_AVISY	P00527 avian sarco
51	37	86.0	536	1	YES_XENLA	P10936 xenopus lae
52	37	86.0	537	2	Q498G3_XENLA	Q498g3 xenopus lae
53	37	86.0	537	2	Q640S9_XENTR	Q640s9 xenopus tro
54	37	86.0	537	2	Q6PF70_XENLA	Q6pf70 xenopus lae
55	37	86.0	538	1	YES_CANFA	Q28923 canis famil
56	37	86.0	540	1	YES_CHICK	P09324 gallus gall
57	37	86.0	540	1	YES_MOUSE	Q04736 mus musculu
58	37	86.0	541	2	Q3TJI7_MOUSE	Q3tji7 mus musculu
59	37	86.0	541	2	Q8C762_MOUSE	Q8c762 mus musculu
60	37	86.0	541	2	Q8CBP1_MOUSE	Q8cbp1 mus musculu
61	37	86.0	541	2	Q99PW1_RAT	Q99pw1 rattus norv
62	37	86.0	542	1	YES_HUMAN	P07947 homo sapien
63	37	86.0	543	2	Q5REC4_PONPY	Q5rec4 pongo pygma
64	37	86.0	922	2	Q3U4N8_MOUSE	Q3u4n8 mus musculu
65	37	86.0	945	2	Q3U1X4_MOUSE	Q3u1x4 mus musculu
66	37	86.0	968	2	Q4W447_HORSE	Q4w447 equus cabal
67	37	86.0	972	1	CSF1R_HUMAN	P07333 homo sapien
68	37	86.0	972	2	Q86VW7_HUMAN	Q86vw7 homo sapien
69	37	86.0	977	1	CSF1R_MOUSE	P09581 mus musculu
70	37	86.0	977	2	Q3U1Y3_MOUSE	Q3u1y3 mus musculu
71	37	86.0	977	2	Q3U210_MOUSE	Q3u210 mus musculu
72	37	86.0	977	2	Q3U3P1_MOUSE	Q3u3p1 m nod-deriv
73	37	86.0	977	2	Q3U3W0_MOUSE	Q3u3w0 mus musculu
74	37	86.0	977	2	Q3UKC6_MOUSE	Q3ukc6 mus musculu
75	37	86.0	977	2	Q6NXV8_MOUSE	Q6nxv8 mus musculu
76	37	86.0	978	1	CSF1R_RAT	Q00495 rattus norv
77	37	86.0	978	1	KFMS_FSVMD	P00545 feline sarc
78	37	86.0	980	1	CSF1R_FELCA	P13369 felis silve
79	37	86.0	1055	1	ACK1_MOUSE	O54967 mus musculu
80	36	83.7	68	2	Q5FYR9_HORSE	Q5fyr9 equus cabal
81	36	83.7	323	2	Q9EQ22_RAT	Q9eq22 rattus norv
82	36	83.7	370	1	KIT_FSVHZ	P04048 feline sarc
83	36	83.7	392	2	Q28414_FLV	Q28414 feline sarc
84	36	83.7	496	2	O93411_XENLA	O93411 xenopus lae
85	36	83.7	498	2	Q5FW27_XENTR	Q5fw27 xenopus tro
86	36	83.7	516	2	Q6R1Y5_ASTMI	Q6r1y5 asterina mi
87	36	83.7	517	1	FGR_MOUSE	P14234 mus musculu
88	36	83.7	517	2	Q63206_RAT	Q63206 rattus norv
89	36	83.7	517	2	Q6GTF2_MOUSE	Q6gtf2 m gardner-r
90	36	83.7	517	2	Q6P6U0_RAT	Q6p6u0 rattus norv
91	36	83.7	517	2	Q8BGM0_MOUSE	Q8bgm0 m adult mal
92	36	83.7	529	1	FGR_HUMAN	P09769 homo sapien
93	36	83.7	545	1	FGR_FSVGR	P00544 feline sarc
94	36	83.7	548	2	Q82M92_STRAW	Q82m92 streptomyce
95	36	83.7	604	2	Q2S794_9GAMM	Q2s794 hahella che
96	36	83.7	724	2	Q9MYN0_BOVIN	Q9myn0 bos taurus
97	36	83.7	742	2	Q3ULJ6_MOUSE	Q3ulj6 mus musculu
98	36	83.7	898	2	Q5D4S1_HORSE	Q5d4s1 equus cabal
99	36	83.7	923	2	O97745_PIG	O97745 sus scrofa
100	36	83.7	939	2	Q5FYR8_HORSE	Q5fyr8 equus cabal

ALIGNMENTS

```
RESULT 1
Q9U8V6_EPTBU
ID   Q9U8V6_EPTBU   PRELIMINARY;   PRT;   249 AA.
AC   Q9U8V6;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 28.
DE   Src-like A (Fragment).
OS   Eptatretus burgeri (Inshore hagfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
OC   Myxinidae; Eptatretinae; Eptatretus.
OX   NCBI_TaxID=7764;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20020330; PubMed=10552041;
RA   Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
RT   "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey:
RT   isoform duplications around the divergence of cyclostomes and
RT   gnathostomes.";
RL   J. Mol. Evol. 49:601-608(1999).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB025546; BAA84736.1; -; mRNA.
DR   HSSP; P06239; 1QPC.
DR   SMR; Q9U8V6; 1-249.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   249 AA;  28636 MW;  D7F37EE197EA580C CRC64;

  Query Match             100.0%;  Score 43;  DB 2;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db         87 QIAEGMAFI 95


RESULT 2
Q3TLX4_MOUSE
ID   Q3TLX4_MOUSE   PRELIMINARY;   PRT;   368 AA.
AC   Q3TLX4;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched
DE   library, clone:G830026O06 product:lymphocyte protein tyrosine kinase,
DE   full insert sequence. (Fragment).
GN   Name=Lck;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
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RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC ---
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC ---
DR EMBL; AK166263; BAE38668.1; -; mRNA.
DR MGI; MGI:96756; Lck.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF07714; Pkinase_Tyr; 1.
DR Pfam; PF00017; SH2; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50001; SH2; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW Tyrosine-protein kinase.
FT NON_TER 1 1
SQ SEQUENCE 368 AA; 42018 MW; 7AB6AE53AF1A5059 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIAEGMAFI 9
|||||||||
Db 206 QIAEGMAFI 214

RESULT 3
Q4FZR6_RAT
ID Q4FZR6_RAT PRELIMINARY; PRT; 379 AA.
AC Q4FZR6;
DT 30-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 30-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Lck_mapped protein (Fragment).
GN Name=Lck_mapped;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

```
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC099218; AAH99218.1; -; mRNA.
DR   SMR; Q4FZR6; 2-379.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   379 AA;  43336 MW;  7CDEB573BAFB53AB CRC64;

  Query Match             100.0%;  Score 43;  DB 2;  Length 379;
  Best Local Similarity   100.0%;  Pred. No. 3.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        217 QIAEGMAFI 225


RESULT 4
HCK_MACFA
ID   HCK_MACFA      STANDARD;      PRT;   503 AA.
AC   Q95M30;
DT   23-JAN-2002, integrated into UniProtKB/Swiss-Prot.
DT   26-SEP-2003, sequence version 2.
DT   07-MAR-2006, entry version 39.
DE   Tyrosine-protein kinase HCK (EC 2.7.1.112) (p56-HCK) (Hemopoietic cell
DE   kinase).
GN   Name=HCK;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Picard C.;
RL   Thesis (2001), University of Marseille, France.
CC   -!- FUNCTION: May serve as part of a signaling pathway coupling the Fc
CC       receptor to the activation of the respiratory burst. May also
CC       contribute to neutrophil migration and may regulate the
CC       degranulation process of neutrophils (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBCELLULAR LOCATION: Membrane; peripheral membrane protein (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ320181; CAC44031.1; -; mRNA.
DR   HSSP; P08631; 4HCK.
DR   SMR; Q95M30; 58-503.
DR   InterPro; IPR000108; Neu_cyt_fact_2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00499; P67PHOX.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; SH2 domain;
KW   SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       By similarity.
FT   CHAIN         1    503       Tyrosine-protein kinase HCK.
FT                                /FTId=PRO_0000088103.
FT   DOMAIN       55    115       SH3.
FT   DOMAIN      121    218       SH2.
FT   DOMAIN      239    492       Protein kinase.
FT   NP_BIND     245    253       ATP (By similarity).
FT   ACT_SITE    358    358       Proton acceptor (By similarity).
FT   BINDING     267    267       ATP (By similarity).
FT   MOD_RES     388    388       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   503 AA;  56965 MW;  B61F9322D2DE3436 CRC64;

  Query Match             100.0%;  Score 43;  DB 1;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
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Db        341 QIAEGMAFI 349


RESULT 5
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LCK_CHICK
ID   LCK_CHICK      STANDARD;      PRT;   507 AA.
AC   P42683; Q53WS8;
DT   01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1995, sequence version 1.
DT   07-MAR-2006, entry version 47.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (Protein-
DE   tyrosine kinase C-TKL) (p56tkl).
GN   Name=LCK;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Spleen;
RA   Gaertner T., Khnel H., Strebhardt K., Ruebsamen-Waigmann H.;
RL   Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 1-88.
RX   MEDLINE=92186854; PubMed=1545804;
RA   Chow L., Ratcliffe M., Veillette A.;
RT   "tkl is the avian homolog of the mammalian lck tyrosine protein kinase
RT   gene.";
RL   Mol. Cell. Biol. 12:1226-1233(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 46-507.
RX   MEDLINE=88097370; PubMed=3321053;
RA   Strebhardt K., Mullins J.I., Bruck C., Ruebsamen-Waigmann H.;
RT   "Additional member of the protein-tyrosine kinase family: the src- and
RT   lck-related protooncogene c-tkl.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:8778-8782(1987).
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD4, CD8 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Bound to the cytoplasmic domain of either
CC       CD4 or CD8 (By similarity).
CC   -!- PTM: Phosphorylated on Tyr-503. This phosphorylation downregulates
CC       catalytic activity. Phosphorylated on Tyr-392 either by itself or
CC       another kinase, leading to increased enzymatic activity.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X60380; CAA42930.1; -; mRNA.
DR   EMBL; M85043; AAA49003.1; -; mRNA.
DR   EMBL; J03579; AAA49081.1; ALT_INIT; mRNA.
DR   HSSP; P06239; 3LCK.
DR   SMR; P42683; 63-507.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    507       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088128.
FT   DOMAIN       59    119       SH3.
FT   DOMAIN      125    222       SH2.
FT   DOMAIN      243    496       Protein kinase.
FT   NP_BIND     249    257       ATP (By similarity).
FT   ACT_SITE    362    362       Proton acceptor (By similarity).
FT   BINDING     271    271       ATP (By similarity).
FT   MOD_RES     392    392       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     503    503       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   507 AA;  58009 MW;  BC83C4FA891B6170 CRC64;

  Query Match             100.0%;  Score 43;  DB 1;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        345 QIAEGMAFI 353


RESULT 6
LCK_AOTNA
ID   LCK_AOTNA      STANDARD;      PRT;   508 AA.
AC   Q5PXS1;
DT   08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT   08-NOV-2005, sequence version 3.
DT   07-MAR-2006, entry version 13.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Aotus nancymaae (Ma's night monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=37293;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Perez-Quintero L.A., Vernot J.P.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Tyrosine kinase that plays an essential role for the
CC       selection and maturation of developing T-cell in the thymus and in
CC       mature T-cell function. Is constitutively associated with the
CC       cytoplasmic portions of the CD4 and CD8 surface receptors and
CC       plays a key role in T-cell antigen receptor(TCR)-linked signal
CC       transduction pathways. Association of the TCR with a peptide
CC       antigen-bound MHC complex facilitates the interaction of CD4 and
CC       CD8 with MHC class II and class I molecules, respectively, and
CC       thereby recruits the associated LCK to the vicinity of the TCR/CD3
CC       complex. LCK then phosphorylates tyrosines residues within the
CC       immunoreceptor tyrosines-based activation motifs (ITAMs) in the
CC       cytoplasmic tails of the TCRgamma chains and CD3 subunits,
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CC       initiating the TCR/CD3 signaling pathway. In addition, contributes
CC       to signaling by other receptor molecules. Associates directly with
CC       the cytoplasmic tail of CD2, and upon engagement of the CD2
CC       molecule, LCK undergoes hyperphosphorylation and activation. Also
CC       plays a role in the IL2 receptor-linked signaling pathway that
CC       controls T-cell proliferative response. Binding of IL2 to its
CC       receptor results in increased activity of LCK. Is expressed at all
CC       stages of thymocyte development and is required for the regulation
CC       of maturation events that are governed by both pre-TCR and mature
CC       alpha beta TCR (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface
CC       receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also
CC       binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to
CC       other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds
CC       to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes
CC       through its SH3 domain and to the tyrosine phosphorylated form of
CC       KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.
CC       Interacts with phosphorylated LIME1. Interacts with CBLB (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.
CC       Present in lipid rafts in an unactive form (By similarity).
CC   -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.
CC       Interaction is regulated by Ser-58 phosphorylation (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY821852; AAV70114.2; -; mRNA.
DR   SMR; Q5PXS1; 64-508.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;
KW   SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       Probable.
FT   CHAIN         1    508       Proto-oncogene tyrosine-protein kinase
FT                                LCK.
FT                                /FTId=PRO_0000088123.
FT   DOMAIN       60    120       SH3.
FT   DOMAIN      126    223       SH2.
FT   DOMAIN      244    497       Protein kinase.
FT   NP_BIND     250    258       ATP (By similarity).
FT   REGION        1     71       Interactions with CD4 and CD8 (By
FT                                similarity).
FT   ACT_SITE    363    363       Proton acceptor (By similarity).
FT   BINDING     272    272       ATP (By similarity).
FT   MOD_RES     393    393       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     504    504       Phosphotyrosine (negative regulation) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   LIPID         4      4       S-palmitoyl cysteine (By similarity).
SQ   SEQUENCE   508 AA;  58041 MW;  8B61951BC192A3A4 CRC64;

  Query Match             100.0%;  Score 43;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        346 QIAEGMAFI 354


RESULT 7
LCK_HUMAN
ID   LCK_HUMAN      STANDARD;      PRT;   508 AA.
AC   P06239; P07100; Q12850; Q13152; Q5TDH8; Q5TDH9; Q96DW4; Q9NYT8;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1994, sequence version 5.
DT   07-MAR-2006, entry version 87.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase) (LSK) (T cell-
DE   specific protein-tyrosine kinase).
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=87133831; PubMed=3493153;
RA   Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
RA   Mak T.W.;
RT   "A human T cell-specific cDNA clone (YT16) encodes a protein with
RT   extensive homology to a family of protein-tyrosine kinases.";
RL   Eur. J. Immunol. 16:1643-1646(1986).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=89123626; PubMed=3265417;
RA   Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F.,
RA   Wilson C.B.;
RT   "Structure and expression of lck transcripts in human lymphoid
RT   cells.";
RL   J. Cell. Biochem. 38:117-126(1988).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=90108697; PubMed=2558056; DOI=10.1016/0378-1119(89)90144-3;
RA   Rouer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
RA   Benarous R.;
RT   "Structure of the human lck gene: differences in genomic organisation
RT   within src-related genes affect only N-terminal exons.";
RL   Gene 84:105-113(1989).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA], VARIANTS LEU-27; GLN-LYS-PRO-231 INS;
RP   VAL-352 AND LEU-446, AND PHOSPHORYLATION SITES TYR-393 AND TYR-504.
RC   TISSUE=Leukemia;
RX   MEDLINE=94187714; PubMed=8139546;
RA   Wright D.D., Sefton B.M., Kamps M.P.;
RT   "Oncogenic activation of the Lck protein accompanies translocation of
RT   the LCK gene in the human HSB2 T-cell leukemia.";
RL   Mol. Cell. Biol. 14:2429-2437(1994).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM SHORT), AND ALTERNATIVE SPLICING.
RC   TISSUE=Leukemic T-cell;
RX   MEDLINE=96085119; PubMed=7495859; DOI=10.1016/0167-4781(95)00162-A;
RA   Vogel L.B., Arthur R., Fujita D.J.;
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RT "An aberrant lck mRNA in two human T-cell lines.";
RL Biochim. Biophys. Acta 1264:168-172(1995).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG Human chromosome 1 international sequencing consortium;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX MEDLINE=89096891; PubMed=2850479;
RA Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT "Structure of the murine lck gene and its rearrangement in a murine
RT lymphoma cell line.";
RL Mol. Cell. Biol. 8:3058-3064(1988).
RN [9]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX MEDLINE=89313764; PubMed=2787474;
RA Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
RA Miyamoto N.G., Mak T.W.;
RT "Structure of the two promoters of the human lck gene: differential
RT accumulation of two classes of lck transcripts in T cells.";
RL Mol. Cell. Biol. 9:2173-2180(1989).
RN [10]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 13-508.
RC TISSUE=Peripheral blood lymphocyte;
RX MEDLINE=20462621; PubMed=11009097;
RX DOI=10.1002/1521-4141(200009)30:9<2632::AID-IMMU2632>3.0.CO;2-C;
RA Boncristiano M., Majolini M.B., D'Elios M.M., Pacini S., Valensin S.,
RA Ulivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,
RA Baldari C.T.;
RT "Defective recruitment and activation of ZAP-70 in common variable
RT immunodeficiency patients with T cell defects.";
RL Eur. J. Immunol. 30:2632-2638(2000).
RN [11]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 367-508.
RX MEDLINE=88217332; PubMed=2835736;
RA Veillette A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.;
RT "Expression of the lck tyrosine kinase gene in human colon carcinoma
RT and other non-lymphoid human tumor cell lines.";
RL Oncogene Res. 1:357-374(1987).
RN [12]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 374-508.
RX MEDLINE=87000726; PubMed=3489486; DOI=10.1016/0167-4889(86)90228-4;
RA Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
RA Linna T.J.;
RT "Human T lymphocytes express a protein-tyrosine kinase homologous to
RT p56LSTRA.";
RL Biochim. Biophys. Acta 888:286-295(1986).
RN [13]
RP PHOSPHORYLATION SITE TYR-504.
RX MEDLINE=92347326; PubMed=1639064;
RA Bergman M., Mustelin T., Oetken C., Partanen J., Flint N.A.,
RA Amrein K.E., Autero M., Burn P., Alitalo K.;
RT "The human p50csk tyrosine kinase phosphorylates p56lck at Tyr-505 and
RT down regulates its catalytic activity.";
RL EMBO J. 11:2919-2924(1992).
RN [14]
RP INTERACTION WITH PI3K.
RX MEDLINE=94067101; PubMed=7504174;
RA Vogel L.B., Fujita D.J.;
RT "The SH3 domain of p56lck is involved in binding to
RT phosphatidylinositol 3'-kinase from T lymphocytes.";
RL Mol. Cell. Biol. 13:7408-7417(1993).
RN [15]
RP INTERACTION WITH KHDRBS1.
RX MEDLINE=95155308; PubMed=7852312; DOI=10.1074/jbc.270.6.2506;
RA Vogel L.B., Fujita D.J.;
RT "p70 phosphorylation and binding to p56lck is an early event in
RT interleukin-2-induced onset of cell cycle progression in T-
RT lymphocytes.";
RL J. Biol. Chem. 270:2506-2511(1995).
RN [16]
RP INTERACTION WITH SQSTM1, AND MUTAGENESIS OF SER-58 AND ARG-153.
RX PubMed=8618896;
RA Park I., Chung J., Walsh C.T., Yun Y., Strominger J.L., Shin J.;
RT "Phosphotyrosine-independent binding of a 62-kDa protein to the src
RT homology 2 (SH2) domain of p56lck and its regulation by
RT phosphorylation of Ser-59 in the lck unique N-terminal region.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:12338-12342(1995).
RN [17]
RP INTERACTION WITH HIV-1 NEF.
RX MEDLINE=96386556; PubMed=8794306;
RA Greenway A.L., Azad A., Mills J., McPhee D.A.;
RT "Human immunodeficiency virus type 1 Nef binds directly to LCK and
RT mitogen-activated protein kinase, inhibiting kinase activity.";
RL J. Virol. 70:6701-6708(1996).
RN [18]
RP REVIEW.
RX PubMed=10848956;
RA Isakov N., Biesinger B.;
RT "Lck protein tyrosine kinase is a key regulator of T-cell activation
RT and a target for signal intervention by Herpesvirus saimiri and other
RT viral gene products.";
RL Eur. J. Biochem. 267:3413-3421(2000).
RN [19]
RP SUBCELLULAR LOCATION.
RX PubMed=12218089;
RA Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT protein/phosphoprotein associated with glycolipid-enriched
RT microdomains in lipid rafts in resting T cells.";
RL J. Immunol. 169:2813-2817(2002).
RN [20]
RP MASS SPECTROMETRY.
RC TISSUE=Mammary cancer;
RX MEDLINE=21829512; PubMed=11840567;
RX DOI=10.1002/1615-9861(200202)2:2<212::AID-PROT212>3.0.CO;2-H;
RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
RA Zvelebil M.J.;
RT "Cluster analysis of an extensive human breast cancer cell line
RT protein expression map database.";
RL Proteomics 2:212-223(2002).
RN [21]
RP INTERACTION WITH LIME1.
RX PubMed=14610046; DOI=10.1084/jem.20031484;
RA Brdickova N., Brdicka T., Angelisova P., Horvath O., Spicka J.,
RA Hilgert I., Paces J., Simeoni L., Kliche S., Merten C., Schraven B.,
RA Horejsi V.;
RT "LIME: a new membrane raft-associated adaptor protein involved in CD4
RT and CD8 coreceptor signaling.";
RL J. Exp. Med. 198:1453-1462(2003).

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RN   [22]
RP   INTERACTION WITH LIME1.

  Query Match             100.0%;  Score 43;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        346 QIAEGMAFI 354


RESULT 8
LCK_MOUSE
ID   LCK_MOUSE      STANDARD;      PRT;   508 AA.
AC   P06240; Q61794; Q61795; Q62320; Q91X65;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   25-OCT-2005, sequence version 3.
DT   07-MAR-2006, entry version 74.
DE   Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
DE   (Lymphocyte cell-specific protein-tyrosine kinase) (LSK).
GN   Name=Lck; Synonyms=Lsk-t;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86079521; PubMed=2416464; DOI=10.1016/0092-8674(85)90169-2;
RA   Marth J.D., Peet R., Krebs E.G., Perlmutter R.M.;
RT   "A lymphocyte-specific protein-tyrosine kinase gene is rearranged and
RT   overexpressed in the murine T cell lymphoma LSTRA.";
RL   Cell 43:393-404(1985).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86146842; PubMed=3081813;
RA   Voronova A.F., Sefton B.M.;
RT   "Expression of a new tyrosine protein kinase is stimulated by
RT   retrovirus promoter insertion.";
RL   Nature 319:682-685(1986).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=NOD; TISSUE=Thymus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX   MEDLINE=89096891; PubMed=2850479;
RA   Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT   "Structure of the murine lck gene and its rearrangement in a murine
RT   lymphoma cell line.";
RL   Mol. Cell. Biol. 8:3058-3064(1988).
RN   [6]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-10.
RX   MEDLINE=88142832; PubMed=3501824;
RA   Voronova A.F., Adler H.T., Sefton B.M.;
RT   "Two lck transcripts containing different 5' untranslated regions are
RT   present in T cells.";
RL   Mol. Cell. Biol. 7:4407-4413(1987).
RN   [7]
RP   MUTAGENESIS OF TYR-504.
RX   MEDLINE=88248001; PubMed=3380790;
RA   Amrein K.E., Sefton B.M.;
RT   "Avian reovirus mRNAs are nonfunctional in infected mouse cells:
RT   translational basis for virus host-range restriction.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:4257-4261(1988).
RN   [8]
RP   INTERACTIONS WITH CD4 AND CD8, AND MUTAGENESIS OF 2-CYS--CYS-4; CYS-19
RP   AND CYS-22.
RX   MEDLINE=90182665; PubMed=2107025; DOI=10.1016/0092-8674(90)90090-2;
RA   Turner J.M., Brodsky M.H., Irving B.A., Levin S.D., Perlmutter R.M.,
RA   Littman D.R.;
RT   "Interaction of the unique N-terminal region of tyrosine kinase p56lck
RT   with cytoplasmic domains of CD4 and CD8 is mediated by cysteine
RT   motifs.";
RL   Cell 60:755-765(1990).
RN   [9]
RP   MUTAGENESIS.
RX   MEDLINE=93059694; PubMed=1279202;
RA   Hurley T.R., Amrein K.E., Sefton B.M.;
RT   "Creation and characterization of temperature-sensitive mutants of the
RT   lck tyrosine protein kinase.";
RL   J. Virol. 66:7406-7413(1992).
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RN   [10]
RP   MUTAGENESIS OF LYS-272.
RX   MEDLINE=91163633; PubMed=1706070; DOI=10.1038/350062a0;
RA   Abraham N., Miceli M.C., Parnes J.C., Veillette A.;
RT   "Enhancement of T-cell responsiveness by the lymphocyte-specific
RT   tyrosine protein kinase p56lck.";
RL   Nature 350:62-66(1991).
RN   [11]
RP   MUTAGENESIS OF TYR-504.
RX   MEDLINE=91219495; PubMed=1708890;
RA   Abraham K.M., Levin S.D., Marth J.D., Forbush K.A., Perlmutter R.M.;
RT   "Thymic tumorigenesis induced by overexpression of p56lck.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981(1991).
RN   [12]
RP   PHOSPHORYLATION BY CSK.
RX   PubMed=8371758; DOI=10.1038/365156a0;
RA   Chow L.M., Fournel M., Davidson D., Veillette A.;
RT   "Negative regulation of T-cell receptor signalling by tyrosine protein
RT   kinase p50csk.";
RL   Nature 365:156-160(1993).
RN   [13]
RP   MUTAGENESIS.
RX   MEDLINE=93133805; PubMed=8421674;
RA   Carrera A.C., Alexandrov K., Roberts T.M.;
RT   "The conserved lysine of the catalytic domain of protein kinases is
RT   actively involved in the phosphotransfer reaction and not required for
RT   anchoring ATP.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:442-446(1993).
RN   [14]
RP   PALMITOYLATION.
RX   MEDLINE=94019312; PubMed=8413237;
RA   Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;
RT   "Palmitylation of an amino-terminal cysteine motif of protein tyrosine
RT   kinases p56lck and p59fyn mediates interaction with glycosyl-
RT   phosphatidylinositol-anchored proteins.";
RL   Mol. Cell. Biol. 13:6385-6392(1993).
RN   [15]
RP   PALMITOYLATION.
RX   MEDLINE=95071286; PubMed=7980442;
RA   Koegl M., Zlatkine P., Ley S.C., Courtneidge S.A., Magee A.I.;
RT   "Palmitoylation of multiple Src-family kinases at a homologous N-
RT   terminal motif.";
RL   Biochem. J. 303:749-753(1994).
RN   [16]
RP   INTERACTION WITH CBLB.
RX   PubMed=10646608; DOI=10.1038/35003228;
RA   Bachmaier K., Krawczyk C., Kozieradzki I., Kong Y.-Y., Sasaki T.,
RA   Oliveira-dos-Santos A., Mariathasan S., Bouchard D., Wakeham A.,
RA   Itie A., Le J., Ohashi P.S., Sarosi I., Nishina H., Lipkowitz S.,
RA   Penninger J.M.;
RT   "Negative regulation of lymphocyte activation and autoimmunity by the
RT   molecular adaptor Cbl-b.";
RL   Nature 403:211-216(2000).
RN   [17]
RP   SUBCELLULAR LOCATION.
RX   PubMed=12218089;
RA   Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA   Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT   "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT   protein/phosphoprotein associated with glycolipid-enriched
RT   microdomains in lipid rafts in resting T cells.";
RL   J. Immunol. 169:2813-2817(2002).
RN   [18]
RP   PHOSPHORYLATION SITE TYR-393, AND MASS SPECTROMETRY.
RX   PubMed=15592455; DOI=10.1038/nbt1046;
RA   Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
RA   Zha X.-M., Polakiewicz R.D., Comb M.J.;
RT   "Immunoaffinity profiling of tyrosine phosphorylation in cancer

  Query Match             100.0%;  Score 43;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
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Db        346 QIAEGMAFI 354


RESULT 9
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ID   Q7RTZ3_HUMAN   PRELIMINARY;   PRT;   509 AA.
AC   Q7RTZ3;
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DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Protein tyrosine kinase.
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22289034; PubMed=12401726;
RA   Nervi S., Nicodeme S., Gartioux C., Atlan C., Lathrop M., Reviron D.,
RA   Naquet P., Matsuda F., Imbert J., Vialettes B.;
RT   "No association between lck gene polymorphisms and protein level in
RT   type 1 diabetes.";
RL   Diabetes 51:3326-3330(2002).
CC   -!- MISCELLANEOUS: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ third party annotation (TPA) entry.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BN000073; CAD55807.1; -; Genomic_DNA.
DR   HSSP; P06239; 1BHF.
DR   SMR; Q7RTZ3; 65-509.
DR   Ensembl; ENSG00000182866; Homo sapiens.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
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DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   509 AA;  58001 MW;  44BFF0D43FFB420D CRC64;

  Query Match             100.0%;  Score 43;  DB 2;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
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Db        347 QIAEGMAFI 355


RESULT 10
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ID   Q95M32_9PRIM   PRELIMINARY;   PRT;   509 AA.
AC   Q95M32;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Lck protein.
GN   Name=lck;
OS   Hylobates sp. (gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Hylobatidae; Hylobates.
OX   NCBI_TaxID=9581;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22031236; PubMed=12033791; DOI=10.1006/viro.2002.1381;
RA   Picard C., Greenway A., Holloway G., Olive D., Collette Y.;
RT   "Interaction with simian Hck tyrosine kinase reveals convergent
RT   evolution of the Nef protein from simian and human immunodeficiency
RT   viruses despite differential molecular surface usage.";
RL   Virology 295:320-327(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Picard C.;
RL   Thesis (2001), Department of Experimental Oncology laboratory, U.
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ320182; CAC44027.1; -; mRNA.
DR   HSSP; P06239; 1LCK.
DR   SMR; Q95M32; 65-509.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
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  Query Match             100.0%;  Score 43;  DB 2;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        347 QIAEGMAFI 355


RESULT 11
Q3ZCM0_BOVIN
ID   Q3ZCM0_BOVIN   PRELIMINARY;   PRT;   509 AA.
AC   Q3ZCM0;
DT   27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   27-SEP-2005, sequence version 1.
DT   07-MAR-2006, entry version 6.
DE   Hypothetical protein MGC126900.
GN   Name=MGC126900;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Crossbred x Angus; TISSUE=Ileum;
RA   Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA   Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA   Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA   Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA   Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA   Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; BC102046; AAI02047.1; -; mRNA.
DR   GO; GO:0045121; C:lipid raft; ISS.
DR   GO; GO:0000242; C:pericentriolar material; ISS.
DR   GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
DR   GO; GO:0042169; F:SH2 domain binding; ISS.
DR   GO; GO:0006919; P:caspase activation; ISS.
DR   GO; GO:0030097; P:hemopoiesis; ISS.
DR   GO; GO:0006917; P:induction of apoptosis; ISS.
DR   GO; GO:0007242; P:intracellular signaling cascade; ISS.
DR   GO; GO:0050870; P:positive regulation of T cell activation; ISS.
DR   GO; GO:0050862; P:positive regulation of T cell receptor sign. . .; ISS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR   GO; GO:0007265; P:Ras protein signal transduction; ISS.
DR   GO; GO:0051249; P:regulation of lymphocyte activation; ISS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; ISS.
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DR   GO; GO:0042493; P:response to drug; ISS.
DR   GO; GO:0030217; P:T cell differentiation; ISS.
DR   GO; GO:0006882; P:zinc ion homeostasis; ISS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   509 AA;  58116 MW;  CE0E80DCD6D0F2F8 CRC64;

  Query Match             100.0%;  Score 43;  DB 2;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        347 QIAEGMAFI 355


RESULT 12
Q573B4_HUMAN
ID   Q573B4_HUMAN   PRELIMINARY;   PRT;   516 AA.
AC   Q573B4;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Proto-oncogene tyrosine-protein kinase LCK.
GN   Name=LCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Blood;
RX   PubMed=16107303; DOI=10.1016/j.gene.2005.06.018;
RA   Nervi S., Guinamard R., Delaval B., Lecine P., Vialettes B.,
RA   Naquet P., Imbert J.;
RT   "A rare mRNA variant of the human lymphocyte-specific protein tyrosine
RT   kinaseLCK gene with intron B retention and exon 7 skipping encodes a
RT   putativeprotein with altered SH3-dependent molecular interactions.";
RL   Gene 359:18-25(2005).
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ865079; CAI23831.1; -; mRNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   516 AA;  58333 MW;  EB9A52D4EBDF14D2 CRC64;

  Query Match             100.0%;  Score 43;  DB 2;  Length 516;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        354 QIAEGMAFI 362


RESULT 13
HCK_HUMAN
ID   HCK_HUMAN      STANDARD;      PRT;   525 AA.
AC   P08631; Q5T7K1; Q5T7K2; Q96CC0; Q9H5Y5; Q9NUA4; Q9UMJ5;
DT   01-AUG-1988, integrated into UniProtKB/Swiss-Prot.
DT   26-SEP-2003, sequence version 4.
DT   07-MAR-2006, entry version 87.
DE   Tyrosine-protein kinase HCK (EC 2.7.1.112) (p59-HCK/p60-HCK)
DE   (Hemopoietic cell kinase).
GN   Name=HCK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE OF 21-525.
RX   MEDLINE=87257942; PubMed=3496523;
RA   Quintrell N., Lebo R., Varmus H., Bishop J.M., Pettenati M.J.,
RA   le Beau M.M., Diaz M.O., Rowley J.D.;
RT   "Identification of a human gene (HCK) that encodes a protein-tyrosine
RT   kinase and is expressed in hemopoietic cells.";
RL   Mol. Cell. Biol. 7:2267-2275(1987).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 21-525.
RX   MEDLINE=87257943; PubMed=3453117;
RA   Ziegler S.F., Marth J.D., Lewis D.B., Perlmutter R.M.;
RT   "Novel protein-tyrosine kinase gene (hck) preferentially expressed in
RT   cells of hematopoietic origin.";
RL   Mol. Cell. Biol. 7:2276-2285(1987).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 21-525.
RC   TISSUE=B-cell;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 21-525.
RC TISSUE=Ileal mucosa;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE OF 178-525.
RC TISSUE=Spleen;
RX MEDLINE=92241680; PubMed=1572549; DOI=10.1016/0378-1119(92)90407-G;
RA Hradetzky D., Strebhardt K., Ruesamen-Waigmann H.;
RT "The genomic locus of the human hemopoietic-specific cell protein
RT tyrosine kinase (PTK)-encoding gene (HCK) confirms conservation of
RT exon-intron structure among human PTKs of the src family.";
RL Gene 113:275-280(1992).
RN [7]
RP NUCLEOTIDE SEQUENCE OF 1-21, AND ALTERNATIVE INITIATION.
RX MEDLINE=91342636; PubMed=1875927;
RA Lock P., Ralph S., Stanley E., Boulet I., Ramsay R., Dunn A.R.;
RT "Two isoforms of murine hck, generated by utilization of alternative
RT translational initiation codons, exhibit different patterns of
RT subcellular localization.";
RL Mol. Cell. Biol. 11:4363-4370(1991).
RN [8]
RP INTERACTION WITH HIV-1 NEF.
RX MEDLINE=97364702; PubMed=9218412; DOI=10.1074/jbc.272.29.17899;
RA Briggs S.D., Sharkey M., Stevenson M., Smithgall T.E.;
RT "SH3-mediated Hck tyrosine kinase activation and fibroblast
RT transformation by the Nef protein of HIV-1.";
RL J. Biol. Chem. 272:17899-17902(1997).
RN [9]
RP INTERACTION WITH HIV-1 VIF.
RX PubMed=11278465; DOI=10.1074/jbc.M009076200;
RA Hassaine G., Courcoul M., Bessou G., Barthalay Y., Picard C.,
RA Olive D., Collette Y., Vigne R., Decroly E.;
RT "The tyrosine kinase Hck is an inhibitor of HIV-1 replication
RT counteracted by the viral vif protein.";
RL J. Biol. Chem. 276:16885-16893(2001).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-525.
RX MEDLINE=97177106; PubMed=9024658; DOI=10.1038/385602a0;
RA Sicheri F., Moarefi I., Kuriyan J.;
RT "Crystal structure of the Src family tyrosine kinase Hck.";
RL Nature 385:602-609(1997).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 80-136.
RX MEDLINE=98453315; PubMed=9778343; DOI=10.1021/bi980989q;
RA Arold S., O'Brien R., Franken P., Strub M.P., Hoh F., Dumas C.,
RA Ladbury J.E.;
RT "RT loop flexibility enhances the specificity of Src family SH3
RT domains for HIV-1 Nef.";
RL Biochemistry 37:14683-14691(1998).
RN [12]
RP STRUCTURE BY NMR OF 77-137.
RX MEDLINE=98239731; PubMed=9571048; DOI=10.1006/jmbi.1998.1690;
RA Horita D.A., Baldisseri D.M., Zhang W., Altieri A.S., Smithgall T.E.,
RA Gmeiner W.H., Byrd R.A.;
RT "Solution structure of the human Hck SH3 domain and identification of
RT its ligand binding site.";
RL J. Mol. Biol. 278:253-265(1998).
RN [13]
RP STRUCTURE BY NMR OF 138-244.
RX MEDLINE=97263487; PubMed=9109402; DOI=10.1016/S0014-5793(97)00255-X;
RA Zhang W., Smithgall T.E., Gmeiner W.H.;
RT "Sequential assignment and secondary structure determination for the
RT Src homology 2 domain of hematopoietic cellular kinase.";
RL FEBS Lett. 406:131-135(1997).
CC -!- FUNCTION: May serve as part of a signaling pathway coupling the Fc
CC receptor to the activation of the respiratory burst. May also
CC contribute to neutrophil migration and may regulate the
CC degranulation process of neutrophils.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- SUBUNIT: May bind to HIV-1 Nef and VIF through its SH3 domain.
CC This interaction would stimulates its tyrosine-kinase activity.
CC -!- INTERACTION:
CC O92969:- (xeno); NbExp=2; IntAct=EBI-346340, EBI-710506;

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CC       P26660:- (xeno); NbExp=1; IntAct=EBI-346340, EBI-706322;
CC       P27958:- (xeno); NbExp=5; IntAct=EBI-346340, EBI-706378;
CC       Q13545:-; NbExp=1; IntAct=EBI-346340, EBI-346574;
CC       Q9UDG1:-; NbExp=1; IntAct=EBI-346340, EBI-346967;
CC       Q9WMX2:- (xeno); NbExp=1; IntAct=EBI-346340, EBI-710918;
CC       Q9Y5K6:CD2AP; NbExp=1; IntAct=EBI-346340, EBI-298152;
CC       Q9ULH1:DDEF1; NbExp=1; IntAct=EBI-346340, EBI-346622;
CC       P50570:DNM2; NbExp=1; IntAct=EBI-346340, EBI-346547;
CC       Q92556:ELMO1; NbExp=4; IntAct=EBI-346340, EBI-346417;
CC       Q9UI08:EVL; NbExp=1; IntAct=EBI-346340, EBI-346653;
CC       Q9H6R7:FLJ21945; NbExp=1; IntAct=EBI-346340, EBI-346906;
CC       P61978:HNRPK; NbExp=1; IntAct=EBI-346340, EBI-304185;

  Query Match             100.0%;  Score 43;  DB 1;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 4.8;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        363 QIAEGMAFI 371


RESULT 14
Q504R5_HUMAN
ID   Q504R5_HUMAN   PRELIMINARY;   PRT;   570 AA.
AC   Q504R5;
DT   07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT   07-JUN-2005, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   Hypothetical protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lymph;
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC094847; AAH94847.1; -; mRNA.
DR   SMR; Q504R5; 125-570.
DR   Ensembl; ENSG00000101336; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW   SH3 domain; Transferase; Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   570 AA;  64194 MW;  824B51745A4D4224 CRC64;

  Query Match             100.0%;  Score 43;  DB 2;  Length 570;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
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Db        408 QIAEGMAFI 416


RESULT 15
Q2VPE2_HUMAN
ID   Q2VPE2_HUMAN   PRELIMINARY;   PRT;   580 AA.
AC   Q2VPE2;
DT   10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT   10-JAN-2006, sequence version 1.
DT   07-MAR-2006, entry version 4.
DE   Hypothetical protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RG   NIH MGC Project;
RL   Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC108931; AAI08932.1; -; mRNA.
DR   EMBL; BC108930; AAI08931.1; -; mRNA.
KW   ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW   SH3 domain; Transferase; Tyrosine-protein kinase.
FT   NON_TER       1       1
SQ   SEQUENCE   580 AA;  65343 MW;  A9D2E429B128891A CRC64;

  Query Match             100.0%;  Score 43;  DB 2;  Length 580;
  Best Local Similarity   100.0%;  Pred. No. 5.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||||
Db        418 QIAEGMAFI 426


RESULT 16
Q9PVV0_LAMRE
ID   Q9PVV0_LAMRE   PRELIMINARY;   PRT;   249 AA.
AC   Q9PVV0;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 28.
DE   Src-like A (Fragment).
OS   Lampetra reissneri (Far Eastern brook lamprey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC   Petromyzontiformes; Petromyzontidae; Lethenteron.
OX   NCBI_TaxID=7753;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20020330; PubMed=10552041;
RA   Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
RT   "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey:
RT   isoform duplications around the divergence of cyclostomes and
RT   gnathostomes.";
RL   J. Mol. Evol. 49:601-608(1999).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB025549; BAA84739.1; -; mRNA.
DR   HSSP; P08631; 1AD5.
DR   SMR; Q9PVV0; 1-246.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Tyrosine-protein kinase.
FT   NON_TER       1       1
SQ   SEQUENCE   249 AA;  28627 MW;  DAC9DBA041F3D941 CRC64;

  Query Match             97.7%;  Score 42;  DB 2;  Length 249;
  Best Local Similarity   88.9%;  Pred. No. 3.9;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |:|||||||
Db         87 QVAEGMAFI 95


RESULT 17
Q4RR72_TETNG
ID   Q4RR72_TETNG   PRELIMINARY;   PRT;   322 AA.
AC   Q4RR72;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   Chromosome 14 SCAF15003, whole genome shotgun sequence. (Fragment).
GN   ORFNames=GSTENG00030294001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC       cycle. It is required in higher cells for entry into S-phase and
CC       mitosis. Component of the kinase complex that phosphorylates the
CC       repetitive C-terminus of RNA polymerase II. Catalytic component of
CC       MPF (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC       mature oocytes (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CAAE01015003; CAG09110.1; -; Genomic_DNA.
DR   SMR; Q4RR72; 2-322.
DR   GO; GO:0005524; F:ATP binding; IEA.
```

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DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   322 AA;  36768 MW;  EC0ED0B6DB1CBB2F CRC64;

  Query Match             93.0%;  Score 40;  DB 2;  Length 322;
  Best Local Similarity   88.9%;  Pred. No. 13;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||:|
Db        135 QIAEGMAYI 143


RESULT 18
Q5TYU7_BRARE
ID   Q5TYU7_BRARE   PRELIMINARY;   PRT;   485 AA.
AC   Q5TYU7;
DT   07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   07-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   Novel protein tyrosine kinase.
GN   Name=si:dkey-33i22.2; Synonyms=OTTDARP00000004623;
GN   ORFNames=DKEY-33I22.2-001;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Dunn M.;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BX842684; CAH69080.1; -; Genomic_DNA.
DR   SMR; Q5TYU7; 42-485.
DR   Ensembl; ENSDARG00000007783; Danio rerio.
DR   ZFIN; ZDB-GENE-040724-106; si:dkey-33i22.2.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   485 AA;  55644 MW;  3ED1878453666747 CRC64;

  Query Match             93.0%;  Score 40;  DB 2;  Length 485;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||:|
Db        324 QIAEGMAYI 332


RESULT 19
O13064_XENLA
ID   O13064_XENLA   PRELIMINARY;   PRT;   488 AA.
AC   O13064;
DT   01-JUL-1997, integrated into UniProtKB/TrEMBL.
DT   01-JUL-1997, sequence version 1.
DT   07-FEB-2006, entry version 29.
DE   Lyn protein tyrosine kinase.
GN   Name=Lyn;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fukami Y., Funabiki K., Sato K.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB003358; BAA20078.1; -; mRNA.
DR   HSSP; P08631; 1AD5.
DR   SMR; O13064; 43-488.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
```

```
KW   Kinase.
SQ   SEQUENCE   488 AA;  55795 MW;  B7E70668B6EA92B2 CRC64;

  Query Match             93.0%;  Score 40;  DB 2;  Length 488;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||:|
Db        326 QIAEGMAYI 334


RESULT 20
Q3U6Q5_MOUSE
ID   Q3U6Q5_MOUSE   PRELIMINARY;   PRT;   491 AA.
AC   Q3U6Q5;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Bone marrow macrophage cDNA, RIKEN full-length enriched library,
DE   clone:I830119M13 product:Yamaguchi sarcoma viral (v-yes-1) oncogene
DE   homolog, full insert sequence.
GN   Name=Lyn;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
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RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK153038; BAE31669.1; -; mRNA.
DR   MGI; MGI:96892; Lyn.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IDA.
DR   GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.
DR   GO; GO:0046777; P:protein amino acid autophosphorylation; IDA.
DR   GO; GO:0046777; P:protein amino acid autophosphorylation; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   491 AA;  56285 MW;  2C82015D510B1F59 CRC64;

  Query Match           93.0%;  Score 40;  DB 2;  Length 491;
  Best Local Similarity  88.9%;  Pred. No. 19;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||:|
Db        329 QIAEGMAYI 337


RESULT 21
Q8CEI0_MOUSE
ID   Q8CEI0_MOUSE   PRELIMINARY;   PRT;   491 AA.
AC   Q8CEI0;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 21.
DE   10 day old male pancreas cDNA, RIKEN full-length enriched library,
DE   clone:1810073A02 product:Yamaguchi sarcoma viral (v-yes-1) oncogene
DE   homolog, full insert sequence.
GN   Name=Lyn;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
```

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RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y.. Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AK028112; BAC25753.1; -; mRNA.
DR   HSSP; P08631; 1AD5.
DR   SMR; Q8CEI0; 46-491.
DR   Ensembl; ENSMUSG00000042228; Mus musculus.
DR   MGI; MGI:96892; Lyn.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IDA.
DR   GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.
DR   GO; GO:0046777; P:protein amino acid autophosphorylation; IDA.
DR   GO; GO:0046777; P:protein amino acid autophosphorylation; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.

  Query Match             93.0%;  Score 40;  DB 2;  Length 491;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||:|
Db        329 QIAEGMAYI 337


RESULT 22
Q5ZMB9_CHICK
ID   Q5ZMB9_CHICK   PRELIMINARY;   PRT;   492 AA.
AC   Q5ZMB9;
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DT   23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT   23-NOV-2004, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   Hypothetical protein.
GN   ORFNames=RCJMB04_2j8;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CB; TISSUE=Bursa;
RA   Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA   Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA   Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT   "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT   genefunction analysis.";
RL   Genome Biol. 6:R6-R6(2005).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ719465; CAG31124.1; -; mRNA.
DR   SMR; Q5ZMB9; 46-492.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   492 AA;  56202 MW;  69D2F0534E33CC1E CRC64;

  Query Match             93.0%;  Score 40;  DB 2;  Length 492;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||:|
Db        330 QIAEGMAYI 338


RESULT 23
HCK_RAT
ID   HCK_RAT        STANDARD;      PRT;   502 AA.
AC   P50545; Q64647;
DT   01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT   26-SEP-2003, sequence version 2.
DT   07-MAR-2006, entry version 54.
DE   Tyrosine-protein kinase HCK (EC 2.7.1.112) (p56-HCK) (Hemopoietic cell
DE   kinase).
GN   Name=Hck;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=92109719; PubMed=1764064;
RA   Okano Y., Sugimoto Y., Fukuoka M., Matsui A., Nagata K.I., Nozawa Y.;
RT   "Identification of rat cDNA encoding hck tyrosine kinase from
RT   megakaryocytes.";
RL   Biochem. Biophys. Res. Commun. 181:1137-1144(1991).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=Wistar; TISSUE=Spleen;
RA   Vijaya Gouri B.S., Rema V., Kamatkar S., Swarup G.;
RT   "Nucleotide sequence of a cDNA coding for rat hck tyrosine kinase and
RT   characterization of its gene product.";
RL   J. Biosci. 19:117-129(1994).
CC   -!- FUNCTION: May serve as part of a signaling pathway coupling the Fc
CC       receptor to the activation of the respiratory burst. May also
CC       contribute to neutrophil migration and may regulate the
CC       degranulation process of neutrophils.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBCELLULAR LOCATION: Membrane-associated.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; S74141; AAB20754.1; -; mRNA.
DR   EMBL; M83666; AAA41312.1; -; mRNA.
DR   EMBL; X62345; CAA44218.1; -; mRNA.
DR   PIR; JQ1321; JQ1321.
DR   HSSP; P08631; 1BU1.
DR   SMR; P50545; 58-502.
DR   Ensembl; ENSRNOG00000009331; Rattus norvegicus.
DR   RGD; 2785; Hck.
DR   InterPro; IPR000108; Neu_cyt_fact_2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00499; P67PHOX.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;
KW   Nucleotide-binding; Palmitate; Phosphorylation; SH2 domain;
KW   SH3 domain; Transferase; Tyrosine-protein kinase.
FT   INIT_MET      0      0       By similarity.
FT   CHAIN         1    502       Tyrosine-protein kinase HCK.
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FT                                /FTId=PRO_0000088104.
FT   DOMAIN       54    114       SH3.
FT   DOMAIN      120    217       SH2.
FT   DOMAIN      238    491       Protein kinase.
FT   NP_BIND     244    252       ATP (By similarity).
FT   ACT_SITE    357    357       Proton acceptor (By similarity).
FT   BINDING     266    266       ATP (By similarity).
FT   MOD_RES     387    387       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   CONFLICT     50     50       F -> V (in Ref. 2).
FT   CONFLICT    204    204       K -> R (in Ref. 2).
FT   CONFLICT    305    305       I -> T (in Ref. 2).
SQ   SEQUENCE   502 AA;  56885 MW;  4CFC1F3F0E82EADF CRC64;

  Query Match             93.0%;  Score 40;  DB 1;  Length 502;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              ||:||||||
Db        340 QISEGMAFI 348


RESULT 24
Q9DDK6_SALSA
ID   Q9DDK6_SALSA   PRELIMINARY;   PRT;   502 AA.
AC   Q9DDK6;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
DT   07-FEB-2006, entry version 20.
DE   Src-family tyrosine kinase SCK.
OS   Salmo salar (Atlantic salmon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX   NCBI_TaxID=8030;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Hordvik I., Male R.;
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF321110; AAG38611.1; -; mRNA.
DR   HSSP; P08631; 1AD5.
DR   SMR; Q9DDK6; 54-502.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   502 AA;  56600 MW;  82DF0D677AA99980 CRC64;

  Query Match             93.0%;  Score 40;  DB 2;  Length 502;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||:|
Db        340 QIAEGMAYI 348


RESULT 25
Q3UD17_MOUSE
ID   Q3UD17_MOUSE   PRELIMINARY;   PRT;   503 AA.
AC   Q3UD17;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   Bone marrow macrophage cDNA, RIKEN full-length enriched library,
DE   clone:I830001J15 product:hemopoietic cell kinase, full insert sequence
DE   (Bone marrow macrophage cDNA, RIKEN full-length enriched library,
DE   clone:I830013O10 product:hemopoietic cell kinase, full insert
DE   sequence) (Activated spleen cDNA, RIKEN full-length enriched library,
DE   clone:F830002M23 product:hemopoietic cell kinase, full insert
DE   sequence) (6 days neonate spleen cDNA, RIKEN full-length enriched
DE   library, clone:F430012D01 product:hemopoietic cell kinase, full insert
DE   sequence) (Bone marrow macrophage cDNA, RIKEN full-length enriched
DE   library, clone:G530014D07 product:hemopoietic cell kinase, full insert
DE   sequence).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
RC   Spleen;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
RC   Spleen;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
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RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
RC Spleen;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
RC Spleen;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
RC Spleen;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
RC Spleen;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
RC Spleen;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, and Bone marrow;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spleen;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
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CC ---
DR EMBL; AK150290; BAE29445.1; -; mRNA.
DR EMBL; AK150709; BAE29787.1; -; mRNA.
DR EMBL; AK155975; BAE33532.1; -; mRNA.
DR EMBL; AK165315; BAE38133.1; -; mRNA.
DR EMBL; AK149736; BAE29054.1; -; mRNA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
DR InterPro; IPR000108; Neu_cyt_fact_2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR000980; SH2.

Query Match 93.0%; Score 40; DB 2; Length 503;

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  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
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Db        341 QISEGMAFI 349


RESULT 26
Q6AYV7_RAT
ID   Q6AYV7_RAT     PRELIMINARY;   PRT;   503 AA.
AC   Q6AYV7;
DT   13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT   13-SEP-2004, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Hck protein.
GN   Name=Hck;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RA   Director MGC Project;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; BC078890; AAH78890.1; -; mRNA.
DR   SMR; Q6AYV7; 59-503.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000108; Neu_cyt_fact_2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00499; P67PHOX.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   503 AA;  56968 MW;  4D4D0777FF3AAC99 CRC64;

  Query Match             93.0%;  Score 40;  DB 2;  Length 503;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              ||:||||||
Db        341 QISEGMAFI 349


RESULT 27
BLK_HUMAN
ID   BLK_HUMAN      STANDARD;      PRT;   504 AA.
AC   P51451; Q16291;
DT   01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-1996, sequence version 1.
DT   07-MAR-2006, entry version 48.
DE   Tyrosine-protein kinase BLK (EC 2.7.1.112) (B lymphocyte kinase) (p55-
DE   BLK).
GN   Name=BLK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=95123078; PubMed=7822795;
RA   Islam K.B., Rabbani H., Larsson C., Sanders R., Smith C.I.;
RT   "Molecular cloning, characterization, and chromosomal localization of
RT   a human lymphoid tyrosine kinase related to murine Blk.";
RL   J. Immunol. 154:1265-1272(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=95148218; PubMed=7845672;
RA   Drebin J.A., Hartzell S.W., Griffin C., Campbell M.J.,
RA   Niederhuber J.E.;
RT   "Molecular cloning and chromosomal localization of the human homologue
RT   of a B-lymphocyte specific protein tyrosine kinase (blk).";
RL   Oncogene 10:477-486(1995).
CC   -!- FUNCTION: May function in a signal transduction pathway that is
CC       restricted to B lymphoid cells.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; Z33998; CAA83965.1; -; mRNA.
DR   EMBL; S76617; AAB33265.1; -; mRNA.
DR   PIR; I37206; I37206.
DR   HSSP; P16277; 1BLK.
DR   SMR; P51451; 62-504.
DR   Ensembl; ENSG00000136573; Homo sapiens.
DR   H-InvDB; HIX0007315; -.
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DR   HGNC; HGNC:1057; BLK.
DR   MIM; 191305; gene.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; TAS.
DR   GO; GO:0007243; P:protein kinase cascade; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; FALSE_NEG.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Lipoprotein; Myristate; Nucleotide-binding;
KW   Phosphorylation; SH2 domain; SH3 domain; Transferase;
KW   Tyrosine-protein kinase.
FT   INIT_MET      0      0       By similarity.
FT   CHAIN         1    504       Tyrosine-protein kinase BLK.
FT                                /FTId=PRO_0000088061.
FT   DOMAIN       57    117       SH3.
FT   DOMAIN      123    219       SH2.
FT   DOMAIN      240    493       Protein kinase.
FT   NP_BIND     246    254       ATP (By similarity).
FT   ACT_SITE    359    359       Proton acceptor (By similarity).
FT   BINDING     268    268       ATP (By similarity).
FT   MOD_RES     388    388       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   CONFLICT    286    286       M -> V (in Ref. 2).
FT   CONFLICT    406    406       I -> Y (in Ref. 2).
SQ   SEQUENCE   504 AA;  57607 MW;  BDB1DF50EC7370C8 CRC64;

  Query Match             93.0%;  Score 40;  DB 1;  Length 504;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||:|
Db        342 QIAEGMAYI 350


RESULT 28
Q96IN1_HUMAN
ID   Q96IN1_HUMAN   PRELIMINARY;   PRT;   505 AA.
AC   Q96IN1;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 24.
DE   B lymphoid tyrosine kinase.
GN   Name=BLK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Blood, and Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lymph;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Blood;
RA   Director MGC Project;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC007371; AAH07371.1; -; mRNA.
DR   EMBL; BC032413; AAH32413.1; -; mRNA.
DR   HSSP; P16277; 1BLK.
DR   SMR; Q96IN1; 63-505.
DR   Ensembl; ENSG00000136573; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   505 AA;  57706 MW;  B5F739BEF8389176 CRC64;

  Query Match             93.0%;  Score 40;  DB 2;  Length 505;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
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Db        343 QIAEGMAYI 351


RESULT 29
Q66I04_BRARE
ID   Q66I04_BRARE   PRELIMINARY;   PRT;   510 AA.
AC   Q66I04;
DT   11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2004, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Zgc:92124.
GN   ORFNames=zgc:92124;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RA   Director MGC Project;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC081601; AAH81601.1; -; mRNA.
DR   SMR; Q66I04; 65-510.
DR   Ensembl; ENSDARG00000031715; Danio rerio.
DR   ZFIN; ZDB-GENE-040912-7; zgc:92124.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   510 AA;  58258 MW;  5EE8F68226569BA2 CRC64;

  Query Match            93.0%;  Score 40;  DB 2;  Length 510;
  Best Local Similarity  88.9%;  Pred. No. 20;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||:|
Db        348 QIAEGMAYI 356


RESULT 30
LYN_HUMAN
ID   LYN_HUMAN      STANDARD;      PRT;   511 AA.
AC   P07948;
DT   01-AUG-1988, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-1994, sequence version 2.
DT   07-MAR-2006, entry version 74.
DE   Tyrosine-protein kinase Lyn (EC 2.7.1.112).
GN   Name=LYN;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=87172710; PubMed=3561390;
RA   Yamanashi Y., Fukushige S., Semba K., Sukegawa J., Miyajima N.,
RA   Matsubara K., Yamamoto T., Toyoshima K.;
RT   "The yes-related cellular gene lyn encodes a possible tyrosine kinase
RT   similar to p56lck.";
RL   Mol. Cell. Biol. 7:237-243(1987).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=94171041; PubMed=8125304; DOI=10.1016/0378-1119(94)90811-7;
RA   Rider L.G., Raben N., Miller L., Jelsema C.;
RT   "The cDNAs encoding two forms of the LYN protein tyrosine kinase are
RT   expressed in rat mast cells and human myeloid cells.";
RL   Gene 138:219-222(1994).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LYN A).
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 368-423.
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RX   MEDLINE=91062389; PubMed=2247464;
RA   Partanen J., Maekelae T.P., Alitalo R., Lehvaeslaiho H., Alitalo K.;
RT   "Putative tyrosine kinases expressed in K-562 human leukemia cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:8913-8917(1990).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 368-423.
RX   MEDLINE=92378604; PubMed=1510669;
RA   Bielke W., Ziemieki A., Kappos L., Miescher G.C.;
RT   "Expression of the B cell-associated tyrosine kinase gene Lyn in
RT   primary neuroblastoma tumours and its modulation during the
RT   differentiation of neuroblastoma cell lines.";
RL   Biochem. Biophys. Res. Commun. 186:1403-1409(1992).
RN   [6]
RP   INTERACTION WITH EPSTEIN-BARR VIRUS LMP2A.
RX   PubMed=7895172;
RA   Miller C.L., Burkhardt A.L., Lee J.H., Stealey B., Longnecker R.,
RA   Bolen J.B., Kieff E.;
RT   "Integral membrane protein 2 of Epstein-Barr virus regulates
RT   reactivation from latency through dominant negative effects on
RT   protein-tyrosine kinases.";
RL   Immunity 2:155-166(1995).
RN   [7]
RP   PHOSPHORYLATION SITE TYR-507, AND MASS SPECTROMETRY.
RX   PubMed=15592455; DOI=10.1038/nbt1046;
RA   Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
RA   Zha X.-M., Polakiewicz R.D., Comb M.J.;
RT   "Immunoaffinity profiling of tyrosine phosphorylation in cancer
RT   cells.";
RL   Nat. Biotechnol. 23:94-101(2005).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Interacts with phosphorylated LIME1 upon BCR activation.
CC       Interacts with Epstein-Barr virus LMP2A.
CC   -!- INTERACTION:
CC       O92969:- (xeno); NbExp=2; IntAct=EBI-79452, EBI-710506;
CC       P26660:- (xeno); NbExp=1; IntAct=EBI-79452, EBI-706322;
CC       P27958:- (xeno); NbExp=5; IntAct=EBI-79452, EBI-706378;
CC       Q9WMX2:- (xeno); NbExp=2; IntAct=EBI-79452, EBI-710918;
CC       P20273:CD22; NbExp=1; IntAct=EBI-79452, EBI-78277;
CC       Q6NVF1:Centd3 (xeno); NbExp=2; IntAct=EBI-79452, EBI-621463;
CC       P67870:CSNK2B; NbExp=1; IntAct=EBI-79452, EBI-348169;
CC       Q9UIF2:gpVI; NbExp=2; IntAct=EBI-79452, EBI-515278;
CC       Q07666:KHDRBS1; NbExp=1; IntAct=EBI-79452, EBI-1364;
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=LYN A;
CC         IsoId=P07948-1; Sequence=Displayed;
CC       Name=LYN B;
CC         IsoId=P07948-2; Sequence=VSP_005002;
CC   -!- TISSUE SPECIFICITY: Expressed in primary neuroblastoma tumors.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; M16038; AAA59540.1; -; mRNA.
DR   EMBL; M79321; AAB50019.1; -; mRNA.
DR   EMBL; BC075001; AAH75001.1; -; mRNA.
DR   EMBL; BC075002; AAH75002.1; -; mRNA.
DR   PIR; A26719; TVHULY.
DR   PDB; 1W1F; NMR; A=60-122.
DR   PDB; 1WA7; NMR; A=60-122.
DR   SMR; P07948; 66-511.
DR   IntAct; P07948; -.
DR   Ensembl; ENSG00000147507; Homo sapiens.
DR   HGNC; HGNC:6735; LYN.
DR   MIM; 165120; gene.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004716; F:receptor signaling protein tyrosine kinase . . .; TAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   3D-structure; Alternative splicing; ATP-binding; Kinase; Lipoprotein;
KW   Myristate; Nucleotide-binding; Palmitate; Phosphoprotein;
KW   Proto-oncogene; SH2 domain; SH3 domain; Transferase;
KW   Tyrosine-protein kinase.
FT   INIT_MET      0      0       By similarity.
FT   CHAIN         1    511       Tyrosine-protein kinase Lyn.
FT                                /FTId=PRO_0000088129.
FT   DOMAIN       62    122       SH3.
FT   DOMAIN      128    225       SH2.
FT   DOMAIN      246    500       Protein kinase.
FT   NP_BIND     252    260       ATP (By similarity).
FT   ACT_SITE    366    366       Proton acceptor (By similarity).
FT   BINDING     274    274       ATP (By similarity).
FT   MOD_RES     396    396       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     507    507       Phosphotyrosine.
FT   LIPID         1      1       N-myristoyl glycine (By similarity).
FT   LIPID         2      2       S-palmitoyl cysteine (By similarity).
FT   VARSPLIC     22     42       Missing (in isoform LYN B).
FT                                /FTId=VSP_005002.
FT   STRAND       65     71
FT   STRAND       73     73
FT   STRAND       77     79
FT   STRAND       83     83
FT   TURN         85     86
FT   STRAND       88     94
FT   STRAND       96    103
FT   TURN        104    106
FT   STRAND      109    113
FT   TURN        114    116
FT   STRAND      117    119
SQ   SEQUENCE   511 AA;  58443 MW;  8419CD461204E364 CRC64;

  Query Match             93.0%;  Score 40;  DB 1;  Length 511;
  Best Local Similarity   88.9%;  Pred. No. 20;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QIAEGMAFI 9
              |||||||:|
Db        349 QIAEGMAYI 357


Search completed: June 29, 2006, 09:29:23
Job time : 109.942 secs
```

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:14 ; Search time 87.8313 Seconds
(without alignments)
46.851 Million cell updates/sec

Title: US-10-062-257A-16
Perfect score: 49
Sequence: 1 DVWSFGILL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	100.0	9	4	AAB73132	Aab73132 Tumour an
2	49	100.0	9	6	ABR84355	Abr84355 Human lck
3	49	100.0	9	8	ADS87127	Ads87127 Human gen
4	49	100.0	12	2	AAW80588	Aaw80588 Peptide f
5	49	100.0	15	2	AAW14809	Aaw14809 fes oncog
6	49	100.0	15	3	AAY52604	Aay52604 v-fes enc
7	49	100.0	15	3	AAY52671	Aay52671 v-fes enc
8	49	100.0	30	1	AAP40384	Aap40384 Sequence
9	49	100.0	30	2	AAW14803	Aaw14803 fes oncog
10	49	100.0	30	3	AAY52601	Aay52601 v-fes enc
11	49	100.0	43	4	AAM17615	Aam17615 Peptide #
12	49	100.0	43	4	ABB36636	Abb36636 Peptide #
13	49	100.0	43	4	AAM30133	Aam30133 Peptide #
14	49	100.0	43	4	ABB31423	Abb31423 Peptide #
15	49	100.0	43	4	ABB21970	Abb21970 Protein #
16	49	100.0	43	4	AAM69792	Aam69792 Human bon
17	49	100.0	43	4	AAM57399	Aam57399 Human bra
18	49	100.0	43	4	ABG51487	Abg51487 Human liv
19	49	100.0	43	4	AAM05274	Aam05274 Peptide #
20	49	100.0	43	5	ABG39421	Abg39421 Human pep
21	49	100.0	49	5	ABP52388	Abp52388 JAK famil
22	49	100.0	65	8	ADT00021	Adt00021 Rat FES p
23	49	100.0	66	8	ADT00022	Adt00022 Chicken F
24	49	100.0	66	8	ADT00018	Adt00018 Human FES
25	49	100.0	66	8	ADT00019	Adt00019 Feline FE
26	49	100.0	66	8	ADT00020	Adt00020 Mouse FES
27	49	100.0	70	9	AED85831	Aed85831 Tyrosine
28	49	100.0	85	4	ABG22262	Abg22262 Novel hum
29	49	100.0	90	3	AAB58188	Aab58188 Lung canc
30	49	100.0	114	7	ADB64505	Adb64505 Human pro
31	49	100.0	169	8	ADQ66418	Adq66418 Novel hum
32	49	100.0	209	4	AAB66603	Aab66603 Human h14
33	49	100.0	211	1	AAP70055	Aap70055 Fes/fps p
34	49	100.0	250	9	ADY52570	Ady52570 Human onc
35	49	100.0	250	9	ADY52571	Ady52571 Human onc
36	49	100.0	251	4	AAB95778	Aab95778 Human pro
37	49	100.0	251	9	ADY52569	Ady52569 Human onc
38	49	100.0	254	1	AAP60009	Aap60009 Sequence
39	49	100.0	256	1	AAP60010	Aap60010 Sequence
40	49	100.0	259	2	AAR32299	Aar32299 Sequence
41	49	100.0	259	2	AAY43957	Aay43957 Human pro
42	49	100.0	259	2	AAY43956	Aay43956 Mouse pro
43	49	100.0	259	2	AAY43950	Aay43950 Human pro
44	49	100.0	259	2	AAY43952	Aay43952 Human pro
45	49	100.0	259	2	AAY43953	Aay43953 Human pro
46	49	100.0	259	2	AAY43955	Aay43955 Human pro
47	49	100.0	260	2	AAY43954	Aay43954 Human pro
48	49	100.0	260	8	ADR88387	Adr88387 CSK tyros
49	49	100.0	262	2	AAY43965	Aay43965 Chicken p
50	49	100.0	262	2	AAY43958	Aay43958 Drosophil
51	49	100.0	262	2	AAY43963	Aay43963 Human pro
52	49	100.0	262	2	AAY43964	Aay43964 Cat prote
53	49	100.0	263	5	ABP52384	Abp52384 Human JAK
54	49	100.0	263	8	ADR88385	Adr88385 LCK tyros
55	49	100.0	265	7	ABR56203	Abr56203 Mutant Ly
56	49	100.0	270	2	AAY43977	Aay43977 Mouse pro
57	49	100.0	271	7	ABR56204	Abr56204 Mutant Ly
58	49	100.0	271	8	ADR88384	Adr88384 HCK tyros
59	49	100.0	272	5	ABB81188	Abb81188 Human KIT
60	49	100.0	273	8	ADR88383	Adr88383 SAC tyros
61	49	100.0	278	9	ADY85453	Ady85453 Catalytic
62	49	100.0	279	9	ADY85449	Ady85449 Catalytic
63	49	100.0	292	9	ADY85497	Ady85497 Catalytic
64	49	100.0	294	9	ADY85470	Ady85470 Catalytic
65	49	100.0	296	9	ADY85501	Ady85501 Catalytic
66	49	100.0	300	9	ADY85468	Ady85468 Catalytic
67	49	100.0	302	9	ADY85467	Ady85467 Catalytic
68	49	100.0	309	9	ADY52576	Ady52576 Human onc
69	49	100.0	312	9	ADY85469	Ady85469 Catalytic
70	49	100.0	314	5	ABB81191	Abb81191 Human PDG
71	49	100.0	316	9	ADY85448	Ady85448 Catalytic
72	49	100.0	319	9	ADY85450	Ady85450 Catalytic
73	49	100.0	346	3	AAY76750	Aay76750 Human pro
74	49	100.0	346	4	AAE06208	Aae06208 Human pro
75	49	100.0	346	5	ABB84435	Abb84435 Human pro
76	49	100.0	348	9	ADY85559	Ady85559 Catalytic
77	49	100.0	351	4	ABG23777	Abg23777 Novel hum
78	49	100.0	355	8	ABM82980	Abm82980 Human dia
79	49	100.0	374	10	AEE72394	Aee72394 Human tar
80	49	100.0	383	7	ADJ68978	Adj68978 Human hea
81	49	100.0	393	5	ABP53494	Abp53494 Human c-S
82	49	100.0	411	9	ADZ64612	Adz64612 Tyrosine
83	49	100.0	417	2	AAR14201	Aar14201 (Beta-gal
84	49	100.0	421	3	AAY44298	Aay44298 Human rec
85	49	100.0	422	3	AAY44297	Aay44297 Human rec
86	49	100.0	422	3	AAY44299	Aay44299 Human rec
87	49	100.0	422	4	AAG66404	Aag66404 Human fib
88	49	100.0	422	8	ADW39286	Adw39286 Tumor gen
89	49	100.0	422	9	ADY17845	Ady17845 PRO polyp
90	49	100.0	422	9	ADY20347	Ady20347 PRO polyp
91	49	100.0	422	9	ADY17698	Ady17698 PRO polyp
92	49	100.0	422	10	AEE72188	Aee72188 Human tar
93	49	100.0	423	8	ADQ97769	Adq97769 Mouse can
94	49	100.0	426	2	AAR26278	Aar26278 Tyrosine
95	49	100.0	436	8	ADN61468	Adn61468 Human KPP
96	49	100.0	437	5	ABB78795	Abb78795 Human NOV

97	49	100.0	438	9	ADY52642	Ady52642 Human tra
98	49	100.0	439	9	ADY52636	Ady52636 Human tra
99	49	100.0	440	9	ADY52635	Ady52635 Human tra
100	49	100.0	444	9	ADY52634	Ady52634 Human tra

ALIGNMENTS

RESULT 1
AAB73132
ID AAB73132 standard; peptide; 9 AA.
XX
AC AAB73132;
XX
DT 09-MAY-2001 (first entry)
XX
DE Tumour antigen peptide #16.
XX
KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS Homo sapiens.
XX
PN WO200111044-A1.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-JP005220.
XX
PR 05-AUG-1999; 99JP-00222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
DR WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and
PT polynucleotides encoding them for treatment of cancer.
XX
PS Claim 1; Page 70; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 1 DVWSFGILL 9

RESULT 2
ABR84355
ID ABR84355 standard; peptide; 9 AA.
XX
AC ABR84355;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human lck HLA-A2 epitope, SEQ ID NO:6.
XX
KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW human; human leukocyte antigen; HLA-A2 epitope.
XX
OS Homo sapiens.
XX
PN JP2002365286-A.
XX
PD 18-DEC-2002.
XX
PF 18-SEP-2001; 2001JP-00283413.
XX
PR 13-NOV-2000; 2000JP-00345094.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2003-508315/48.
XX
PT A detection method of antigen specific T-cells, comprises the use of
PT plural antigenic peptides, useful in semi-quantitative determination of
PT cancer specific T-cell frequencies and for monitoring cellular immunity.
XX
PS Example 7; Page 8; 18pp; Japanese.
XX
CC The invention relates to a method for the detection of antigen specific T
CC -cells in a blood sample involving the use of a plurality of antigenic
CC peptides. The method comprises sampling of peripheral blood monocytes;
CC stimulation of the collected peripheral blood monocytes with antigens
CC without direct use of antigen presenting cells; and detection of T-cells
CC specific to the antigen in the stimulated monocytes. The method is
CC particularly used for the detection of cancer as it can be used in semi-
CC quantitative determination of cancer specific T-cells. It can also be
CC used for cancer vaccine therapy for patients with cervical or prostate
CC cancer. The method can additionally be used to monitor of cellular
CC immunity and cancer immune therapy by detection of specific T-cell
CC frequencies. Sequences ABR84350-ABR84365 represent HLA-A2 (human
CC leukocyte antigen) peptides of human origin used in an example from the
CC invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 49; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 1 DVWSFGILL 9

RESULT 3
ADS87127
ID ADS87127 standard; peptide; 9 AA.
XX
AC ADS87127;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human genetic vaccine/ubiquitin (Ub)/Lck-related epitope peptide 5.
XX
KW vaccine; ubiquitin; Ub; T-cell target; melanoma; sarcoma;
KW Hodgkins lymphoma; non-Hodgkins; leukaemia; neuroblastoma; myeloma;
KW lung cancer; stomach; skin; thyroid; ovary; prostate; womb; pancreas;
KW colon; bladder; breast; oesophagus; kidney; brain; human; epitope; Lck.
XX
OS Homo sapiens.
XX
PN WO2004035085-A1.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-JP013279.
XX
PR 17-OCT-2002; 2002JP-00302816.
XX
PA (KYUS-) KYUSHU TLO CO LTD.
XX

PI Himeno K, Furue M, Maehara Y;
XX
DR WPI; 2004-357144/33.
XX
PT Gene vaccine containing cancer antigen genes ligated to ubiquitin genes
PT or cytokine genes for prevention and treatment of cancer.
XX
PS Disclosure; SEQ ID NO 143; 266pp; Japanese.
XX
CC The invention relates to a novel genetic vaccine containing the ubiquitin
CC gene together with a gene encoding an antigenic protein containing a T-
CC cell target sequence. The vaccine of the invention may be useful for
CC prevention and treatment of cancers including melanoma, sarcoma, lymphoma
CC (Hodgkins or non-Hodgkins), leukaemia, neuroblastoma, myeloma and cancer
CC of the lung, stomach, skin, thyroid, ovary, prostate, womb, pancreas,
CC colon, bladder, breast, oesophagus, kidney or brain. The current sequence
CC is that of a human genetic vaccine/ubiquitin (Ub)-related epitope peptide
CC of the invention.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 49; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 1 DVWSFGILL 9

RESULT 4
AAW80588
ID AAW80588 standard; peptide; 12 AA.
XX
AC AAW80588;
XX
DT 18-DEC-1998 (first entry)
XX
DE Peptide fragment from kinase domain of src-family tyrosine kinases.
XX
KW src-family tyrosine kinase; serine phosphorylation-mediated degradation;
KW mutation; T cell activation; immune response; screening; cancerous cell;
KW therapy; immunity; allogenic transplant; xenogeneic organ transplant.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "can be replaced with Ala"
FT Misc-difference 9
FT /note= "can be replaced with Ala"
FT Misc-difference 10
FT /note= "can be replaced with Ala"
XX
PN WO9846996-A2.
XX
PD 22-OCT-1998.
XX
PF 10-APR-1998; 98WO-IB000801.
XX
PR 11-APR-1997; 97US-0041878P.
XX
PA (ROBA-) ROBARTS RES INST JOHN P.
XX
PI Madrenas J;
XX
DR WPI; 1998-583294/49.
XX
PT Detection of levels of T cell activation - by measuring increase in
PT amount of serine phosphorylated Ick relative to total Ick as indicative
PT of increased T cell activation.
XX
PS Claim 21, 23; Page 23; 48pp; English.
XX
CC This represents a peptide fragment from the kinase domain of src-family
CC tyrosine kinase polypeptide. The invention provides src-family tyrosine
CC kinase peptide fragments (AAW80586 to AAW80591), which on mutation
CC reduces the serine phosphorylation-mediated degradation of the
CC polypeptide. The mutation could be a mutation of the serine residue
CC located at the amino terminus to alanine and/or could be a mutation that
CC results in a leucine -leucine to alanine-alanine change in the
CC polypeptide. The invention also provides methods for detecting the level
CC of T cell activation; for detecting a compound that modulates T cell
CC activation; and for generating a src-family tyrosine kinase polypeptide
CC that has a reduced level of serine phosphorylation-mediated degradation.
CC The methods can be used for the rapid detection of an antigen-specific
CC immune response. They can also be used for screening candidate
CC therapeutic compounds and protocols for the efficacy in either
CC stimulating or blocking the antigen-specific immune response.
CC Identification and development of such compounds and protocols is useful
CC for enhancing, decreasing or preventing antigen- specific immune
CC responses. Therapies which enhance the immune response aid in the
CC development of immunity to antigens derived from pathogens and cancerous
CC cells. Therapies which prevent or decrease the development of an antigen-
CC specific immune response are useful in preventing an immune response to
CC antigens derived from e.g. allogenic or xenogeneic organ transplants
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 49; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 2 DVWSFGILL 10

RESULT 5
AAW14809
ID AAW14809 standard; peptide; 15 AA.
XX
AC AAW14809;
XX
DT 27-AUG-2003 (revised)
DT 23-MAY-1997 (first entry)
XX
DE fes oncogene protein residues 690-704.
XX
KW Oncogene; monoclonal receptor; antibody; immunoglobulin; ligand;
KW immunogen; epitope; oncoprotein; detection.
XX
OS Feline leukemia virus.
XX
PN US5030565-A.
XX
PD 09-JUL-1991.
XX
PF 15-FEB-1985; 85US-00701954.
XX
PR 17-AUG-1983; 83US-00524084.
PR 17-AUG-1984; 84US-00001304.
PR 16-APR-1987; 87US-00039534.
XX
DR WPI; 1991-222277/30.
XX
PT Monoclonal receptors to protein, esp. onco-protein ligands - prepd. using
PT a polypeptide corresp. to a portion of the protein aminoacid sequence.
XX
PS Disclosure; Page; 41pp; English.
XX
CC The sequences given in AAW14803-32 represent peptides derived from
CC oncogenes which are bound by the monoclonal receptors of the invention.
CC The monoclonal receptor molecules are immunoglobulins which bind to both
CC (a) a protein ligand and (b) a polypeptide having an amino acid residue
CC sequence containing 7-40 amino acid residues corresponding to a sequence

CC of a portion of the protein, the receptor molecule having been raised to
CC an immunogen containing the polypeptide. High yields of monoclonal
CC receptors can be obtained which bind to or immunoreact with known
CC predetermined epitopes of protein molecules such as oncoproteins. The
CC receptors can be used for e.g. detection of oncoprotein ligands or in
CC affinity sorbants for binding and purifying oncoprotein ligands. (Updated
CC on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 49; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 5 DVWSFGILL 13

RESULT 6
AAY52604
ID AAY52604 standard; peptide; 15 AA.
XX
AC AAY52604;
XX
DT 06-AUG-2003 (revised)
DT 28-FEB-2000 (first entry)
XX
DE v-fes encoded oncoprotein epitope #4.
XX
KW Oncoprotein; epitope; oncogene; retroviral; infection; cellular;
KW monoclonal; antibody; MAb; purification; cancer; tumour; growth factor;
KW mitogenic; expression; detection; diagnosis; prognosis; immunoassay;
KW growth; development; neoplasia; foetus; non-invasive. oncoprotein.
XX
OS Synthetic.
OS Feline sarcoma virus; strain Snyder-Theilen.
XX
PN US5985587-A.
XX
PD 16-NOV-1999.
XX
PF 02-JUN-1995; 95US-00461584.
XX
PR 17-AUG-1984; 84WO-US001304.
PR 15-FEB-1985; 85US-00702954.
PR 21-MAY-1985; 85US-00736545.
PR 07-OCT-1991; 91US-00772702.
PR 02-SEP-1994; 94US-00300068.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Lerner RA, Niman HL;
XX
DR WPI; 2000-022278/02.
XX
PT Purifying oncoprotein ligands using monoclonal antibodies, useful for
PT diagnosing cancers caused by retroviruses.
XX
PS Disclosure; Col 23-24; 52pp; English.
XX
CC Sequences AAY52601-Y52675 represent oncoprotein epitopes used to raise
CC monoclonal antibodies which bind to both the epitopes and the proteins
CC that comprise them. Certain retroviruses are able to cause the formation
CC of solid tumours within a short period of time after infection of the
CC host. Oncogenes, and the oncoproteins they encode, are responsible for
CC the tumorigenic potential of these retroviruses. Retroviral oncogenes are
CC closely related to and are derived from cellular oncogenes, which encode
CC proteins with mitogenic activity such as growth factors. The invention
CC relates to monoclonal anti-oncoprotein antibodies, and the method used to
CC purify them. The method of the invention may be used for obtaining
CC purified oncoprotein ligands from aqueous solutions. It may be used in
CC this way to detect proteins produced in tumour cells to diagnose cancers
CC caused by retroviruses. It may also be used for the prognostication of
CC foetal development (and other growth states including neoplasia) using
CC either urine or other body fluid obtained by non invasive methods, the
CC antibodies being used to assay for oncoprotein. As the antibodies bind to
CC epitopes of known amino acid sequence, the type of oncoprotein being
CC expressed in the patient may be determined. (Updated on 06-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 49; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 5 DVWSFGILL 13

RESULT 7
AAY52671
ID AAY52671 standard; peptide; 15 AA.
XX
AC AAY52671;
XX
DT 06-AUG-2003 (revised)
DT 28-FEB-2000 (first entry)
XX
DE v-fes encoded oncoprotein epitope 71.
XX
KW Oncoprotein; epitope; oncogene; retroviral; infection; cellular;
KW monoclonal; antibody; MAb; purification; cancer; tumour; growth factor;
KW mitogenic; expression; detection; diagnosis; prognosis; immunoassay;
KW growth; development; neoplasia; foetus; non-invasive. oncoprotein.
XX
OS Synthetic.
OS Feline sarcoma virus.
XX
PN US5985587-A.
XX
PD 16-NOV-1999.
XX
PF 02-JUN-1995; 95US-00461584.
XX
PR 17-AUG-1984; 84WO-US001304.
PR 15-FEB-1985; 85US-00702954.
PR 21-MAY-1985; 85US-00736545.
PR 07-OCT-1991; 91US-00772702.
PR 02-SEP-1994; 94US-00300068.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Lerner RA, Niman HL;
XX
DR WPI; 2000-022278/02.
XX
PT Purifying oncoprotein ligands using monoclonal antibodies, useful for
PT diagnosing cancers caused by retroviruses.
XX
PS Claim 5; Col 52; 52pp; English.
XX
CC Sequences AAY52601-Y52675 represent oncoprotein epitopes used to raise
CC monoclonal antibodies which bind to both the epitopes and the proteins
CC that comprise them. Certain retroviruses are able to cause the formation
CC of solid tumours within a short period of time after infection of the
CC host. Oncogenes, and the oncoproteins they encode, are responsible for
CC the tumorigenic potential of these retroviruses. Retroviral oncogenes are
CC closely related to and are derived from cellular oncogenes, which encode
CC proteins with mitogenic activity such as growth factors. The invention
CC relates to monoclonal anti-oncoprotein antibodies, and the method used to
CC purify them. The method of the invention may be used for obtaining
CC purified oncoprotein ligands from aqueous solutions. It may be used in
CC this way to detect proteins produced in tumour cells to diagnose cancers

```
CC   caused by retroviruses. It may also be used for the prognostication of
CC   foetal development (and other growth states including neoplasia) using
CC   either urine or other body fluid obtained by non invasive methods, the
CC   antibodies being used to assay for oncoprotein. As the antibodies bind to
CC   epitopes of known amino acid sequence, the type of oncoprotein being
CC   expressed in the patient may be determined. (Updated on 06-AUG-2003 to
CC   correct OS field.)
XX
SQ   Sequence 15 AA;

  Query Match             100.0%;  Score 49;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.069;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db          5 DVWSFGILL 13


RESULT 8
AAP40384
ID   AAP40384 standard; peptide; 30 AA.
XX
AC   AAP40384;
XX
DT   09-JAN-2003  (revised)
DT   09-JAN-1992  (first entry)
XX
DE   Sequence of synthetic antigenic peptide 7 from group A-fes/fps family of
DE   oncoproteins.
XX
KW   Vaccine; neoplasia; tumour location; diagnosis; oncogenic virus; antigen;
KW   oncoprotein; viral oncogene.
XX
OS   Synthetic.
XX
PN   WO8403087-A.
XX
PD   16-AUG-1984.
XX
PF   14-FEB-1984;   84WO-US000190.
XX
PR   14-FEB-1983;   83US-00466329.
XX
PA   (SENA/) SEN A.
XX
PI   Sen A,  Lerner RA,  Houghten R,  Bittle JL;
XX
DR   WPI; 1984-213376/34.
XX
PT   Synthetic polypeptide(s) - useful for immunisation against neoplastic
PT   growth and in detection of neoplastic disease.
XX
PS   Example; Table 4, Page 53; 84pp; English.
XX
CC   The synthetic peptides of the invention corresp. to an AA residue SQ of a
CC   first determinant domain of a first oncoprotein produced by cells
CC   transformed by an oncogenic virus. The determinant domain is vicinal to,
CC   but exclusive of, an active site of the oncoprotein. (Updated on 09-JAN-
CC   2003 to add missing OS field.)
XX
SQ   Sequence 30 AA;

  Query Match             100.0%;  Score 49;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db          2 DVWSFGILL 10


RESULT 9
AAW14803
ID   AAW14803 standard; peptide; 30 AA.
XX
AC   AAW14803;
XX
DT   27-AUG-2003  (revised)
DT   23-MAY-1997  (first entry)
XX
DE   fes oncogene protein residues 693-722.
XX
KW   Oncogene; monoclonal receptor; antibody; immunoglobulin; ligand;
KW   immunogen; epitope; oncoprotein; detection.
XX
OS   Feline leukemia virus.
XX
PN   US5030565-A.
XX
PD   09-JUL-1991.
XX
PF   15-FEB-1985;   85US-00701954.
XX
PR   17-AUG-1983;   83US-00524084.
PR   17-AUG-1984;   84US-00001304.
PR   16-APR-1987;   87US-00039534.
XX
DR   WPI; 1991-222277/30.
XX
PT   Monoclonal receptors to protein, esp. onco-protein ligands - prepd. using
PT   a polypeptide corresp. to a portion of the protein aminoacid sequence.
XX
PS   Disclosure; Page; 41pp; English.
XX
CC   The sequences given in AAW14803-32 represent peptides derived from
CC   oncogenes which are bound by the monoclonal receptors of the invention.
CC   The monoclonal receptor molecules are immunoglobulins which bind to both
CC   (a) a protein ligand and (b) a polypeptide having an amino acid residue
CC   sequence containing 7-40 amino acid residues corresponding to a sequence
CC   of a portion of the protein, the receptor molecule having been raised to
CC   an immunogen containing the polypeptide. High yields of monoclonal
CC   receptors can be obtained which bind to or immunoreact with known
CC   predetermined epitopes of protein molecules such as oncoproteins. The
CC   receptors can be used for e.g. detection of oncoprotein ligands or in
CC   affinity sorbants for binding and purifying oncoprotein ligands. (Updated
CC   on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 30 AA;

  Query Match             100.0%;  Score 49;  DB 2;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db          2 DVWSFGILL 10


RESULT 10
AAY52601
ID   AAY52601 standard; peptide; 30 AA.
XX
AC   AAY52601;
XX
DT   06-AUG-2003  (revised)
DT   28-FEB-2000  (first entry)
XX
DE   v-fes encoded oncoprotein epitope #1.
XX
KW   Oncoprotein; epitope; oncogene; retroviral; infection; cellular;
KW   monoclonal; antibody; MAb; purification; cancer; tumour; growth factor;
KW   mitogenic; expression; detection; diagnosis; prognosis; immunoassay;
KW   growth; development; neoplasia; foetus; non-invasive. oncoprotein.
XX
OS   Synthetic.
```

OS Feline sarcoma virus; strain Snyder-Theilen.
XX
PN US5985587-A.
XX
PD 16-NOV-1999.
XX
PF 02-JUN-1995; 95US-00461584.
XX
PR 17-AUG-1984; 84WO-US001304.
PR 15-FEB-1985; 85US-00702954.
PR 21-MAY-1985; 85US-00736545.
PR 07-OCT-1991; 91US-00772702.
PR 02-SEP-1994; 94US-00300068.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Lerner RA, Niman HL;
XX
DR WPI; 2000-022278/02.
XX
PT Purifying oncoprotein ligands using monoclonal antibodies, useful for
PT diagnosing cancers caused by retroviruses.
XX
PS Claim 5; Col 23-24; 52pp; English.
XX
CC Sequences AAY52601-Y52675 represent oncoprotein epitopes used to raise
CC monoclonal antibodies which bind to both the epitopes and the proteins
CC that comprise them. Certain retroviruses are able to cause the formation
CC of solid tumours within a short period of time after infection of the
CC host. Oncogenes, and the oncoproteins they encode, are responsible for
CC the tumorigenic potential of these retroviruses. Retroviral oncogenes are
CC closely related to and are derived from cellular oncogenes, which encode
CC proteins with mitogenic activity such as growth factors. The invention
CC relates to monoclonal anti-oncoprotein antibodies, and the method used to
CC purify them. The method of the invention may be used for obtaining
CC purified oncoprotein ligands from aqueous solutions. It may be used in
CC this way to detect proteins produced in tumour cells to diagnose cancers
CC caused by retroviruses. It may also be used for the prognostication of
CC foetal development (and other growth states including neoplasia) using
CC either urine or other body fluid obtained by non invasive methods, the
CC antibodies being used to assay for oncoprotein. As the antibodies bind to
CC epitopes of known amino acid sequence, the type of oncoprotein being
CC expressed in the patient may be determined. (Updated on 06-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 30 AA;

Query Match 100.0%; Score 49; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 2 DVWSFGILL 10

RESULT 11
AAM17615
ID AAM17615 standard; protein; 43 AA.
XX
AC AAM17615;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #4049 encoded by probe for measuring cervical gene expression.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000670.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human cervical epithelial cells.
XX
PS Claim 27; SEQ ID NO 22441; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 49; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 23 DVWSFGILL 31

RESULT 12
ABB36636
ID ABB36636 standard; peptide; 43 AA.
XX
AC ABB36636;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #4142 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX

```
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483447/52.
XX
PT   Human genome-derived single exon nucleic acid probes useful for analyzing
PT   gene expression in human fetal liver.
XX
PS   Claim 27; SEQ ID NO 29271; 639pp + Sequence Listing; English.
XX
CC   The invention relates to a single exon nucleic acid probe for measuring
CC   human gene expression in a sample derived from human foetal liver. The
CC   single exon nucleic acid probes may be used for predicting, measuring and
CC   displaying gene expression in samples derived from human fetal liver. The
CC   present sequence is a peptide encoded by a single exon nucleic acid probe
CC   of the invention. Note: The sequence data for this patent did not form
CC   part of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 43 AA;

  Query Match             100.0%;  Score 49;  DB 4;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 0.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db         23 DVWSFGILL 31


RESULT 13
AAM30133
ID   AAM30133 standard; protein; 43 AA.
XX
AC   AAM30133;
XX
DT   17-OCT-2001  (first entry)
XX
DE   Peptide #4170 encoded by probe for measuring placental gene expression.
XX
KW   Probe; microarray; human; placenta; antenatal diagnosis;
KW   genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200157272-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000663.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488897/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for analyzing
PT   gene expression in human placenta.
XX
PS   Claim 27; SEQ ID NO 30402; 654pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes (SENP:
CC   see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC   such probe. The probes are useful for producing a microarray for
CC   predicting, measuring and displaying gene expression in samples derived
CC   from human placenta. The probes are useful for antenatal diagnosis of
CC   human genetic disorders
XX
SQ   Sequence 43 AA;

  Query Match             100.0%;  Score 49;  DB 4;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 0.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db         23 DVWSFGILL 31


RESULT 14
ABB31423
ID   ABB31423 standard; peptide; 43 AA.
XX
AC   ABB31423;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Peptide #4074 encoded by breast cell single exon nucleic acid probe.
XX
KW   Human; microarray; single exon probe; gene expression; breast; disease;
KW   cancer.
XX
OS   Homo sapiens.
XX
PN   WO200157271-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000662.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-496933/54.
XX
PT   New spatially-addressable set of single exon nucleic acid probes, useful
PT   for measuring gene expression in sample derived from human breast,
PT   comprises number of single exon nucleic acid probes.
XX
PS   Claim 27; SEQ ID NO 14391; 327pp + Sequence Listing; English.
XX
CC   The invention relates to a spatially-addressable set of single exon
CC   nucleic acid probes for measuring gene expression in a sample derived
CC   from human breast and BT 474 cells. The method involves contacting the
CC   probes with a collection of detectably labelled nucleic acids derived
CC   from mRNA of human breast, and then measuring the label bound to each
CC   probe of the microarray. The probes are useful for verifying the
CC   expression of regions of genomic DNA predicted to encode proteins. They
CC   are useful for gene discovery, and for determining predisposition and/or
CC   prognosing breast disease. Gene expression analysis is useful for
CC   assessing the toxicity of chemical agents on cells. The microarray of
CC   this invention presents a far greater diversity of probes for measuring
CC   gene expression, with far less bias than expressed sequence tag
CC   microarrays. The method is suitable for rapid production of functional
CC   information from genomic sequence. The present sequence is a peptide
CC   encoded by a single exon nucleic acid probe of the invention. Note: The
CC   sequence data for this patent did not form part of the printed
```

```
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 43 AA;

  Query Match             100.0%;  Score 49;  DB 4;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 0.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db         23 DVWSFGILL 31


RESULT 15
ABB21970
ID   ABB21970 standard; protein; 43 AA.
XX
AC   ABB21970;
XX
DT   23-JAN-2002  (first entry)
XX
DE   Protein #3969 encoded by probe for measuring heart cell gene expression.
XX
KW   Human; gene expression; heart; microarray; vascular system;
KW   cardiovascular disease; hypertension; cardiac arrhythmia;
KW   congenital heart disease.
XX
OS   Homo sapiens.
XX
PN   WO200157274-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000666.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488899/53.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   hearts.
XX
PS   Claim 15; SEQ ID NO 23740; 530pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes for
CC   measuring human gene expression in a sample derived from human heart (see
CC   ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC   probe. The probes may be used for predicting, measuring and displaying
CC   gene expression in samples derived from the human heart via microarrays.
CC   By measuring gene expression, the probes are useful for predicting,
CC   diagnosing, grading, staging, monitoring and prognosing diseases of the
CC   human heart and vascular system e.g. cardiovascular disease,
CC   hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 43 AA;

  Query Match             100.0%;  Score 49;  DB 4;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 0.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db         23 DVWSFGILL 31


RESULT 16
AAM69792
ID   AAM69792 standard; protein; 43 AA.
XX
AC   AAM69792;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human bone marrow expressed probe encoded protein SEQ ID NO: 30098.
XX
KW   Human; bone marrow expressed exon; gene expression analysis; probe;
KW   microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS   Homo sapiens.
XX
PN   WO200157276-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000668.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488900/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for analyzing
PT   gene expression in human bone marrow.
XX
PS   Example 4; SEQ ID NO 30098; 658pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   bone marrow. They can be used to measure gene expression in bone marrow
CC   samples, which may enable the improved diagnosis and treatment of cancers
CC   such as lymphoma, leukaemia and myeloma. The present sequence is a
CC   protein encoded by one of the probes of the invention
XX
SQ   Sequence 43 AA;

  Query Match             100.0%;  Score 49;  DB 4;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 0.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db         23 DVWSFGILL 31


RESULT 17
AAM57399
ID   AAM57399 standard; protein; 43 AA.
XX
AC   AAM57399;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 29504.
```

XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
PS Example 4; SEQ ID NO 29504; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 49; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 23 DVWSFGILL 31

RESULT 18
ABG51487
ID ABG51487 standard; peptide; 43 AA.
XX
AC ABG51487;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID No 30135.
XX
KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488898/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
PS Claim 27; SEQ ID NO 30135; 658pp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 49; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 23 DVWSFGILL 31

RESULT 19
AAM05274
ID AAM05274 standard; protein; 43 AA.
XX
AC AAM05274;
XX
DT 09-OCT-2001 (first entry)
XX
DE Peptide #3956 encoded by probe for measuring breast gene expression.
XX
KW Probe; human; breast disease; breast cancer; development disorder;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS Homo sapiens.
XX
PN WO200157270-A2.
XX
PD 09-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US000661.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.

```
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-476286/51.
XX
PT   Novel single exon nucleic acid probe used to measuring gene expression in
PT   a human breast.
XX
PS   Claim 27; SEQ ID NO 14014; 322pp; English.
XX
CC   The present invention relates to novel single exon nucleic acid probes
CC   (see AAI00010-AAI10067). The present sequence is a peptide encoded by one
CC   such probe. The probes are useful for measuring human gene expression in
CC   a human breast sample, where the probe hybridises at high stringency to a
CC   nucleic acid expressed in the human breast. The probes are useful for
CC   predicting, diagnosing, grading, staging, monitoring and prognosing
CC   diseases of the human breast, particularly those diseases with polygenic
CC   aetiology. The diseases include: breast cancer, disorders of development,
CC   inflammatory diseases of the breast, fibrocystic changes, proliferative
CC   breast disease and non-carcinoma tumours. Note: The sequence data for
CC   this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 43 AA;

  Query Match             100.0%;  Score 49;  DB 4;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 0.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db         23 DVWSFGILL 31


RESULT 20
ABG39421
ID   ABG39421 standard; peptide; 43 AA.
XX
AC   ABG39421;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human peptide encoded by genome-derived single exon probe SEQ ID 29086.
XX
KW   Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW   chronic obstructive pulmonary disease; interstitial lung disease;
KW   familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW   tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW   Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW   pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome;
KW   pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW   primary ciliary dyskinesis; pulmonary hypertension;
KW   hyaline membrane disease.
XX
OS   Homo sapiens.
XX
PN   WO200186003-A2.
XX
PD   15-NOV-2001.
XX
PF   30-JAN-2001; 2001WO-US000665.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2002-114183/15.
XX
PT   Spatially-addressable set of single exon nucleic acid probes, used to
PT   measure gene expression in human lung samples.
XX
PS   Claim 27; SEQ ID NO 29086; 634pp; English.
XX
CC   The invention relates to a spatially-addressable set of single exon
CC   nucleic acid probes for measuring gene expression in a sample derived
CC   from human lung comprising single exon nucleic acid probes having one of
CC   12614 nucleic acid sequences mentioned in the specification, or their
CC   complements or the 12387 open reading frames derived from the 12614
CC   probes. Also included are a microarray comprising the novel set of probes
CC   ; the novel set of probes which hybridise at high stringency to a nucleic
CC   acid expressed in the human lung; measuring gene expression in a sample
CC   derived from human lung, comprising (a) contacting the array with a
CC   collection of detectably labeled nucleic acids derived from human lung
CC   mRNA, and (b) measuring the label detectably bound to each probe of the
CC   array; identifying exons in a eukaryotic genome, comprising (a)
CC   algorithmically predicting at least one exon from genomic sequences of
CC   the eukaryote; and (b) detecting specific hybridisation of detectably
CC   labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC   having a fragment identical to the predicted exon, the probe is included
CC   in the above mentioned microarray; assigning exons to a single gene,
CC   comprising (a) identifying exons from genomic sequence by the method
CC   above and (b) measuring the expression of each of the exons in several
CC   tissues and/or cell types using hybridisation to a single exon
CC   microarrays having a probe with the exon, where a common pattern of
CC   expression of the exons in the tissues and/or cell types indicates that
CC   the exons should be assigned to a single gene; a peptide comprising one
CC   of 12011 sequences, mentioned in the specification, or encoded by the
CC   probes/open reading frames (ORF). The probes are used for gene expression
CC   analysis, and for identifying exons in a gene, particularly using human
CC   lung derived mRNA and for the study of lung diseases such as asthma, lung
CC   cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC   disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC   tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC   Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC   histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis,
CC   Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC   dyskinesis, pulmonary hypertension and hyaline membrane disease. The
CC   present sequence is a peptide/protein encoded by a single exon probe of
CC   the invention. Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 43 AA;

  Query Match             100.0%;  Score 49;  DB 5;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 0.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db         23 DVWSFGILL 31


RESULT 21
ABP52388
ID   ABP52388 standard; peptide; 49 AA.
XX
AC   ABP52388;
XX
DT   21-OCT-2002  (first entry)
XX
DE   JAK family human SRC related peptide SEQ ID NO:28.
XX
KW   Human; JAK; protein kinase signalling; protein tyrosine kinase; enzyme;
KW   kinase like domain; pseudo-substrate loop; anti-asthmatic; anti-allergic;
KW   dermatological; anti-inflammatory; anti-tumour; cytostatic;
KW   immunostimulant; JAK inhibitor; JAK modulator; asthma; eczema;
```

KW food allergy; inflammatory bowel disease; Crohn's disease; leukaemia;
KW lymphoma; cutaneous inflammation; immune suppression; solid tumour;
KW prostate cancer.
XX
OS Homo sapiens.
XX
PN WO200260927-A1.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-AU000088.
XX
PR 30-JAN-2001; 2001AU-00002791.
XX
PA (CYTO-) CYTOPIA PTY LTD.
XX
PI Wilks AF, Atkin J, Fantino E;
XX
DR WPI; 2002-608498/65.
XX
PT Method of selecting or designing a compound useful in the treatment of
PT e.g. asthma by assessing the ability of the compound to modulate the
PT interaction of the pseudo-substrate loop with the kinase like domain.
XX
PS Disclosure; Page 23; 82pp; English.
XX
CC The present invention describes a method (M1) of selecting or designing a
CC compound for the regulation of JAK activity involving assessing the
CC ability of the compound to modulate the interaction of the pseudo-
CC substrate loop (PSL) with the kinase like domain (KLD) of JAK. JAK family
CC proteins are protein tyrosine kinases. Also described is a compound (C1)
CC which interacts with PSL or the KLD (interacts with the binding of the
CC PSL with the KLD), which reduces the activity of the JAK compared to that
CC of the JAK in the absence of the compound. JAK has anti-asthmatic, anti-
CC allergic, dermatological, anti-inflammatory, immunostimulant, anti-tumour
CC and cytostatic. The method can be used for designing or selecting a
CC compound with the ability to regulate JAK activity; for the treatment of
CC a subject suffering from a JAK-associated disease state such as asthma,
CC eczema, food allergy, inflammatory bowel disease, Crohn's disease,
CC leukaemia, lymphoma, cutaneous inflammation, immune suppression by solid
CC tumour and prostate cancer. The method provides a number of target points
CC at which a chemical entity regulates JAK activity. The present sequence
CC represents a JAK family related amino acid sequence, which is given in
CC the exemplification of the present invention
XX
SQ Sequence 49 AA;

Query Match 100.0%; Score 49; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 2 DVWSFGILL 10

RESULT 22
ADT00021
ID ADT00021 standard; protein; 65 AA.
XX
AC ADT00021;
XX
DT 16-DEC-2004 (first entry)
XX
DE Rat FES partial protein sequence SeqID9.
XX
KW tyrosine kinase; cancer; anti-cancer agent; signalling molecule;
KW tumourigenesis; somatic alteration; colorectal cancer; NTRK3; FES;
KW GUCY2F; MCCK; MLK4; kinase domain; cytostatic; tyrosine kinase inhibitor;
KW guanylate cyclase stimulator; rat.
XX
OS Rattus norvegicus.
XX
PN WO2004082458-A2.
XX
PD 30-SEP-2004.
XX
PF 18-FEB-2004; 2004WO-US004452.
XX
PR 21-FEB-2003; 2003US-0448537P.
PR 29-MAY-2003; 2003US-0473895P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Bardelli A, Parsons W, Velculescu V, Kinzler KW, Vogelstein B;
XX
DR WPI; 2004-718702/70.
XX
PT Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCCK) and
PT associated methods for diagnosing cancer and screening for anti-cancer
PT agents.
XX
PS Example 4; SEQ ID NO 9; 363pp; English.
XX
CC This invention relates to a novel activated mutant protein tyrosine
CC kinases and associated methods for diagnosing cancer and screening for
CC anti-cancer agents. Protein kinases are signalling molecules involved in
CC tumourigenesis. Mutational analysis of the human tyrosine kinase gene
CC family identified somatic alteration sin 1 in 5 colorectal cancers, with
CC the majority of mutations occurring in the NTRK3, FES, GUCY2F and
CC MCCK/MLK4 genes. Most were identified in the kinase domain. The invention
CC may be useful for the production of compounds with a cytostatic activity
CC acting as protein tyrosine kinase inhibitors or guanylate cyclase
CC stimulators. The invention may be useful for developing methods for
CC detecting mutations involved in cancer or screening for anti-cancer
CC agents. The present sequence is that of a partial protein which was used
CC in the exemplification of the invention.
XX
SQ Sequence 65 AA;

Query Match 100.0%; Score 49; DB 8; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 48 DVWSFGILL 56

RESULT 23
ADT00022
ID ADT00022 standard; protein; 66 AA.
XX
AC ADT00022;
XX
DT 16-DEC-2004 (first entry)
XX
DE Chicken FES partial protein sequence SeqID10.
XX
KW tyrosine kinase; cancer; anti-cancer agent; signalling molecule;
KW tumourigenesis; somatic alteration; colorectal cancer; NTRK3; FES;
KW GUCY2F; MCCK; MLK4; kinase domain; cytostatic; tyrosine kinase inhibitor;
KW guanylate cyclase stimulator; chicken.
XX
OS Gallus gallus.
XX
PN WO2004082458-A2.
XX
PD 30-SEP-2004.
XX
PF 18-FEB-2004; 2004WO-US004452.
XX
PR 21-FEB-2003; 2003US-0448537P.
PR 29-MAY-2003; 2003US-0473895P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.

XX
PI Bardelli A, Parsons W, Velculescu V, Kinzler KW, Vogelstein B;
XX
DR WPI; 2004-718702/70.
XX
PT Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCCK) and
PT associated methods for diagnosing cancer and screening for anti-cancer
PT agents.
XX
PS Example 4; SEQ ID NO 10; 363pp; English.
XX
CC This invention relates to a novel activated mutant protein tyrosine
CC kinases and associated methods for diagnosing cancer and screening for
CC anti-cancer agents. Protein kinases are signalling molecules involved in
CC tumourigenesis. Mutational analysis of the human tyrosine kinase gene
CC family identified somatic alteration sin 1 in 5 colorectal cancers, with
CC the majority of mutations occurring in the NTRK3, FES, GUCY2F and
CC MCCK/MLK4 genes. Most were identified in the kinase domain. The invention
CC may be useful for the production of compounds with a cytostatic activity
CC acting as protein tyrosine kinase inhibitors or guanylate cyclase
CC stimulators. The invention may be useful for developing methods for
CC detecting mutations involved in cancer or screening for anti-cancer
CC agents. The present sequence is that of a partial protein which was used
CC in the exemplification of the invention.
XX
SQ Sequence 66 AA;

Query Match 100.0%; Score 49; DB 8; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 49 DVWSFGILL 57

RESULT 24
ADT00018
ID ADT00018 standard; protein; 66 AA.
XX
AC ADT00018;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human FES partial protein sequence SeqID6.
XX
KW tyrosine kinase; cancer; anti-cancer agent; signalling molecule;
KW tumourigenesis; somatic alteration; colorectal cancer; NTRK3; FES;
KW GUCY2F; MCCK; MLK4; kinase domain; cytostatic; tyrosine kinase inhibitor;
KW guanylate cyclase stimulator; human.
XX
OS Homo sapiens.
XX
PN WO2004082458-A2.
XX
PD 30-SEP-2004.
XX
PF 18-FEB-2004; 2004WO-US004452.
XX
PR 21-FEB-2003; 2003US-0448537P.
PR 29-MAY-2003; 2003US-0473895P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Bardelli A, Parsons W, Velculescu V, Kinzler KW, Vogelstein B;
XX
DR WPI; 2004-718702/70.
XX
PT Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCCK) and
PT associated methods for diagnosing cancer and screening for anti-cancer
PT agents.
XX
PS Example 4; SEQ ID NO 6; 363pp; English.
XX
CC This invention relates to a novel activated mutant protein tyrosine
CC kinases and associated methods for diagnosing cancer and screening for
CC anti-cancer agents. Protein kinases are signalling molecules involved in
CC tumourigenesis. Mutational analysis of the human tyrosine kinase gene
CC family identified somatic alteration sin 1 in 5 colorectal cancers, with
CC the majority of mutations occurring in the NTRK3, FES, GUCY2F and
CC MCCK/MLK4 genes. Most were identified in the kinase domain. The invention
CC may be useful for the production of compounds with a cytostatic activity
CC acting as protein tyrosine kinase inhibitors or guanylate cyclase
CC stimulators. The invention may be useful for developing methods for
CC detecting mutations involved in cancer or screening for anti-cancer
CC agents. The present sequence is that of a partial protein which was used
CC in the exemplification of the invention.
XX
SQ Sequence 66 AA;

Query Match 100.0%; Score 49; DB 8; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 49 DVWSFGILL 57

RESULT 25
ADT00019
ID ADT00019 standard; protein; 66 AA.
XX
AC ADT00019;
XX
DT 16-DEC-2004 (first entry)
XX
DE Feline FES partial protein sequence SeqID7.
XX
KW tyrosine kinase; cancer; anti-cancer agent; signalling molecule;
KW tumourigenesis; somatic alteration; colorectal cancer; NTRK3; FES;
KW GUCY2F; MCCK; MLK4; kinase domain; cytostatic; tyrosine kinase inhibitor;
KW guanylate cyclase stimulator; cat; feline.
XX
OS Felis catus.
XX
PN WO2004082458-A2.
XX
PD 30-SEP-2004.
XX
PF 18-FEB-2004; 2004WO-US004452.
XX
PR 21-FEB-2003; 2003US-0448537P.
PR 29-MAY-2003; 2003US-0473895P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Bardelli A, Parsons W, Velculescu V, Kinzler KW, Vogelstein B;
XX
DR WPI; 2004-718702/70.
XX
PT Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCCK) and
PT associated methods for diagnosing cancer and screening for anti-cancer
PT agents.
XX
PS Example 4; SEQ ID NO 7; 363pp; English.
XX
CC This invention relates to a novel activated mutant protein tyrosine
CC kinases and associated methods for diagnosing cancer and screening for
CC anti-cancer agents. Protein kinases are signalling molecules involved in
CC tumourigenesis. Mutational analysis of the human tyrosine kinase gene
CC family identified somatic alteration sin 1 in 5 colorectal cancers, with
CC the majority of mutations occurring in the NTRK3, FES, GUCY2F and
CC MCCK/MLK4 genes. Most were identified in the kinase domain. The invention
CC may be useful for the production of compounds with a cytostatic activity
CC acting as protein tyrosine kinase inhibitors or guanylate cyclase

CC stimulators. The invention may be useful for developing methods for
CC detecting mutations involved in cancer or screening for anti-cancer
CC agents. The present sequence is that of a partial protein which was used
CC in the exemplification of the invention.
XX
SQ Sequence 66 AA;

Query Match 100.0%; Score 49; DB 8; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 49 DVWSFGILL 57

RESULT 26
ADT00020
ID ADT00020 standard; protein; 66 AA.
XX
AC ADT00020;
XX
DT 16-DEC-2004 (first entry)
XX
DE Mouse FES partial protein sequence SeqID8.
XX
KW tyrosine kinase; cancer; anti-cancer agent; signalling molecule;
KW tumourigenesis; somatic alteration; colorectal cancer; NTRK3; FES;
KW GUCY2F; MCCK; MLK4; kinase domain; cytostatic; tyrosine kinase inhibitor;
KW guanylate cyclase stimulator; mouse; murine.
XX
OS Mus musculus.
XX
PN WO2004082458-A2.
XX
PD 30-SEP-2004.
XX
PF 18-FEB-2004; 2004WO-US004452.
XX
PR 21-FEB-2003; 2003US-0448537P.
PR 29-MAY-2003; 2003US-0473895P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Bardelli A, Parsons W, Velculescu V, Kinzler KW, Vogelstein B;
XX
DR WPI; 2004-718702/70.
XX
PT Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCCK) and
PT associated methods for diagnosing cancer and screening for anti-cancer
PT agents.
XX
PS Example 4; SEQ ID NO 8; 363pp; English.
XX
CC This invention relates to a novel activated mutant protein tyrosine
CC kinases and associated methods for diagnosing cancer and screening for
CC anti-cancer agents. Protein kinases are signalling molecules involved in
CC tumourigenesis. Mutational analysis of the human tyrosine kinase gene
CC family identified somatic alteration sin 1 in 5 colorectal cancers, with
CC the majority of mutations occurring in the NTRK3, FES, GUCY2F and
CC MCCK/MLK4 genes. Most were identified in the kinase domain. The invention
CC may be useful for the production of compounds with a cytostatic activity
CC acting as protein tyrosine kinase inhibitors or guanylate cyclase
CC stimulators. The invention may be useful for developing methods for
CC detecting mutations involved in cancer or screening for anti-cancer
CC agents. The present sequence is that of a partial protein which was used
CC in the exemplification of the invention.
XX
SQ Sequence 66 AA;

Query Match 100.0%; Score 49; DB 8; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 49 DVWSFGILL 57

RESULT 27
AED85831
ID AED85831 standard; protein; 70 AA.
XX
AC AED85831;
XX
DT 12-JAN-2006 (first entry)
XX
DE Tyrosine kinase alpha-FG region from c-Src.
XX
KW c-Src; tyrosine kinase; protein structure; crystallography;
KW protein co-ordinate data; drug discovery;
KW severe combined immunodeficiency; immunostimulant.
XX
OS Unidentified.
XX
PN WO2005105988-A2.
XX
PD 10-NOV-2005.
XX
PF 26-APR-2005; 2005WO-US014216.
XX
PR 28-APR-2004; 2004US-0566393P.
PR 08-APR-2005; 2005US-0669771P.
XX
PA (VERT-) VERTEX PHARM INC.
XX
PI Zuccola H, Jacobs M, Swenson L, Saxena K;
XX
DR WPI; 2005-759248/77.
XX
PT Crystal of human janus kinase 3 domain, domain complex or its homolog,
PT useful for screening kinase inhibitor.
XX
PS Disclosure; SEQ ID NO 6; 190pp; English.
XX
CC The invention relates to a crystal (I) of human janus kinase 3 (JAK3)
CC domain, domain complex or its homolog. Also included are a crystallizable
CC composition comprising JAK3 domain, a computer (comprising a machine-
CC readable data storage medium, working memory, CPU and output hardware),
CC using a computer for selecting an orientation of a chemical entity that
CC interacts favorably with a binding pocket/domain, using a computer for
CC selecting an orientation of a chemical entity with a favorable shape
CC complementarity in a binding pocket of JAK3, identifying a candidate
CC inhibitor of a molecule/molecular complex comprising a binding pocket or
CC domain, designing a compound/complex that interacts with a binding
CC pocket/domain, utilizing molecular replacement to obtain structural
CC information of a molecule/a molecular complex of unknown structure (where
CC the molecule is sufficiently homologous to human JAK3 domain); and
CC identifying a candidate inhibitor that interacts with a binding site of a
CC human JAK3 or its homolog. The human JAK3 domain complex of (I) comprises
CC human JAK3 domain and a chemical entity chosen from adenosine, ATP, ATP
CC analog, AMP-PNP, nucleotide triphosphate, nucleotide diphosphate,
CC phosphate and active site inhibitor (preferably AMP-PNP). The JAK3 domain
CC is chosen from amino acid residues 810-1100, 810-1104, 810-1115, 810-1124
CC and 813-1100 of human JAK3 (appearing as AED85826). The crystal is useful
CC for screening kinase inhibitor useful as drugs for treating severe
CC combined immunodeficiency (SCID). The present sequence is the alpha-FG
CC region from another tyrosine kinase used as comparator for the alpha-FG
CC region of JAK3.
XX
SQ Sequence 70 AA;

Query Match 100.0%; Score 49; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 DVWSFGILL 9
              |||||||||
Db         41 DVWSFGILL 49
```

RESULT 28
ABG22262
ID ABG22262 standard; protein; 85 AA.
XX
AC ABG22262;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22253.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS86449.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 52621; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 85 AA;

```
  Query Match             100.0%;  Score 49;  DB 4;  Length 85;
  Best Local Similarity   100.0%;  Pred. No. 0.41;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
```

```
Db         55 DVWSFGILL 63
```

RESULT 29
AAB58188
ID AAB58188 standard; protein; 90 AA.
XX
AC AAB58188;
XX
DT 14-MAR-2001 (first entry)
XX
DE Lung cancer associated polypeptide sequence SEQ ID 526.
XX
KW Human; lung cancer associated protein; neuroprotective; cytostatic;
KW cardioactive; immunomodulatory; muscular active; vulnerary;
KW gastrointestinal; nephrotropic; antiinfective; gynecological;
KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
KW proliferative disorder; wound healing; infectious disease.
XX
OS Homo sapiens.
XX
PN WO200055180-A2.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005918.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Ruben SM;
XX
DR WPI; 2000-587514/55.
DR N-PSDB; AAF18064.
XX
PT Lung cancer associated gene sequences, referred to as lung cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as lung cancer.
XX
PS Claim 11; Page 1015-1016; 1425pp; English.
XX
CC Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC associated proteins and polynucleotide sequences, their agonists, and
CC antagonists may have neuroprotective; cytostatic; cardioactive;
CC immunomodulatory; muscular active general; vulnerary; gastrointestinal
CC general; nephrotropic; antiinfective; gynecological; or antibacterial
CC activity. The invention also includes antibodies specific for the protein
CC or polynucleotide sequences. The lung cancer associated polynucleotide
CC sequences may be used for detection of lung cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The proteins may be used to treat disorders such as
CC neural, immune, muscular, reproductive, gastrointestinal, pulmonary,
CC cardiovascular, renal, and proliferative disorders. The proteins may also
CC be used in the treatment of wounds and infectious diseases.
CC Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are
CC used in the course of the invention for the identification and
CC characterisation of the polynucleotide and protein sequences
XX
SQ Sequence 90 AA;

```
  Query Match             100.0%;  Score 49;  DB 3;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 0.43;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db         40 DVWSFGILL 48
```

RESULT 30

ADB64505
ID ADB64505 standard; protein; 114 AA.
XX
AC ADB64505;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human protein encoded by clone HLUNG20011260.
XX
KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW cell regeneration; membrane protein; signal transduction-related protein;
KW transcription-related protein; osteoporosis; neurological disease;
KW cancer; tumour.
XX
OS Homo sapiens.
XX
PN EP1308459-A2.
XX
PD 07-MAY-2003.
XX
PF 28-MAR-2002; 2002EP-00007401.
XX
PR 05-NOV-2001; 2001JP-00379298.
PR 25-JAN-2002; 2002US-00350978.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-450961/43.
DR N-PSDB; ADB62535.
XX
PT New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
PS Claim 1; Page; 222pp; English.
XX
CC The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesising the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.
XX
SQ Sequence 114 AA;

Query Match 100.0%; Score 49; DB 7; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 71 DVWSFGILL 79

Search completed: June 29, 2006, 09:13:09
Job time : 89.8313 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 09:13:45 ; Search time 13.3373 Seconds
(without alignments)
64.927 Million cell updates/sec

Title: US-10-062-257A-16
Perfect score: 49
Sequence: 1 DVWSFGILL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	100.0	181	2	I50406	proto-fps protein
2	49	100.0	323	2	S04328	protein-tyrosine k
3	49	100.0	392	2	S04205	protein-tyrosine k
4	49	100.0	422	2	T48680	hypothetical prote
5	49	100.0	450	1	JH0559	protein-tyrosine k
6	49	100.0	450	1	S15094	protein-tyrosine k
7	49	100.0	450	2	A41973	protein-tyrosine k
8	49	100.0	450	2	I48929	protein-tyrosine k
9	49	100.0	451	1	S49016	protein-tyrosine k
10	49	100.0	453	2	I49663	tyrosine kinase (f
11	49	100.0	477	1	TVMVCS	protein-tyrosine k
12	49	100.0	496	2	T22405	protein-tyrosine k
13	49	100.0	496	2	A56040	protein-tyrosine k
14	49	100.0	503	1	JQ1321	protein-tyrosine k
15	49	100.0	503	1	TVMSHC	protein-tyrosine k
16	49	100.0	505	1	TVHUHC	protein-tyrosine k
17	49	100.0	505	2	I38396	protein-tyrosine k
18	49	100.0	507	1	A39939	protein-tyrosine k
19	49	100.0	509	1	I48845	protein-tyrosine k
20	49	100.0	509	1	OKHULK	protein-tyrosine k
21	49	100.0	512	1	I56160	protein-tyrosine k
22	49	100.0	512	1	TVHULY	protein-tyrosine k
23	49	100.0	512	2	I49552	protein-tyrosine k
24	49	100.0	517	2	A43807	protein-tyrosine k
25	49	100.0	517	2	S24547	protein-tyrosine k
26	49	100.0	523	1	TVFVMT	protein-tyrosine k
27	49	100.0	526	1	OKFVYR	protein-tyrosine k
28	49	100.0	526	1	TVFV60	protein-tyrosine k
29	49	100.0	526	1	TVFVR	protein-tyrosine k
30	49	100.0	526	2	S15582	protein-tyrosine k
31	49	100.0	526	2	S20808	protein-tyrosine k
32	49	100.0	526	2	S26420	protein-tyrosine k
33	49	100.0	528	1	TVFVG9	protein-tyrosine k
34	49	100.0	529	1	TVHUFR	protein-tyrosine k
35	49	100.0	532	1	B34104	protein-tyrosine k
36	49	100.0	532	1	A34104	protein-tyrosine k
37	49	100.0	533	1	TVCHS	protein-tyrosine k
38	49	100.0	533	1	TVFVFP	protein-tyrosine k
39	49	100.0	534	1	A44991	protein-tyrosine k
40	49	100.0	534	1	S33568	protein-tyrosine k
41	49	100.0	536	2	S33569	protein-tyrosine k
42	49	100.0	537	1	A43806	protein-tyrosine k
43	49	100.0	537	1	A45501	protein-tyrosine k
44	49	100.0	537	1	TVHUSY	protein-tyrosine k
45	49	100.0	537	2	I51592	protein-tyrosine k
46	49	100.0	539	2	B49114	protein-tyrosine k
47	49	100.0	541	1	A43610	protein-tyrosine k
48	49	100.0	541	1	TVCHYS	protein-tyrosine k
49	49	100.0	542	1	TVHUSC	protein-tyrosine k
50	49	100.0	542	2	A49114	protein-tyrosine k
51	49	100.0	544	2	I51593	protein-tyrosine k
52	49	100.0	545	2	S52313	protein-tyrosine k
53	49	100.0	546	2	S52314	protein-tyrosine k
54	49	100.0	557	1	TVFVS2	protein-tyrosine k
55	49	100.0	568	1	TVFVS1	protein-tyrosine k
56	49	100.0	587	1	TVFVPR	protein-tyrosine k
57	49	100.0	609	1	TVMVGC	protein-tyrosine k
58	49	100.0	650	1	JC1450	fibroblast growth
59	49	100.0	663	1	TVMVRR	protein-tyrosine k
60	49	100.0	802	1	TVHUF4	fibroblast growth
61	49	100.0	820	1	TVCTFF	protein-tyrosine k
62	49	100.0	820	2	I48347	protein-tyrosine k
63	49	100.0	822	1	TVHUFE	protein-tyrosine k
64	49	100.0	822	1	TVHUFF	protein-tyrosine k
65	49	100.0	824	2	I50618	c-fps proto oncoge
66	49	100.0	873	1	TVFVF	protein-tyrosine k
67	49	100.0	873	1	TVFVFS	protein-tyrosine k
68	49	100.0	1087	2	I51552	platelet-derived g
69	49	100.0	1098	1	PFMSRB	platelet-derived g
70	49	100.0	1106	1	PFHUGB	platelet-derived g
71	49	100.0	1375	1	JC5148	hepatocyte growth
72	48	98.0	241	2	PC4221	protein-tyrosine k
73	48	98.0	358	1	S71887	serine/threonine-s
74	48	98.0	388	2	I51023	fibroblast growth
75	48	98.0	402	2	B34735	protein-tyrosine k
76	48	98.0	430	2	T33178	hypothetical prote
77	48	98.0	435	2	JN0290	protein-tyrosine k
78	48	98.0	465	2	I48926	protein-tyrosine k
79	48	98.0	467	2	I56579	protein-tyrosine k
80	48	98.0	477	2	JN0291	protein-tyrosine k
81	48	98.0	499	1	A40092	protein-tyrosine k
82	48	98.0	505	2	I37206	protein-tyrosine k
83	48	98.0	505	2	I59296	protein-tyrosine k
84	48	98.0	507	2	A55625	protein-tyrosine k
85	48	98.0	527	2	A49865	protein-tyrosine k
86	48	98.0	729	2	A56795	fibroblast growth
87	48	98.0	733	2	I49293	fibroblast growth
88	48	98.0	797	2	S38579	fibroblast growth
89	48	98.0	800	1	TVHU2F	fibroblast growth
90	48	98.0	800	2	A48991	heparin-binding gr
91	48	98.0	801	2	I55363	fibroblast growth
92	48	98.0	801	4	TVHURE	transforming prote
93	48	98.0	806	1	TVHUF3	fibroblast growth
94	48	98.0	806	2	A35963	protein-tyrosine k
95	48	98.0	812	1	A36477	fibroblast growth
96	48	98.0	814	1	A39752	fibroblast growth
97	48	98.0	816	2	A49151	fibroblast growth
98	48	98.0	819	1	TVCHFG	fibroblast growth
99	48	98.0	822	1	TVHUFG	fibroblast growth
100	48	98.0	822	1	TVMSFG	fibroblast growth

ALIGNMENTS

RESULT 1
I50406
proto-fps protein - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50406
R;Pfaff, S.L.; Zhou, R.
Virology 146, 307-314, 1985
A;Title: Defining the borders of the chicken proto-fps gene, a precursor of Fujinami sar
A;Reference number: I50405; MUID:86020620; PMID:2996222
A;Accession: I50406
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-181 <PFA>
A;Cross-references: UNIPROT:Q90943; UNIPARC:UPI00000FDB36; GB:M11611; NID:g212542; PIDN:
C;Genetics:
A;Introns: 41/2; 94/1; 135/1
C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology
C;Keywords: ATP
F;1-180/Domain: protein kinase homology (fragment) <KIN>

Query Match 100.0%; Score 49; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 101 DVWSFGILL 109

RESULT 2
S04328
protein-tyrosine kinase (EC 2.7.1.112) flk - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: S04328
R;Letwin, K.; Yee, S.P.; Pawson, T.
Oncogene 3, 621-627, 1988
A;Title: Novel protein-tyrosine kinase cDNAs related to fps/fes and eph cloned using ant
A;Reference number: S04327; MUID:94167102; PMID:2485255
A;Accession: S04328
A;Molecule type: mRNA
A;Residues: 1-323 <LET>
A;Cross-references: UNIPROT:P09760; UNIPARC:UPI000012AA08; EMBL:X13412; NID:g56169; PIDN
C;Genetics:
A;Gene: flk
C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; tyrosine-speci
F;62-322/Domain: protein kinase homology <KIN>
F;70-78/Region: protein kinase ATP-binding motif

Query Match 100.0%; Score 49; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 243 DVWSFGILL 251

RESULT 3
S04205
protein-tyrosine kinase (EC 2.7.1.112) - feline sarcoma virus (fragment)
N;Alternate names: gag-onc fusion protein
C;Species: feline sarcoma virus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S04205
R;Kappes, B.; Ziemiecki, A.; Mueller, R.G.; Theilen, G.H.; Bauer, H.; Barnekow, A.
Oncogene 4, 363-372, 1989
A;Title: The TP1 isolate of feline sarcoma virus encodes a fgr-related oncogene lacking
A;Reference number: S04205; MUID:89201884; PMID:2539576
A;Accession: S04205
A;Molecule type: DNA
A;Residues: 1-392 <KAP>
A;Cross-references: UNIPROT:Q28414; UNIPARC:UPI00001046DB; EMBL:X14842; NID:g1089; PIDN:
C;Superfamily: feline sarcoma virus protein-tyrosine kinase fgr; protein kinase homology
C;Keywords: ATP; autophosphorylation; myristylation; oncogene; phosphoprotein; phosphotra
F;7-104/Domain: SH2 homology <SH2>
F;124-382/Domain: protein kinase homolcgy <KIN>
F;132-140/Region: protein kinase ATP-binding motif
F;154/Active site: Lys #status predicted
F;275,386/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 100.0%; Score 49; DB 2; Length 392;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 303 DVWSFGILL 311

RESULT 4
T48680
hypothetical protein DKFZp761P1010.1 - human
C;Species: Homo sapiens (man)
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: T48680
R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24533
A;Accession: T48680
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-422 <AAA>
A;Cross-references: UNIPROT:Q9NSH1; UNIPARC:UPI000006F5DF; EMBL:AL353940
A;Experimental source: adult amygdala; clone DKFZp761P1010
C;Genetics:
A;Note: DKFZp761P1010.1

Query Match 100.0%; Score 49; DB 2; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 308 DVWSFGILL 316

RESULT 5
JH0559
protein-tyrosine kinase (EC 2.7.1.112) CSK - human
N;Alternate names: protein-tyrosine kinase cyl; protein-tyrosine kinase T2
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 20-Aug-1994 #text_change 05-Oct-2004
C;Accession: JH0559; S38818; S19024; S19025
R;Braeuninger, A.; Holtrich, U.; Strebhardt, K.; Ruebsamen-Waigmann, H.
Gene 110, 205-211, 1992
A;Title: Isolation and characterization of a human gene that encodes a new subclass of p
A;Reference number: JH0559; MUID:92165060; PMID:1371489
A;Accession: JH0559
A;Molecule type: mRNA
A;Residues: 1-450 <BRA>
A;Cross-references: UNIPROT:P41240; UNIPARC:UPI0000128541; EMBL:X59932; NID:g30255; PIDN
A;Experimental source: lung
R;Braeuninger, A.; Karn, T.; Strebhardt, K.; Ruebsamen-Waigmann, H.
Oncogene 8, 1365-1369, 1993
A;Title: Characterization of the human CSK locus.
A;Reference number: S38818; MUID:93241739; PMID:7683131
A;Accession: S38818
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-450 <BR2>

A;Cross-references: UNIPARC:UPI0000128541; EMBL:X74765; NID:g402582; PIDN:CAB58562.1; PI
R;Partanen, J.; Armstrong, E.; Bergman, M.; Maekelae, T.P.; Hirvonen, H.; Huebner, K.; A
Oncogene 6, 2013-2018, 1991
A;Title: cyl encodes a putative cytoplasmic tyrosine kinase lacking the conserved tyrosi
A;Reference number: S19024; MUID:92050797; PMID:1945408
A;Accession: S19024
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-450 <PAR>
A;Cross-references: UNIPARC:UPI0000128541; EMBL:X60114; NID:g30314; PIDN:CAA42713.1; PID
R;Holtrich, U.; Braeuninger, A.; Strebhardt, K.; Ruebsamen-Waigmann, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 10411-10415, 1991
A;Title: Two additional protein-tyrosine kinases expressed in human lung: fourth member
A;Reference number: S19025; MUID:92073297; PMID:1720539
A;Accession: S19025
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-450 <HOL>
A;Cross-references: UNIPARC:UPI0000128541; EMBL:X59932; NID:g30255; PIDN:CAA42556.1; PID
A;Note: this sequence was submitted to the EMBL Data Library, June 1991
C;Comment: This protein lacks the N-myristylation and autophosphorylation sites present
C;Genetics:
A;Gene: GDB:CSK
A;Cross-references: GDB:131642; OMIM:124095
A;Map position: 15q23-15q25
A;Introns: 5/3; 43/3; 81/2; 154/3; 186/1; 208/1; 241/2; 271/3; 296/2; 361/3; 390/3
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;16-65/Domain: SH3 homology <SH3>
F;82-171/Domain: SH2 homology <SH2>
F;193-447/Domain: protein kinase homology <KIN>
F;201-209/Region: protein kinase ATP-binding motif
F;222/Active site: Lys #status predicted

  Query Match 100.0%; Score 49; DB 1; Length 450;
  Best Local Similarity 100.0%; Pred. No. 2.7;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
 |||||||||
Db 368 DVWSFGILL 376

RESULT 6
S15094
protein-tyrosine kinase (EC 2.7.1.112) CSK - rat
N;Alternate names: c-src kinase; tyro-13 kinase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 05-Oct-2004
C;Accession: S15094; S18500; PT0195
R;Nada, S.; Okada, M.; MacAuley, A.; Cooper, J.A.; Nakagawa, H.
Nature 351, 69-72, 1991
A;Title: Cloning of a complementary DNA for a protein-tyrosine kinase that specifically
A;Reference number: S15094; MUID:91226538; PMID:1709258
A;Accession: S15094
A;Molecule type: mRNA
A;Residues: 1-450 <NAD1>
A;Cross-references: UNIPROT:P32577; UNIPARC:UPI00001132C9; EMBL:X58631; NID:g57507; PIDN
A;Accession: S18500
A;Molecule type: protein
A;Residues: 44-49;54-67;77-86;126-137;330-337;352-360;367-376;394-401 <NAD>
A;Cross-references: UNIPARC:UPI000017258F; UNIPARC:UPI0000172590; UNIPARC:UPI0000172591;
596
R;Lai, C.; Lemke, G.
Neuron 6, 691-704, 1991
A;Title: An extended family of protein-tyrosine kinase genes differentially expressed in
A;Reference number: PT0183; MUID:91222560; PMID:2025425
A;Accession: PT0195
A;Molecule type: mRNA
A;Residues: 319-367 <LAI>
A;Cross-references: UNIPARC:UPI0000149DAC
A;Experimental source: sciatic nerve
C;Genetics:
A;Gene: tyro-13
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; tyrosine-speci
F;16-65/Domain: SH3 homology <SH3>
F;82-171/Domain: SH2 homology <SH2>
F;193-447/Domain: protein kinase homology <KIN>
F;201-209/Region: protein kinase ATP-binding motif
F;222/Active site: Lys #status predicted

  Query Match 100.0%; Score 49; DB 1; Length 450;
  Best Local Similarity 100.0%; Pred. No. 2.7;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
 |||||||||
Db 368 DVWSFGILL 376

RESULT 7
A41973
protein-tyrosine kinase (EC 2.7.1.112) CSK - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
C;Accession: A41973
R;Sabe, H.; Knudsen, B.; Okada, M.; Nada, S.; Nakagawa, H.; Hanafusa, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 2190-2194, 1992
A;Title: Molecular cloning and expression of chicken C-terminal Src kinase: lack of stab
A;Reference number: A41973; MUID:92196083; PMID:1372437
A;Accession: A41973
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-450 <SAB>
A;Cross-references: UNIPROT:P41239; UNIPARC:UPI0000128540; GB:M85039; NID:g212701; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:88058, NCBIP:88059)
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; tyrosine-speci
F;16-65/Domain: SH3 homology <SH3>
F;82-171/Domain: SH2 homology <SH2>
F;193-447/Domain: protein kinase homology <KIN>
F;201-209/Region: protein kinase ATP-binding motif

  Query Match 100.0%; Score 49; DB 2; Length 450;
  Best Local Similarity 100.0%; Pred. No. 2.7;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
 |||||||||
Db 368 DVWSFGILL 376

RESULT 8
I48929
protein-tyrosine kinase (EC 2.7.1.112) Csk - mouse
N;Alternate names: protein-tyrosine kinase Mpk-2
C;Species: Mus musculus (house mouse)
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 05-Oct-2004
C;Accession: I48929; S30498
R;Klages, S.; Adam, D.; Class, K.; Fargnoli, J.; Bolen, J.B.; Penhallow, R.C.
Proc. Natl. Acad. Sci. U.S.A. 91, 2597-2601, 1994
A;Title: Ctk: a protein-tyrosine kinase related to Csk that defines an enzyme family.
A;Reference number: A53469; MUID:94195789; PMID:7511815
A;Accession: I48929
A;Molecule type: mRNA
A;Residues: 1-450 <RES>
A;Cross-references: UNIPROT:P41241; UNIPARC:UPI00000276FA; EMBL:U05247; NID:g452471; PID
R;Gilardi-Hebenstreit, P.; Nieto, M.A.; Frain, M.; Mattei, M.G.; Chestier, A.; Wilkinson
Oncogene 7, 2499-2506, 1992
A;Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed in t
A;Reference number: S30496; MUID:93096484; PMID:1281307
A;Accession: S30498
A;Molecule type: mRNA

```
A;Residues: 316-367 <GIL>
A;Cross-references: UNIPARC:UPI000016CF22; EMBL:X57242; NID:g53189; PIDN:CAA40518.1; PID
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;16-65/Domain: SH3 homology <SH3>
F;82-171/Domain: SH2 homology <SH2>
F;193-447/Domain: protein kinase homology <KIN>
F;201-209/Region: protein kinase ATP-binding motif

  Query Match             100.0%;  Score 49;  DB 2;  Length 450;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        368 DVWSFGILL 376


RESULT 9
S49016
protein-tyrosine kinase (EC 2.7.1.112) brk - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: S49016
R;Mitchell, P.J.; Barker, K.T.; Martindale, J.E.; Kamalati, T.; Lowe, P.N.; Page, M.J.;
Oncogene 9, 2383-2390, 1994
A;Title: Cloning and characterisation of cDNAs encoding a novel non-receptor tyrosine ki
A;Reference number: S49016; MUID:94309916; PMID:8036022
A;Accession: S49016
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-451 <MIT>
A;Cross-references: UNIPROT:Q13882; UNIPARC:UPI000004F1D9; EMBL:X78549; NID:g515025; PID
C;Genetics:
A;Gene: GDB:BRK
A;Cross-references: GDB:378058
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;15-67/Domain: SH3 homology <SH3>
F;78-170/Domain: SH2 homology <SH2>
F;189-448/Domain: protein kinase homology <KIN>
F;197-205/Region: protein kinase ATP-binding motif

  Query Match             100.0%;  Score 49;  DB 1;  Length 451;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        369 DVWSFGILL 377


RESULT 10
I49663
tyrosine kinase (ferT) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Dec-2004
C;Accession: I49663
R;Fischman, K.; Edman, J.C.; Shackleford, G.M.; Turner, J.A.; Rutter, W.J.; Nir, U.
Mol. Cell. Biol. 10, 146-153, 1990
A;Title: A murine fer testis-specific transcript (ferT) encodes a truncated fer protein.
A;Reference number: I49663; MUID:90097822; PMID:2294399
A;Accession: I49663
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-453 <RES>
A;Cross-references: UNIPROT:Q61561; UNIPARC:UPI00000289C9; GB:M32054; NID:g193276; PIDN:
C;Keywords: ATP
F;91-177/Domain: SH2 homology <SH2>
F;192-452/Domain: protein kinase homology <KIN>
F;200-208/Region: protein kinase ATP-binding motif

  Query Match             100.0%;  Score 49;  DB 2;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        373 DVWSFGILL 381


RESULT 11
TVMVCS
protein-tyrosine kinase (EC 2.7.1.112) fes - feline sarcoma virus (strain Snyder-Theilen)
C;Species: feline sarcoma virus
A;Note: host Felis sp. (cat)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
C;Accession: A00652
R;Hampe, A.; Laprevotte, I.; Galibert, F.; Fedele, L.A.; Sherr, C.J.
Cell 30, 775-785, 1982
A;Title: Nucleotide sequences of feline retroviral oncogenes (v-fes) provide evidence fo
A;Reference number: A00651; MUID:83050963; PMID:6183005
A;Accession: A00652
A;Molecule type: DNA
A;Residues: 1-477 <HAM>
A;Cross-references: UNIPROT:P00543; UNIPARC:UPI000012A6F2
C;Comment: This protein is synthesized as a gag-fes polyprotein.
C;Genetics:
A;Gene: fes
C;Superfamily: protein-tyrosine kinase fps; protein kinase homology; SH2 homology
C;Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; trans
F;115-200/Domain: SH2 homology <SH2>
F;214-476/Domain: protein kinase homology <KIN>
F;222-230/Region: protein kinase ATP-binding motif
F;245/Active site: Lys #status predicted

  Query Match             100.0%;  Score 49;  DB 1;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        397 DVWSFGILL 405


RESULT 12
T22405
protein-tyrosine kinase (EC 2.7.1.112) F49B2.5 [similarity] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004
C;Accession: T22405
R;Kershaw, J.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19561
A;Accession: T22405
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-496 <WIL>
A;Cross-references: UNIPROT:O45539; UNIPARC:UPI00001755F8; EMBL:Z81543; PIDN:CAB04427.1;
A;Experimental source: clone F49B2
C;Genetics:
A;Gene: CESP:F49B2.5
A;Map position: 1
A;Introns: 82/3; 123/2; 153/1; 219/1; 242/3; 330/3; 427/1
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;
C;Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; thiol
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;4/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match             100.0%;  Score 49;  DB 2;  Length 496;
  Best Local Similarity   100.0%;  Pred. No. 2.9;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        406 DVWSFGILL 414
```

RESULT 13
A56040
protein-tyrosine kinase (EC 2.7.1.112) Srm, nonreceptor type - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 31-Dec-2004
C;Accession: A56040; I56322
R;Kohmura, N.; Yagi, T.; Tomooka, Y.; Oyanagi, M.; Kominami, R.; Takeda, N.; Chiba, J.;
Mol. Cell. Biol. 14, 6915-6925, 1994
A;Title: A novel nonreceptor tyrosine kinase, Srm: cloning and targeted disruption.
A;Reference number: A56040; MUID:95021220; PMID:7935409
A;Accession: A56040
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-496 <KOH>
A;Cross-references: UNIPROT:Q62270; UNIPARC:UPI000004F1F4; GB:D26186; NID:g529072; PIDN:
R;Kawachi, Y.; Nakauchi, H.; Otsuka, F.
J. Invest. Dermatol. 21, 533-538, 1995
A;Title: Identification of a novel cDNA clone encoding protein tyrosine kinase in murine
A;Reference number: I56322
A;Accession: I56322
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-77,'R',79-235,'LRK',239-277,'N',279-496 <KAW>
A;Cross-references: UNIPARC:UPI000004F1F5; GB:D49427; NID:g684971; PIDN:BAA08406.1; PID:
C;Genetics:
A;Map position: 2
C;Superfamily: SH2 homology; SH3 homology
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;62-111/Domain: SH3 homology <SH3>
F;124-216/Domain: SH2 homology <SH2>
F;232-491/Domain: protein kinase homology <KIN>
F;240-248/Region: protein kinase ATP-binding motif

  Query Match 100.0%; Score 49; DB 2; Length 496;
  Best Local Similarity 100.0%; Pred. No. 2.9;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 412 DVWSFGILL 420

RESULT 14
JQ1321
protein-tyrosine kinase (EC 2.7.1.112) hck - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: JQ1321; S18974
R;Okano, Y.; Sugimoto, Y.; Fukuoka, M.; Matsui, A.; Nagata, K.; Nozawa, Y.
Biochem. Biophys. Res. Commun. 181, 1137-1144, 1991
A;Title: Identification of rat cDNA encoding hck tyrosine kinase from megakaryocytes.
A;Reference number: JQ1321; MUID:92109719; PMID:1764064
A;Accession: JQ1321
A;Molecule type: mRNA
A;Residues: 1-503 <OKA>
A;Cross-references: UNIPROT:P50545; UNIPARC:UPI000012C350; GB:S74141; NID:g241436; PIDN:
A;Experimental source: megakaryocyte
R;Rema, V.; Swarup, G.
submitted to the EMBL Data Library, December 1991
A;Reference number: S18974
A;Accession: S18974
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-50,'V',52-204,'R',206-305,'T',307-503 <REM>
A;Cross-references: UNIPARC:UPI0000170BD7; EMBL:X62345; NID:g57581; PIDN:CAA44218.1; PID
C;Genetics:
A;Gene: hck
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro
n kinase
F;62-110/Domain: SH3 homology <SH3>
F;121-218/Domain: SH2 homology <SH2>
F;237-495/Domain: protein kinase homology <KIN>
F;245-253/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;267/Active site: Lys #status predicted
F;388/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match 100.0%; Score 49; DB 1; Length 503;
  Best Local Similarity 100.0%; Pred. No. 3;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 416 DVWSFGILL 424

RESULT 15
TVMSHC
protein-tyrosine kinase (EC 2.7.1.112) hck - mouse
N;Alternate names: kinase-related transforming protein (bmk)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C;Accession: A27282; A39973
R;Klemsz, M.J.; McKercher, S.R.; Maki, R.A.
Nucleic Acids Res. 15, 9600, 1987
A;Title: Nucleotide sequence of the mouse hck gene.
A;Reference number: A27282; MUID:88067781; PMID:3684607
A;Accession: A27282
A;Molecule type: mRNA
A;Residues: 1-503 <KLE>
A;Cross-references: UNIPROT:P08103; UNIPARC:UPI00000018DD; GB:Y00487; NID:g51209; PIDN:C
R;Holtzman, D.A.; Cook, W.D.; Dunn, A.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 8325-8329, 1987
A;Title: Isolation and sequence of a cDNA corresponding to a src-related gene expressed
A;Reference number: A39973; MUID:88068587; PMID:3317404
A;Accession: A39973
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-503 <HOL>
A;Cross-references: UNIPARC:UPI00000018DD; GB:J03023; NID:g192212; PIDN:AAA37305.1; PID:
C;Genetics:
A;Gene: hck
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;62-110/Domain: SH3 homology <SH3>
F;121-218/Domain: SH2 homology <SH2>
F;237-495/Domain: protein kinase homology <KIN>
F;245-253/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;267/Active site: Lys #status predicted
F;388,499/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match 100.0%; Score 49; DB 1; Length 503;
  Best Local Similarity 100.0%; Pred. No. 3;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
|||||||||
Db 416 DVWSFGILL 424

RESULT 16
TVHUHC
protein-tyrosine kinase (EC 2.7.1.112) hck - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 10-Nov-1995 #text_change 05-Oct-2004
C;Accession: A27811; A27812; JC1149; C38268; S31103
R;Quintrell, N.; Lebo, R.; Varmus, H.; Bishop, J.M.; Pettenati, M.J.; Le Beau, M.M.; Dia
Mol. Cell. Biol. 7, 2267-2275, 1987
A;Title: Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and
A;Reference number: A27811; MUID:87257942; PMID:3496523

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A;Accession: A27811
A;Molecule type: mRNA
A;Residues: 1-505 <QUI>
A;Cross-references: UNIPROT:P08631; UNIPARC:UPI000015C528; GB:M16591
A;Note: the codon given for 3-Cys (TCG) is inconsistent with the authors' translation
R;Ziegler, S.F.; Marth, J.D.; Lewis, D.B.; Perlmutter, R.M.
Mol. Cell. Biol. 7, 2276-2285, 1987
A;Title: Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of h
A;Reference number: A27812; MUID:87257943; PMID:3453117
A;Accession: A27812
A;Molecule type: mRNA
A;Residues: 1-505 <ZIE>
A;Cross-references: UNIPARC:UPI000015C528; GB:M16592; NID:g183913; PIDN:AAA52644.1; PID:
R;Hradetzky, D.; Strebhardt, K.; Ruebsamen-Waigmann, H.
Gene 113, 275-280, 1992
A;Title: The genomic locus of the human hemopoietic-specific cell protein tyrosine kinas
A;Reference number: JC1149; MUID:92241680; PMID:1572549
A;Accession: JC1149
A;Molecule type: DNA
A;Residues: 157-505 <HRA>
A;Cross-references: UNIPARC:UPI0000172589; EMBL:X59741
R;Partanen, J.; Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A;Reference number: A38268; MUID:91062389; PMID:2247464
A;Accession: C38268
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 362-417 <PAR>
A;Cross-references: UNIPARC:UPI000017258A
C;Genetics:
A;Gene: GDB:HCK
A;Cross-references: GDB:119303; OMIM:142370
A;Map position: 20q11-20q12
A;Introns: 207/1; 258/1; 318/1; 343/3; 395/1; 439/1
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;2-505/Product: protein-tyrosine kinase hck #status predicted <MAT>
F;64-112/Domain: SH3 homology <SH3>
F;123-220/Domain: SH2 homology <SH2>
F;239-497/Domain: protein kinase homology <KIN>
F;247-255/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;269/Active site: Lys #status predicted
F;390/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             100.0%;  Score 49;  DB 1;  Length 505;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        418 DVWSFGILL 426


RESULT 17
I38396
protein-tyrosine kinase (EC 2.7.1.112) FRK - human
N;Alternate names: FYN-related kinase (FRK)
C;Species: Homo sapiens (man)
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 05-Oct-2004
C;Accession: I38396
R;Lee, J.; Wang, Z.; Luoh, S.M.; Wood, W.I.; Scadden, D.T.
Gene 138, 247-251, 1994
A;Title: Cloning of FRK, a novel intracellular SRC-like tyrosine kinase-encoding gene.
A;Reference number: I38396; MUID:94171047; PMID:7510261
A;Accession: I38396
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-505 <RES>
A;Cross-references: UNIPROT:P42685; UNIPARC:UPI000012AC35; EMBL:U00803; NID:g392887; PIDI
C;Genetics:
A;Gene: GDB:FRK
A;Cross-references: GDB:355675
A;Map position: 4q35-4q35
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;49-105/Domain: SH3 homology <SH3>
F;116-208/Domain: SH2 homology <SH2>
F;232-494/Domain: protein kinase homology <KIN>
F;240-248/Region: protein kinase ATP-binding motif
F;262/Active site: Lys #status predicted

  Query Match             100.0%;  Score 49;  DB 2;  Length 505;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        415 DVWSFGILL 423


RESULT 18
A39939
protein-tyrosine kinase (EC 2.7.1.112) tkl [similarity] - chicken
N;Alternate names: kinase-related transforming protein (tkl); T-cell surface antigen ass
C;Species: Gallus gallus (chicken)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 05-Oct-2004
C;Accession: A42126; A39939
R;Chow, L.M.; Ratcliffe, M.J.; Veillette, A.
Mol. Cell. Biol. 12, 1226-1233, 1992
A;Title: tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene.
A;Reference number: A42126; MUID:92186854; PMID:1545804
A;Accession: A42126
A;Molecule type: mRNA
A;Residues: 1-88 <CHO>
A;Cross-references: UNIPARC:UPI0000172587; GB:M85043
A;Experimental source: thymus, spleen
A;Note: sequence extracted from NCBI backbone (NCBIN:88831, NCBIP:88833)
R;Strebhardt, K.; Mullins, J.I.; Bruck, C.; Ruebsamen-Waigmann, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987
A;Title: Additional member of the protein-tyrosine kinase family: the src-and lck-relate
A;Reference number: A39939; MUID:88097370; PMID:3321053
A;Accession: A39939
A;Molecule type: mRNA
A;Residues: 52-507 <STR>
A;Cross-references: UNIPARC:UPI00001713B3; GB:J03579; NID:g212712; PIDN:AAA49081.1; PID:g
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phos
F;66-114/Domain: SH3 homology <SH3>
F;125-222/Domain: SH2 homology <SH2>
F;241-499/Domain: protein kinase homology <KIN>
F;249-257/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             100.0%;  Score 49;  DB 1;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        420 DVWSFGILL 428


RESULT 19
I48845
protein-tyrosine kinase (EC 2.7.1.112) lck, lymphocyte - mouse
N;Alternate names: p56; protein-tyrosine kinase tck
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: I48845; A23639; I57629; I77452
R;Voronova, A.F.; Sefton, B.M.
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Nature 319, 682-685, 1986
A;Title: Expression of a new tyrosine protein kinase is stimulated by retrovirus promote
A;Reference number: I48845; MUID:86146842; PMID:3081813
A;Accession: I48845
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-509 <VOR1>
A;Cross-references: UNIPROT:Q91X65; UNIPARC:UPI000000418D; EMBL:X03533; NID:g54813; PIDN
R;Marth, J.D.; Peet, R.; Krebs, E.G.; Perimutter, R.M.
Cell 43, 393-404, 1985
A;Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpres
A;Reference number: A23639; MUID:86079521; PMID:2416464
A;Accession: A23639
A;Molecule type: mRNA
A;Residues: 1-282,'VP',285-509 <MAR>
A;Cross-references: UNIPARC:UPI0000172586; GB:M12056; NID:g198763
A;Note; the sequence is revised in GenBank entry MUSLCK, release 116.0, (PIDN:AAB59674.1
R;Voronova, A.F.; Adler, H.T.; Sefton, B.M.
Mol. Cell. Biol. 7, 4407-4413, 1987
A;Title: Two lck transcripts containing different 5' untranslated regions are present in
A;Reference number: I57629; MUID:88142832; PMID:3501824
A;Accession: I57629
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <VOR>
A;Cross-references: UNIPARC:UPI000016CE9D; GB:M18098; NID:g198766; PIDN:AAA39421.1; PID:
R;Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
Mol. Cell. Biol. 8, 3058-3064, 1988
A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel
A;Reference number: I57636; MUID:89096891; PMID:2850479
A;Accession: I77452
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-35,'VR' <GAR>
A;Cross-references: UNIPARC:UPI000016CE9E; GB:M21511; NID:g198768; PIDN:AAA39422.1; PID:
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro
F;68-116/Domain: SH3 homology <SH3>
F;127-224/Domain: SH2 homology <SH2>
F;243-501/Domain: protein kinase homology <KIN>
F;251-259/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;273/Active site: Lys #status predicted
F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match           100.0%;  Score 49;  DB 1;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        422 DVWSFGILL 430


RESULT 20
OKHULK
protein-tyrosine kinase (EC 2.7.1.112) lck - human
N;Alternate names: kinase-related transforming protein (lck)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 05-Oct-2004
C;Accession: JQ0152; S07822; S07200; S01879; S07143; A32797; I57636
R;Rouer, E.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R.
Gene 84, 105-113, 1989
A;Title: Structure of the human lck gene: differences in genomic organisation within src
A;Reference number: JQ0152; MUID:90108697; PMID:2558056
A;Accession: JQ0152
A;Molecule type: DNA
A;Residues: 1-509 <ROU>
A;Cross-references: UNIPROT:P06239; UNIPARC:UPI0000151F17; EMBL:X14053
R;Perlmutter, R.M.; Marth, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, C.B.
J. Cell. Biochem. 38, 117-126, 1988
A;Title: Structure and expression of lck transcripts in human lymphoid cells.
A;Reference number: S07822; MUID:89123626; PMID:3265417
A;Accession: S07822
A;Molecule type: mRNA
A;Residues: 1-86,'P',88-509 <PER>
A;Cross-references: UNIPARC:UPI0000163BD5; EMBL:X13529; NID:g34294; PIDN:CAA31884.1; PID
R;Koga, Y.; Caccia, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikai, Y.; Mak, T.W.
Eur. J. Immunol. 16, 1643-1646, 1986
A;Title: A human T cell-specific cDNA clone (YT16) encodes a protein with extensive homo
A;Reference number: S07200; MUID:87133831; PMID:3493153
A;Accession: S07200
A;Molecule type: mRNA
A;Residues: 1-205,'ASAITPI',212-257,'RCGW',262,'TTT',266,'T',268-281,'AGRLP',287-503,'ST
A;Cross-references: UNIPARC:UPI000016B09E; EMBL:X05027; NID:g36807; PIDN:CAA28691.1; PID
R;Veillette, A.; Foss, F.M.; Sausville, E.A.; Bolen, J.B.; Rosen, N.
Oncogene Res. 1, 357-374, 1987
A;Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other n
A;Reference number: S01879; MUID:88217332; PMID:2835736
A;Accession: S01879
A;Molecule type: mRNA
A;Residues: 368-471,'H',473-509 <VEI>
A;Cross-references: UNIPARC:UPI000016ABFC; EMBL:X06369; NID:g34288; PIDN:CAA29667.1; PID
R;Trevillyan, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Linna, T.J.
Biochim. Biophys. Acta 888, 286-295, 1986
A;Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56(LSTRA).
A;Reference number: S07143; MUID:87000726; PMID:3489486
A;Accession: S07143
A;Molecule type: mRNA
A;Residues: 'A',376-509 <TRE>
A;Cross-references: UNIPARC:UPI000016AF39; EMBL:X04476; NID:g35779; PIDN:CAA28165.1; PID
R;Takadera, T.; Leung, S.; Gernone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.W
Mol. Cell. Biol. 9, 2173-2180, 1989
A;Title: Structure of the two promoters of the human lck gene: differential accumulation
A;Reference number: A32797; MUID:89313764; PMID:2787474
A;Accession: A32797
A;Molecule type: DNA
A;Residues: 1-35 <TAK>
A;Cross-references: UNIPARC:UPI000016ABFF; GB:M26692; NID:g341523; PIDN:AAA59503.1; PID:g
R;Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
Mol. Cell. Biol. 8, 3058-3064, 1988
A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel
A;Reference number: I57636; MUID:89096891; PMID:2850479
A;Accession: I57636
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-35,'VR' <RES>
A;Cross-references: UNIPARC:UPI000016ABFD; GB:M21510; NID:g187031; PIDN:AAA59501.1; PID:g
C;Comment: Protein tyrosine kinases play important roles in the control of cell growth a
C;Genetics:
A;Gene: GDB:LCK
A;Cross-references: GDB:119360; OMIM:153390
A;Map position: 1p35-1p34.3
A;Introns: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology;
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phos
F;2-509/Product: protein-tyrosine kinase lck #status predicted <MAT>
F;68-116/Domain: SH3 homology <SH3>
F;127-224/Domain: SH2 homology <SH2>
F;243-501/Domain: protein kinase homology <KIN>
F;251-259/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3,5/Binding site: palmitate (Cys) (covalent) #status predicted
F;273/Active site: Lys #status predicted
F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi

  Query Match           100.0%;  Score 49;  DB 1;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        422 DVWSFGILL 430
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```
RESULT 21
I56160
protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - rat
N;Contains: protein-tyrosine kinase lyn, splice form B
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: I56160; I67811; I67812
R;Minoguchi, K.; Nishikata, H.; Siraganian, R.P.
J. Immunol. 150, 222, 1993
A;Title: Bacterially expressed rat p56lyn binds several proteins in rat basophilic leuke
A;Reference number: I56160
A;Accession: I56160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-512 <MIN>
A;Cross-references: UNIPROT:Q07014; UNIPARC:UPI0000167AC2; GB:L14951; NID:g294582; PIDN:
R;Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.
Gene 138, 219-222, 1994
A;Title: The cDNAs encoding two forms of the LYN protein tyrosine kinase are expressed i
A;Reference number: I53715; MUID:94171041; PMID:8125304
A;Accession: I67811
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-230,'L',232-307,'A',309-418,'Y',420-512 <RID1>
A;Cross-references: UNIPARC:UPI0000170BE3; GB:L14782; NID:g294578; PIDN:AAA20944.1; PID:
A;Note: in Genbank entry RATLYNATYR, release 116.0, PIDN:AAA20944.1, the source is desig
A;Accession: I67812
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-24,46-230,'L',232-307,'A',309-418,'Y',420-512 <RID2>
A;Cross-references: UNIPARC:UPI0000170BE2; GB:L14823; NID:g294580; PIDN:AAA20945.1; PID:
A;Note: in Genbank entry RATLYNBTYR, release 116.0, PIDN:AAA20945.1, the source is desig
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
F;2-512/Product: protein-tyrosine kinase lyn, splice form A #status predicted <MATA>
F;2-24,46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <MAT
F;70-118/Domain: SH3 homology <SH3>
F;129-226/Domain: SH2 homology <SH2>
F;245-504/Domain: protein kinase homology <KIN>
F;253-261/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;275/Active site: Lys #status predicted
F;397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             100.0%;  Score 49;  DB 1;  Length 512;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        425 DVWSFGILL 433


RESULT 22
TVHULY
protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - human
N;Contains: protein-tyrosine kinase lyn, splice form B
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 05-Oct-2004
C;Accession: A26719; D38268; PH0949; I53715
R;Yamanashi, Y.; Fukushige, S.I.; Semba, K.; Sukegawa, J.; Miyajima, N.; Matsubara, K.;
Mol. Cell. Biol. 7, 237-243, 1987
A;Title: The yes-related cellular gene lyn encodes a possible tyrosine kinase similar to
A;Reference number: A26719; MUID:87172710; PMID:3561390
A;Accession: A26719
A;Molecule type: mRNA
A;Residues: 1-512 <YAM>
A;Cross-references: UNIPROT:P07948; UNIPARC:UPI000013DACD; GB:M16038; NID:g187268; PIDN:
R;Partanen, J.; Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A;Reference number: A38268; MUID:91062389; PMID:2247464
A;Accession: D38268
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 369-424 <PAR>
A;Cross-references: UNIPARC:UPI0000172583
R;Bielke, W.; Ziemieki, A.; Kappos, L.; Miescher, G.C.
Biochem. Biophys. Res. Commun. 186, 1403-1409, 1992
A;Title: Expression of the B cell-associated tyrosine kinase gene lyn in primary neurobla
A;Reference number: PH0949; MUID:92378604; PMID:1510669
A;Accession: PH0949
A;Molecule type: mRNA
A;Residues: 369-424 <BIE>
A;Cross-references: UNIPARC:UPI0000172583
A;Experimental source: neuroblastoma SK-IN cell
R;Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.
Gene 138, 219-222, 1994
A;Title: The cDNAs encoding two forms of the LYN protein tyrosine kinase are expressed i
A;Reference number: I53715; MUID:94171041; PMID:8125304
A;Accession: I53715
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-24,46-512 <RID>
A;Cross-references: UNIPARC:UPI000016AC37; GB:M79321; NID:g187270; PIDN:AAB50019.1; PID:
A;Experimental source: splice form B
C;Genetics:
A;Gene: GDB:LYN
A;Cross-references: GDB:120159; OMIM:165120
A;Map position: 8q13-8qter
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
yrosine-specific protein kinase
F;2-512/Product: protein-tyrosine kinase lyn, splice form A #status predicted <MATA>
F;2-24,46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <MAT
F;70-118/Domain: SH3 homology <SH3>
F;129-226/Domain: SH2 homology <SH2>
F;245-504/Domain: protein kinase homology <KIN>
F;253-261/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;275/Active site: Lys #status predicted
F;397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

  Query Match             100.0%;  Score 49;  DB 1;  Length 512;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        425 DVWSFGILL 433


RESULT 23
I49552
protein-tyrosine kinase (EC 2.7.1.112) bsk/iyk - mouse
N;Alternate names: intestinal tyrosine kinase
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I49552; I48608
R;Oberg-Welsh, C.; Welsh, M.
Gene 152, 239-242, 1995
A;Title: Cloning of BSK, a murine FRK homologue with a specific pattern of tissue distrib
A;Reference number: I49552; MUID:95137395; PMID:7835707
A;Accession: I49552
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-512 <RES>
A;Cross-references: UNIPROT:Q61364; UNIPARC:UPI00000E734B; GB:L36132; NID:g556287; PIDN:
R;Thuveson, M.; Albrecht, D.; Zurcher, G.; Andres, A.C.; Ziemiecki, A.
Biochem. Biophys. Res. Commun. 209, 582-589, 1995
A;Title: iyk, a novel intracellular protein tyrosine kinase differentially expressed in t
A;Reference number: I48608; MUID:95251656; PMID:7733928
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A;Accession: I48608
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-153,'T',155-236,'H',238-512 <RE2>
A;Cross-references: UNIPARC:UPI00000E8172; EMBL:Z48757; NID:g736263; PIDN:CAA88658.1; PI
C;Genetics:
A;Gene: BSK
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; blocked amino end; intestine; lipoprotein; myristylation; phosphotransf
F;56-112/Domain: SH3 homology <SH3>
F;123-215/Domain: SH2 homology <SH2>
F;239-501/Domain: protein kinase homology <KIN>
F;247-255/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;5/Binding site: palmitate (Cys) (covalent) #status predicted
F;269/Active site: Lys #status predicted

  Query Match             100.0%;  Score 49;  DB 2;  Length 512;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        422 DVWSFGILL 430


RESULT 24
A43807
protein-tyrosine kinase (EC 2.7.1.112) fgr - mouse
N;Alternate names: kinase-related transforming protein (fgr)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 05-Oct-2004
C;Accession: A43807; S10072; A33127
R;King, F.J.; Cole, M.D.
Oncogene 5, 337-344, 1990
A;Title: Molecular cloning and sequencing of the murine c-fgr gene.
A;Reference number: A43807; MUID:90191719; PMID:2179817
A;Accession: A43807
A;Molecule type: mRNA
A;Residues: 1-517 <KIN>
A;Cross-references: UNIPROT:P14234; UNIPARC:UPI00000041D4; GB:X52191; NID:g50395; PIDN:C
A;Experimental source: monocyte tumor cell line from strain Balb/c
R;Yi, T.L.; Willman, C.L.
Oncogene 4, 1081-1087, 1989
A;Title: Cloning of the murine c-fgr proto-oncogene cDNA and induction of c-fgr expressi
A;Reference number: S10072; MUID:89385605; PMID:2674853
A;Accession: S10072
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-40,'N',42-211,'Q',213-517 <YIA>
A;Cross-references: UNIPARC:UPI0000028C67; EMBL:X16440; NID:g50393; PIDN:CAA34463.1; PID
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;72-121/Domain: SH3 homology <SH3>
F;132-229/Domain: SH2 homology <SH2>
F;249-507/Domain: protein kinase homology <KIXX>
F;257-265/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;279/Active site: Lys #status predicted
F;511/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             100.0%;  Score 49;  DB 2;  Length 517;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        428 DVWSFGILL 436


RESULT 25
S24547
protein-tyrosine kinase (EC 2.7.1.112) fgr - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C;Accession: S24547; PT0200
R;Yue, C.C.
submitted to the EMBL Data Library, December 1990
A;Reference number: S24547
A;Accession: S24547
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-517 <YUE>
A;Cross-references: UNIPROT:Q63206; UNIPARC:UPI00000E7676; EMBL:X57018; NID:g56145; PIDN
R;Yue, C.C.
Mol. Immunol. 28, 399-408, 1991
A;Title: Novel putative protein kinase clones from a rat large granular lymphocyte tumor
A;Reference number: PT0196; MUID:91287726; PMID:2062320
A;Accession: PT0200
A;Molecule type: mRNA
A;Residues: 371-427 <YU2>
A;Cross-references: UNIPARC:UPI00001755F4
A;Experimental source: lymphocyte cell line
C;Genetics:
A;Gene: FGR
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F;72-121/Domain: SH3 homology <SH3>
F;132-229/Domain: SH2 homology <SH2>
F;249-507/Domain: protein kinase homology <KIN>
F;257-265/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;279/Active site: Lys #status predicted
F;511/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             100.0%;  Score 49;  DB 2;  Length 517;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        428 DVWSFGILL 436


RESULT 26
TVFVMT
protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain PA101T)
C;Species: Rous sarcoma virus
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 05-Oct-2004
C;Accession: A42994
R;Dezelee, P.; Barnier, J.V.; Hampe, A.; Laugier, D.; Marx, M.; Galibert, F.; Calothy, G
Virology 189, 556-567, 1992
A;Title: Small deletion in v-src SH3 domain of a transformation defective mutant of Rous
A;Reference number: A42994; MUID:92351554; PMID:1322589
A;Accession: A42994
A;Molecule type: DNA
A;Residues: 1-523 <DEZ>
A;Cross-references: UNIPROT:P31693; UNIPARC:UPI0000135F2B; GB:M84475
C;Genetics:
A;Gene: src
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F;85-134/Domain: SH3 homology <SH3>
F;145-242/Domain: SH2 homology <SH2>
F;262-520/Domain: protein kinase homology <KIN>
F;270-278/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;292/Active site: Lys #status predicted
F;413/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experime

  Query Match             100.0%;  Score 49;  DB 1;  Length 523;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
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Db        441 DVWSFGILL 449


RESULT 27
OKFVYR
protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain H-19)
N;Alternate names: kinase-related transforming protein src
C;Species: Rous sarcoma virus
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004
C;Accession: S09609
R;Bodor, J.; Poliak, E.; Pichrtova, J.; Geryk, J.; Svoboda, J.
Nucleic Acids Res. 17, 8869, 1989
A;Title: Complete nucleotide sequence of LTR, v-src, LTR provirus H-19.
A;Reference number: S09609; MUID:90067864; PMID:2587228
A;Accession: S09609
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-526 <BOD>
A;Cross-references: UNIPROT:P25020; UNIPARC:UPI0000135F2A; EMBL:X15345; NID:g61706; PIDN
C;Genetics:
A;Gene: src
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             100.0%;  Score 49;  DB 1;  Length 526;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        444 DVWSFGILL 452


RESULT 28
TVFV60
protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
C;Species: Rous sarcoma virus
C;Date: 22-May-1981 #sequence_revision 17-Dec-1982 #text_change 05-Oct-2004
C;Accession: A38017; A00631; S02726; A38018
R;Czernilofsky, A.P.; Levinson, A.D.; Varmus, H.E.; Bishop, J.M.; Tischer, E.; Goodman,
Nature 301, 736-738, 1983
A;Title: Corrections to the nucleotide sequence of the src gene of Rous sarcoma virus.
A;Reference number: A38017; MUID:83141780; PMID:6298633
A;Accession: A38017
A;Molecule type: DNA
A;Residues: 1-526 <CZE>
A;Cross-references: UNIPROT:P00524; UNIPARC:UPI0000170DC3; GB:L29199; GB:J02018; GB:J020
A;Experimental source: strain Schmidt-Ruppin
R;Takeya, T.; Hanafusa, H.
Cell 32, 881-890, 1983
A;Title: Structure and sequence of the cellular gene homologous to the RSV sec gene and
A;Reference number: A00630; MUID:83155664; PMID:6299580
A;Accession: A00631
A;Molecule type: DNA
A;Residues: 1-62,'D',64-95,'T',97-123,'V',125-300,'N',302-526 <TAK>
A;Cross-references: UNIPARC:UPI0000172582
A;Experimental source: strain Schmidt-Ruppin
R;Barnier, J.V.; Dezelee, P.; Marx, M.; Calothy, G.
Nucleic Acids Res. 17, 1252, 1989
A;Title: Nucleotide sequence of the src gene of the Schmidt-Ruppin strain of Rous Sarcom
A;Reference number: S02726; MUID:89160256; PMID:2537953
A;Accession: S02726
A;Molecule type: DNA
A;Residues: 1-9,'G',11-62,'D',64-123,'V',125-319,'K',321-495,'S',497-526 <BAR>
A;Cross-references: UNIPARC:UPI0000135F2C; EMBL:X13745; NID:g61908; PIDN:CAA32012.1; PID
R;Takeya, T.; Feldman, R.A.; Hanafusa, H.
J. Virol. 44, 1-11, 1982
A;Title: DNA sequence of the viral and cellular src gene of chickens: I. Complete nucleot
A;Reference number: A38018; MUID:83059858; PMID:6292477
A;Accession: A38018
A;Molecule type: DNA
A;Residues: 1-15,'C',17-94,'RT',97-116,'D',118-337,'T',339-526 <TA2>
A;Cross-references: UNIPARC:UPI0000135F24; GB:K00928; NID:g210187; PIDN:AAA42565.1; PID:g
A;Experimental source: strain rASV1441
R;Neil, J.C.; Ghysdael, J.; Vogt, P.K.; Smart, J.E.
Nature 291, 675-677, 1981
A;Title: Homologous tyrosine phosphorylation sites in transformation-specific gene produ
A;Reference number: A38019; MUID:81220979; PMID:6264320
A;Contents: annotation; phosphorylation site
C;Comment: The sequence from the Schmidt-Ruppin strain is shown.
C;Genetics:
A;Gene: src
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experimer

  Query Match             100.0%;  Score 49;  DB 1;  Length 526;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        444 DVWSFGILL 452


RESULT 29
TVFVR
protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain Prague C)
C;Species: Rous sarcoma virus
C;Date: 01-Sep-1981 #sequence_revision 17-Dec-1982 #text_change 05-Oct-2004
C;Accession: A00632
R;Schwartz, D.; Tizard, R.; Gilbert, W.
submitted to the Nucleic Acid Sequence Database, September 1982
A;Reference number: A00632
A;Accession: A00632
A;Molecule type: genomic RNA
A;Residues: 1-526 <SCH>
A;Cross-references: UNIPROT:P00526; UNIPROT:O92806; UNIPARC:UPI000002BA63
A;Note: as a result of base variations, residues 242 and 288 may be replaced by Thr and
R;Neil, J.C.; Ghysdael, J.; Vogt, P.K.; Smart, J.E.
Nature 291, 675-677, 1981
A;Title: Homologous tyrosine phosphorylation sites in transformation-specific gene produ
A;Reference number: A38019; MUID:81220979; PMID:6264320
A;Contents: annotation; phosphorylation site
C;Genetics:
A;Gene: src
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experimer

  Query Match             100.0%;  Score 49;  DB 1;  Length 526;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        444 DVWSFGILL 452
```

RESULT 30
S15582
protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus (strain Prague A)
C;Species: Rous sarcoma virus
A;Variety: strain Prague A
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Oct-2004
C;Accession: S15582; S09665
R;Liu, Z.; Hackett, P.B.
Nucleic Acids Res. 17, 3986, 1989
A;Title: Sequence variation of the Rous sarcoma virus PrA src gene.
A;Reference number: S15582; MUID:89282411; PMID:2543959
A;Accession: S15582
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-526 <LIU>
A;Cross-references: UNIPROT:Q64994; UNIPROT:O92806; UNIPROT:Q60567; UNIPROT:Q07461; UNIP
A;Experimental source: strain Prague A
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989
A;Note: only a list of differences from sequence S09665 is given; however, the list is i
R;Fincham, V.J.; Wyke, J.A.
J. Virol. 58, 694-699, 1986
A;Title: Localization of temperature-sensitive transformation mutations and back mutatio
A;Reference number: S09665; MUID:86200422; PMID:3009882
A;Accession: S09665
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 231-241,'TH',244-287,'G',289-463,'P',465-501,'N',503-526 <FIN>
A;Cross-references: UNIPARC:UPI00001755F1
C;Genetics:
A;Gene: src
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; onc
F;88-137/Domain: SH3 homology <SH3>
F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase homology <KIN>
F;273-281/Region: protein kinase ATP-binding motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;295/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match 100.0%; Score 49; DB 2; Length 526;
  Best Local Similarity 100.0%; Pred. No. 3.1;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVWSFGILL 9
 |||||||||
Db 444 DVWSFGILL 452

Search completed: June 29, 2006, 09:31:36
Job time : 14.3373 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:39 ; Search time 105.831 Seconds
(without alignments)
78.664 Million cell updates/sec

Title: US-10-062-257A-16
Perfect score: 49
Sequence: 1 DVWSFGILL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	100.0	113	2	P78483_HUMAN	P78483 homo sapien
2	49	100.0	181	2	Q90943_CHICK	Q90943 gallus gall
3	49	100.0	215	2	Q8BIS9_MOUSE	Q8bis9 mus musculu
4	49	100.0	235	2	Q5U175_DROME	Q5u175 drosophila
5	49	100.0	245	2	Q9PVU9_LAMRE	Q9pvu9 lampetra re
6	49	100.0	246	2	Q9U8V5_EPTBU	Q9u8v5 eptatretus
7	49	100.0	249	2	Q9PVV0_LAMRE	Q9pvv0 lampetra re
8	49	100.0	249	2	Q9U8V6_EPTBU	Q9u8v6 eptatretus
9	49	100.0	251	2	Q9H7V3_HUMAN	Q9h7v3 homo sapien
10	49	100.0	252	2	Q9U8V2_BRABE	Q9u8v2 branchiosto
11	49	100.0	252	2	Q9U8V3_BRABE	Q9u8v3 branchiosto
12	49	100.0	259	2	Q9BDK8_PIG	Q9bdk8 sus scrofa
13	49	100.0	291	2	Q2L6P6_TRISI	Q2l6p6 trionyx sin
14	49	100.0	322	2	Q4RR72_TETNG	Q4rr72 tetraodon n
15	49	100.0	323	1	FLK_RAT	P09760 rattus norv
16	49	100.0	355	2	Q70W05_CIOIN	Q70w05 ciona intes
17	49	100.0	368	2	Q3TLX4_MOUSE	Q3tlx4 mus musculu
18	49	100.0	379	2	Q4FZR6_RAT	Q4fzr6 rattus norv
19	49	100.0	392	2	Q28414_FLV	Q28414 feline sarc
20	49	100.0	393	2	Q8BQI4_MOUSE	Q8bqi4 mus musculu
21	49	100.0	395	2	Q70W10_CIOIN	Q70w10 ciona intes
22	49	100.0	408	2	Q4R6L8_MACFA	Q4r6l8 macaca fasc
23	49	100.0	408	2	Q4RAT6_TETNG	Q4rat6 tetraodon n
24	49	100.0	422	1	STYK1_HUMAN	Q6j9g0 homo sapien
25	49	100.0	422	2	Q52LR3_HUMAN	Q52lr3 homo sapien
26	49	100.0	449	2	Q53EL3_HUMAN	Q53el3 homo sapien
27	49	100.0	449	2	Q80UI3_MOUSE	Q80ui3 mus musculu
28	49	100.0	450	1	CSK_CHICK	P41239 gallus gall
29	49	100.0	450	1	CSK_HUMAN	P41240 homo sapien
30	49	100.0	450	1	CSK_MOUSE	P41241 mus musculu
31	49	100.0	450	1	CSK_RAT	P32577 rattus norv
32	49	100.0	450	2	Q2M3N2_HUMAN	Q2m3n2 homo sapien
33	49	100.0	450	2	Q3UVH2_MOUSE	Q3uvh2 mus musculu
34	49	100.0	450	2	Q4G003_RAT	Q4g003 rattus norv
35	49	100.0	450	2	Q8VCW1_MOUSE	Q8vcw1 m c-src tyr
36	49	100.0	450	2	O73786_XENLA	O73786 xenopus lae
37	49	100.0	451	1	PTK6_HUMAN	Q13882 homo sapien
38	49	100.0	451	2	Q58F01_HUMAN	Q58f01 homo sapien
39	49	100.0	451	2	Q4RML6_TETNG	Q4rml6 tetraodon n
40	49	100.0	453	2	Q61561_MOUSE	Q61561 mus musculu
41	49	100.0	454	2	Q4RH41_TETNG	Q4rh41 tetraodon n
42	49	100.0	466	2	Q4RNX3_TETNG	Q4rnx3 tetraodon n
43	49	100.0	467	2	O77132_HYDAT	O77132 hydra atten
44	49	100.0	477	1	FES_FSVST	P00543 feline sarc
45	49	100.0	478	2	Q70W11_CIOIN	Q70w11 ciona intes
46	49	100.0	482	2	Q8N5D7_HUMAN	Q8n5d7 homo sapien
47	49	100.0	485	2	Q5R3A8_HUMAN	Q5r3a8 homo sapien
48	49	100.0	485	2	Q5TYU7_BRARE	Q5tyu7 brachydanio
49	49	100.0	491	2	Q3U6Q5_MOUSE	Q3u6q5 mus musculu
50	49	100.0	491	2	Q8CEI0_MOUSE	Q8cei0 mus musculu
51	49	100.0	492	2	Q5ZMB9_CHICK	Q5zmb9 gallus gall
52	49	100.0	496	1	SRMS_MOUSE	Q62270 mus musculu
53	49	100.0	502	1	HCK_RAT	P50545 rattus norv
54	49	100.0	502	2	Q8QGJ9_FUGRU	Q8qgj9 fugu rubrip
55	49	100.0	502	2	Q9DDK6_SALSA	Q9ddk6 salmo salar
56	49	100.0	503	1	HCK_MACFA	Q95m30 macaca fasc
57	49	100.0	503	2	Q3UD17_MOUSE	Q3ud17 m bone marr
58	49	100.0	503	2	Q6AYV7_RAT	Q6ayv7 rattus norv
59	49	100.0	505	1	FRK_HUMAN	P42685 homo sapien
60	49	100.0	505	2	Q9NTR5_HUMAN	Q9ntr5 homo sapien
61	49	100.0	506	2	Q62662_RAT	Q62662 rattus norv
62	49	100.0	507	1	LCK_CHICK	P42683 gallus gall
63	49	100.0	507	2	O45539_CAEEL	O45539 caenorhabdi
64	49	100.0	507	2	Q5FVG7_RAT	Q5fvg7 rattus norv
65	49	100.0	508	1	LCK_AOTNA	Q5pxs1 aotus nancy
66	49	100.0	508	1	LCK_HUMAN	P06239 homo sapien
67	49	100.0	508	1	LCK_MOUSE	P06240 mus musculu
68	49	100.0	508	2	Q7PPB4_ANOGA	Q7ppb4 anopheles g
69	49	100.0	509	2	Q7RTZ3_HUMAN	Q7rtz3 homo sapien
70	49	100.0	509	2	Q95M32_9PRIM	Q95m32 hylobates s
71	49	100.0	509	2	Q3ZCM0_BOVIN	Q3zcm0 bos taurus
72	49	100.0	509	2	Q4RNL0_TETNG	Q4rnl0 tetraodon n
73	49	100.0	511	1	LYN_HUMAN	P07948 homo sapien
74	49	100.0	511	1	LYN_MOUSE	P25911 mus musculu
75	49	100.0	511	1	LYN_RAT	Q07014 rattus norv
76	49	100.0	512	2	Q61LW2_CAEBR	Q61lw2 caenorhabdi
77	49	100.0	512	2	Q3TCS3_MOUSE	Q3tcs3 m nod-deriv
78	49	100.0	512	2	Q61364_MOUSE	Q61364 mus musculu
79	49	100.0	512	2	Q61745_MOUSE	Q61745 mus musculu
80	49	100.0	512	2	Q922K9_MOUSE	Q922k9 m fyn-relat
81	49	100.0	516	2	Q573B4_HUMAN	Q573b4 homo sapien
82	49	100.0	517	1	FGR_MOUSE	P14234 mus musculu
83	49	100.0	517	1	SRC42_DROME	Q9v9j3 drosophila
84	49	100.0	517	2	O77050_ANTCR	O77050 anthocidari
85	49	100.0	517	2	Q63206_RAT	Q63206 rattus norv
86	49	100.0	517	2	Q6GTF2_MOUSE	Q6gtf2 m gardner-r
87	49	100.0	517	2	Q6P6U0_RAT	Q6p6u0 rattus norv
88	49	100.0	517	2	Q8BGM0_MOUSE	Q8bgm0 m adult mal
89	49	100.0	520	2	Q6R1Y4_ASTMI	Q6r1y4 asterina mi
90	49	100.0	521	2	Q4RML8_TETNG	Q4rml8 tetraodon n
91	49	100.0	522	1	SRC_RSVPA	P31693 rous sarcom
92	49	100.0	523	1	HCK_MOUSE	P08103 mus musculu
93	49	100.0	523	2	Q45QJ2_RAT	Q45qj2 rattus norv
94	49	100.0	523	2	Q85477_9RETR	Q85477 rous sarcom
95	49	100.0	525	1	HCK_HUMAN	P08631 homo sapien
96	49	100.0	525	1	SRC_AVISR	P00525 avian sarco
97	49	100.0	525	1	SRC_RSVH1	P25020 rous sarcom
98	49	100.0	525	1	SRC_RSVP	P00526 rous sarcom
99	49	100.0	525	1	SRC_RSVSA	P00524 rous sarcom
100	49	100.0	525	1	SRC_RSVSE	P63185 rous sarcom

ALIGNMENTS

```
RESULT 1
P78483_HUMAN
ID   P78483_HUMAN   PRELIMINARY;   PRT;   113 AA.
AC   P78483;
DT   01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT   01-MAY-1997, sequence version 1.
DT   07-FEB-2006, entry version 28.
DE   C-src-2 protein (Fragment).
GN   Name=FGR;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=85187981; PubMed=2581127;
RA   Parker R.C., Mardon G., Lebo R.V., Varmus H.E., Bishop J.M.;
RT   "Isolation of duplicated human c-src genes located on chromosomes 1
RT   and 20.";
RL   Mol. Cell. Biol. 5:831-838(1985).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; K03219; AAA60585.1; -; Genomic_DNA.
DR   HSSP; P00523; 2PTK.
DR   SMR; P78483; 1-111.
DR   Ensembl; ENSG00000000938; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   113 AA;  13027 MW;  65882C8E64A18DA6 CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 113;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db         24 DVWSFGILL 32


RESULT 2
Q90943_CHICK
ID   Q90943_CHICK   PRELIMINARY;   PRT;   181 AA.
AC   Q90943;
DT   01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 2.
DT   07-FEB-2006, entry version 28.
DE   Fps proto-oncogene, 3' end. (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86020620; PubMed=2996222;
RA   Pfaff S.L., Zhou R.-P., Young J.C., Hayflick J., Duesberg P.H.;
RT   "Defining the borders of the chicken proto-fps gene, a precursor of
RT   Fujinami sarcoma virus.";
RL   Virology 146:307-314(1985).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; M11611; AAA49008.1; -; Genomic_DNA.
DR   PIR; I50406; I50406.
DR   HSSP; P11362; 1FGK.
DR   Ensembl; ENSGALG00000008340; Gallus gallus.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Tyrosine-protein kinase.
FT   NON_TER     181    181
SQ   SEQUENCE   181 AA;  20808 MW;  351873AB8DD35188 CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 181;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        101 DVWSFGILL 109


RESULT 3
Q8BIS9_MOUSE
ID   Q8BIS9_MOUSE   PRELIMINARY;   PRT;   215 AA.
AC   Q8BIS9;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 2.
DT   07-FEB-2006, entry version 24.
DE   10, 11 days embryo whole body cDNA, RIKEN full-length enriched
DE   library, clone:2810409K13 product:c-src tyrosine kinase, full insert
DE   sequence. (Fragment).
GN   Name=Csk;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
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RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC ---
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC ---
DR EMBL; AK013057; BAC25388.2; -; mRNA.
DR SMR; Q8BIS9; 1-182.
DR MGI; MGI:88537; Csk.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF07714; Pkinase_Tyr; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

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KW   Kinase; Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   215 AA;  24394 MW;  41D8521DE365FE11 CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
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Db        133 DVWSFGILL 141


RESULT 4
Q5U175_DROME
ID   Q5U175_DROME   PRELIMINARY;   PRT;   235 AA.
AC   Q5U175;
DT   07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   07-DEC-2004, sequence version 1.
DT   21-FEB-2006, entry version 13.
DE   RE19378p.
GN   Name=Src42A;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Berkeley;
RA   Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA   Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
RL   Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC       protein (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BT016017; AAV36902.1; -; mRNA.
DR   FlyBase; FBgn0004603; Src42A.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   ATP-binding; Developmental protein; Kinase; Membrane;
KW   Nucleotide-binding; Receptor; Transferase; Transmembrane;
KW   Tyrosine-protein kinase.
SQ   SEQUENCE   235 AA;  27038 MW;  8B9F65DB2EE15B9A CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 235;
  Best Local Similarity   100.0%;  Pred. No. 2.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
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Db        146 DVWSFGILL 154


RESULT 5
Q9PVU9_LAMRE
ID   Q9PVU9_LAMRE   PRELIMINARY;   PRT;   245 AA.
AC   Q9PVU9;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 28.
DE   Src-like B (Fragment).
OS   Lampetra reissneri (Far Eastern brook lamprey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC   Petromyzontiformes; Petromyzontidae; Lethenteron.
OX   NCBI_TaxID=7753;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20020330; PubMed=10552041;
RA   Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
RT   "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey:
RT   isoform duplications around the divergence of cyclostomes and
RT   gnathostomes.";
RL   J. Mol. Evol. 49:601-608(1999).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB025550; BAA84740.1; -; mRNA.
DR   HSSP; P12931; 1FMK.
DR   SMR; Q9PVU9; 1-245.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   245 AA;  28028 MW;  B73B5C2B64AA0FD5 CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 245;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
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Db        156 DVWSFGILL 164


RESULT 6
Q9U8V5_EPTBU
ID   Q9U8V5_EPTBU   PRELIMINARY;   PRT;   246 AA.
AC   Q9U8V5;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 28.
DE   Src-like B (Fragment).
OS   Eptatretus burgeri (Inshore hagfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
OC   Myxinidae; Eptatretinae; Eptatretus.
OX   NCBI_TaxID=7764;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20020330; PubMed=10552041;
RA   Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
RT   "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey:
RT   isoform duplications around the divergence of cyclostomes and
RT   gnathostomes.";
RL   J. Mol. Evol. 49:601-608(1999).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
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CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB025547; BAA84737.1; -; mRNA.
DR   HSSP; P12931; 1FMK.
DR   SMR; Q9U8V5; 1-246.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   246 AA;  28117 MW;  212CBEE658C6E04D CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 246;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        156 DVWSFGILL 164


RESULT 7
Q9PVV0_LAMRE
ID   Q9PVV0_LAMRE   PRELIMINARY;   PRT;   249 AA.
AC   Q9PVV0;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 28.
DE   Src-like A (Fragment).
OS   Lampetra reissneri (Far Eastern brook lamprey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC   Petromyzontiformes; Petromyzontidae; Lethenteron.
OX   NCBI_TaxID=7753;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20020330; PubMed=10552041;
RA   Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
RT   "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey:
RT   isoform duplications around the divergence of cyclostomes and
RT   gnathostomes.";
RL   J. Mol. Evol. 49:601-608(1999).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB025549; BAA84739.1; -; mRNA.
DR   HSSP; P08631; 1AD5.
DR   SMR; Q9PVV0; 1-246.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   249 AA;  28627 MW;  DAC9DBA041F3D941 CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        162 DVWSFGILL 170


RESULT 8
Q9U8V6_EPTBU
ID   Q9U8V6_EPTBU   PRELIMINARY;   PRT;   249 AA.
AC   Q9U8V6;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 28.
DE   Src-like A (Fragment).
OS   Eptatretus burgeri (Inshore hagfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
OC   Myxinidae; Eptatretinae; Eptatretus.
OX   NCBI_TaxID=7764;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20020330; PubMed=10552041;
RA   Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
RT   "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey:
RT   isoform duplications around the divergence of cyclostomes and
RT   gnathostomes.";
RL   J. Mol. Evol. 49:601-608(1999).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB025546; BAA84736.1; -; mRNA.
DR   HSSP; P06239; 1QPC.
DR   SMR; Q9U8V6; 1-249.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   249 AA;  28636 MW;  D7F37EE197EA580C CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        162 DVWSFGILL 170


RESULT 9
Q9H7V3_HUMAN
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ID   Q9H7V3_HUMAN   PRELIMINARY;   PRT;   251 AA.
AC   Q9H7V3;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
DT   07-MAR-2006, entry version 32.
DE   Hypothetical protein FLJ14219 (OTTHUMP00000030929).
GN   Name=SRC; ORFNames=RP5-823N20.1-004;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA   Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA   Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA   Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA   Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA   Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA   Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA   Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA   Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA   Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Wallis J.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK024281; BAB14871.1; -; mRNA.
DR   EMBL; AL133293; CAI22921.1; -; Genomic_DNA.
DR   HSSP; P12931; 2SRC.
DR   SMR; Q9H7V3; 1-251.
DR   Ensembl; ENSG00000197122; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   ATP-binding; Kinase; Membrane; Nucleotide-binding; Receptor;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
SQ   SEQUENCE   251 AA;  28721 MW;  ECA7468046D6657A CRC64;

  Query Match            100.0%;  Score 49;  DB 2;  Length 251;
  Best Local Similarity  100.0%;  Pred. No. 2.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        162 DVWSFGILL 170


RESULT 10
Q9U8V2_BRABE
ID   Q9U8V2_BRABE   PRELIMINARY;   PRT;   252 AA.
AC   Q9U8V2;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 28.
DE   Src-like A-1 (Fragment).
OS   Branchiostoma belcheri (Amphoxius).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7741;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20020330; PubMed=10552041;
RA   Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
RT   "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey:
RT   isoform duplications around the divergence of cyclostomes and
RT   gnathostomes.";
RL   J. Mol. Evol. 49:601-608(1999).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB025551; BAA84741.1; -; mRNA.
DR   HSSP; P00523; 2PTK.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Tyrosine-protein kinase.
FT   NON_TER       1       1
SQ   SEQUENCE   252 AA;  28752 MW;  3C6348FDE12A7D7F CRC64;

  Query Match            100.0%;  Score 49;  DB 2;  Length 252;
  Best Local Similarity  100.0%;  Pred. No. 2.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        163 DVWSFGILL 171


RESULT 11
Q9U8V3_BRABE
ID   Q9U8V3_BRABE   PRELIMINARY;   PRT;   252 AA.
AC   Q9U8V3;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
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DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 32.
DE   Src-like A-2.
OS   Branchiostoma belcheri (Amphoxius).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7741;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20020330; PubMed=10552041;
RA   Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
RT   "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey:
RT   isoform duplications around the divergence of cyclostomes and
RT   gnathostomes.";
RL   J. Mol. Evol. 49:601-608(1999).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB025551; BAA84765.1; -; mRNA.
DR   HSSP; P00523; 2PTK.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   ATP-binding; Kinase; Membrane; Nucleotide-binding; Transferase;
KW   Transmembrane; Tyrosine-protein kinase.
SQ   SEQUENCE   252 AA;  28798 MW;  B331B41E7AFEE2A7 CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 252;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        163 DVWSFGILL 171


RESULT 12
Q9BDK8_PIG
ID   Q9BDK8_PIG     PRELIMINARY;   PRT;   259 AA.
AC   Q9BDK8;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 24.
DE   Platelet-derived growth factor receptor beta (Fragment).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Remillard P.E., Lacroix D.A., Murphy B.D.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AF347051; AAK31152.1; -; mRNA.
DR   HSSP; P11362; 1FGK.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Phosphorylation; Receptor; Tyrosine-protein kinase.
FT   NON_TER       1      1
FT   NON_TER     259    259
SQ   SEQUENCE   259 AA;  28776 MW;  F1A432566282D951 CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 259;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        234 DVWSFGILL 242


RESULT 13
Q2L6P6_TRISI
ID   Q2L6P6_TRISI   PRELIMINARY;   PRT;   291 AA.
AC   Q2L6P6;
DT   07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT   07-MAR-2006, sequence version 1.
DT   07-MAR-2006, entry version 1.
DE   Fibroblast growth factor receptor 4 (Fragment).
GN   Name=PsFGFR4;
OS   Trionyx sinensis (Chinese softshell turtle) (Pelodiscus sinensis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Testudines; Cryptodira; Trionychoidea; Trionychidae; Pelodiscus.
OX   NCBI_TaxID=13735;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole embryo;
RA   Kuraku S., Ishijima J., Nishida-Umehara C., Agata K., Kuratani S.,
RA   Matsuda Y.;
RT   "cDNA-based gene mapping and GC3 profiling in the soft-shelled turtle
RT   suggest a chromosomal size-dependent GC bias shared by sauropsids.";
RL   Chromosome Res. 0:0-0(2006).
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB188373; BAE78797.1; -; mRNA.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER     291    291
SQ   SEQUENCE   291 AA;  33348 MW;  4A1CE92660C5720C CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 291;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        191 DVWSFGILL 199
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RESULT 14
Q4RR72_TETNG
ID   Q4RR72_TETNG   PRELIMINARY;   PRT;   322 AA.
AC   Q4RR72;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   Chromosome 14 SCAF15003, whole genome shotgun sequence. (Fragment).
GN   ORFNames=GSTENG00030294001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC       cycle. It is required in higher cells for entry into S-phase and
CC       mitosis. Component of the kinase complex that phosphorylates the
CC       repetitive C-terminus of RNA polymerase II. Catalytic component of
CC       MPF (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC       mature oocytes (By similarity).
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CAAE01015003; CAG09110.1; -; Genomic_DNA.
DR   SMR; Q4RR72; 2-322.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   322 AA;  36768 MW;  EC0ED0B6DB1CBB2F CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        209 DVWSFGILL 217


RESULT 15
FLK_RAT
ID   FLK_RAT        STANDARD;      PRT;   323 AA.
AC   P09760;
DT   01-JUL-1989, integrated into UniProtKB/Swiss-Prot.
DT   01-JUL-1989, sequence version 1.
DT   07-MAR-2006, entry version 56.
DE   Tyrosine-protein kinase FLK (EC 2.7.1.112) (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=Wistar; TISSUE=Brain;
RX   MEDLINE=94167102; PubMed=2485255;
RA   Letwin K., Yee S.P., Pawson T.;
RT   "Novel protein-tyrosine kinase cDNAs related to fps/fes and eph cloned
RT   using anti-phosphotyrosine antibody.";
RL   Oncogene 3:621-627(1988).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. Fes/fps
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X13412; CAA31778.1; -; mRNA.
DR   PIR; S04328; S04328.
DR   HSSP; P54763; 1JPA.
DR   Ensembl; ENSRNOG00000015898; Rattus norvegicus.
DR   LinkHub; P09760; -.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; PARTIAL.
DR   PROSITE; PS50002; SH3; PARTIAL.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation; SH2 domain;
KW   Transferase; Tyrosine-protein kinase.
FT   CHAIN        <1    323       Tyrosine-protein kinase FLK.
FT                                 /FTId=PRO_0000088093.
FT   DOMAIN       <1     51       SH2.
FT   DOMAIN       64    315       Protein kinase.
FT   NP_BIND      70     78       ATP (By similarity).
FT   ACT_SITE    185    185       Proton acceptor (By similarity).
FT   BINDING      92     92       ATP (By similarity).
```

```
FT   MOD_RES      215    215       Phosphotyrosine (by autocatalysis) (By
FT                                 similarity).
FT   NON_TER        1      1
SQ   SEQUENCE   323 AA;  37104 MW;  D7BA8BDE50C3EAC1 CRC64;

  Query Match             100.0%;  Score 49;  DB 1;  Length 323;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        243 DVWSFGILL 251


RESULT 16
Q70W05_CIOIN
ID   Q70W05_CIOIN   PRELIMINARY;   PRT;   355 AA.
AC   Q70W05;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 16.
DE   Src protein (Fragment).
GN   Name=src;
OS   Ciona intestinalis.
OC   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC   Phlebobranchia; Cionidae; Ciona.
OX   NCBI_TaxID=7719;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Leveugle M., Prat K., Popovici C., Birnbaum D., Coulier F.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ534320; CAD58838.1; -; mRNA.
DR   HSSP; P11362; 1AGW.
DR   Ensembl; ENSCING00000005826; Ciona intestinalis.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 2.
DR   Pfam; PF00017; SH2; 2.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00326; SH3; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER        1      1
SQ   SEQUENCE   355 AA;  40337 MW;  24348637494EC157 CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        273 DVWSFGILL 281


RESULT 17
Q3TLX4_MOUSE
ID   Q3TLX4_MOUSE   PRELIMINARY;   PRT;   368 AA.
AC   Q3TLX4;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched
DE   library, clone:G830026O06 product:lymphocyte protein tyrosine kinase,
DE   full insert sequence. (Fragment).
GN   Name=Lck;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
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```
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK166263; BAE38668.1; -; mRNA.
DR   MGI; MGI:96756; Lck.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   368 AA;  42018 MW;  7AB6AE53AF1A5059 CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 368;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        281 DVWSFGILL 289


RESULT 18
Q4FZR6_RAT
ID   Q4FZR6_RAT     PRELIMINARY;   PRT;   379 AA.
AC   Q4FZR6;
DT   30-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   30-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Lck_mapped protein (Fragment).
GN   Name=Lck_mapped;
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OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC099218; AAH99218.1; -; mRNA.
DR   SMR; Q4FZR6; 2-379.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   379 AA;  43336 MW;  7CDEB573BAFB53AB CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 379;
  Best Local Similarity   100.0%;  Pred. No. 4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        292 DVWSFGILL 300


RESULT 19
Q28414_FLV
ID   Q28414_FLV     PRELIMINARY;   PRT;   392 AA.
AC   Q28414;
DT   01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1996, sequence version 1.
DT   07-FEB-2006, entry version 38.
DE   Gag-onc fusion protein (Fragment).
OS   Feline sarcoma virus.
OC   Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC   Gammaretrovirus.
OX   NCBI_TaxID=11772;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Fibrosarcoma;
RX   MEDLINE=89201884; PubMed=2539576;
RA   Kappes B., Ziemiecki A., Mueller R.G., Theilen G.H., Bauer H.,
RA   Barnekow A.;
RT   "The TPI isolate of feline sarcoma virus encodes a fgr-related
RT   oncogene lacking gamma-actin sequences.";
RL   Oncogene 4:363-372(1989).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X14842; CAA32947.1; -; Genomic_DNA.
DR   PIR; S04205; S04205.
DR   HSSP; P00523; 2PTK.
DR   SMR; Q28414; 5-390.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Oncogene; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   392 AA;  44776 MW;  70CF642A7766F684 CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 392;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
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Db        303 DVWSFGILL 311
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RESULT 20
Q8BQI4_MOUSE
ID   Q8BQI4_MOUSE   PRELIMINARY;   PRT;   393 AA.
AC   Q8BQI4;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 24.
DE   7 days embryo whole body cDNA, RIKEN full-length enriched library,
DE   clone:C430045O19 product:src-related kinase lacking C-terminal
DE   regulatory tyrosine and N-terminal myristylation sites, full insert
DE   sequence. (Fragment).
GN   Name=Srms;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK049582; BAC33825.1; -; mRNA.
DR   HSSP; P11362; 1FGK.
DR   Ensembl; ENSMUSG00000027579; Mus musculus.
DR   MGI; MGI:101865; Srms.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

  Query Match            100.0%;  Score 49;  DB 2;  Length 393;
  Best Local Similarity  100.0%;  Pred. No. 4.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
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Db        309 DVWSFGILL 317


RESULT 21
Q70W10_CIOIN
ID   Q70W10_CIOIN   PRELIMINARY;   PRT;   395 AA.
AC   Q70W10;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Fibroblast growth factor receptor (Fragment).
GN   Name=fgfr;
OS   Ciona intestinalis.
OC   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC   Phlebobranchia; Cionidae; Ciona.
OX   NCBI_TaxID=7719;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Leveugle M., Prat K., Popovici C., Birnbaum D., Coulier F.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ534315; CAD58833.1; -; mRNA.
DR   HSSP; P11362; 1AGW.
DR   Ensembl; ENSCING00000000875; Ciona intestinalis.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR013098; I-set.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Receptor; Tyrosine-protein kinase.
FT   NON_TER       1      1
FT   NON_TER     395    395
SQ   SEQUENCE   395 AA;  45825 MW;  0F0D870A8ECFF499 CRC64;

  Query Match            100.0%;  Score 49;  DB 2;  Length 395;
  Best Local Similarity  100.0%;  Pred. No. 4.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        313 DVWSFGILL 321


RESULT 22
Q4R6L8_MACFA
ID   Q4R6L8_MACFA   PRELIMINARY;   PRT;   408 AA.
AC   Q4R6L8;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Testis cDNA, clone: QtsA-17706, similar to human fyn-related kinase
DE   (FRK),.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15944441; DOI=10.1093/molbev/msi187;
RA   Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA   Sugano S., Gojobori T., Shen C.-K.J., Wu C.I., Hashimoto K.;
RT   "Substitution Rate and Structural Divergence of 5'UTR Evolution:
RT   Comparative Analysis Between Human and Cynomolgus Monkey cDNAs.";
RL   Mol. Biol. Evol. 22:1976-1982(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
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RG   International consortium for macaque cDNA sequencing and analysis;
RT   "DNA sequences of macaque genes expressed in brain or testis and its
RT   evolutionary implications.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB169165; BAE01257.1; -; mRNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   Kinase.
SQ   SEQUENCE   408 AA;  47153 MW;  1AFE91AC88554555 CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 408;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
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Db        318 DVWSFGILL 326


RESULT 23
Q4RAT6_TETNG
ID   Q4RAT6_TETNG   PRELIMINARY;   PRT;   408 AA.
AC   Q4RAT6;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   Chromosome undetermined SCAF22943, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00036856001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC       cycle. It is required in higher cells for entry into S-phase and
CC       mitosis. Component of the kinase complex that phosphorylates the
CC       repetitive C-terminus of RNA polymerase II. Catalytic component of
CC       MPF (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC       mature oocytes (By similarity).
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CAAE01022943; CAG14497.1; -; Genomic_DNA.
DR   SMR; Q4RAT6; 6-405.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
FT   NON_TER     408    408
SQ   SEQUENCE   408 AA;  46231 MW;  F6DCC51EBD5B603E CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 408;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        366 DVWSFGILL 374


RESULT 24
STYK1_HUMAN
ID   STYK1_HUMAN    STANDARD;      PRT;   422 AA.
AC   Q6J9G0; Q9BXY2; Q9NSH1;
DT   26-APR-2005, integrated into UniProtKB/Swiss-Prot.
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DT   26-APR-2005, sequence version 2.
DT   07-MAR-2006, entry version 16.
DE   Tyrosine protein-kinase STYK1 (EC 2.7.1.112)
DE   (Serine/threonine/tyrosine kinase 1) (Novel oncogene with kinase-
DE   domain) (Protein PK-unique).
GN   Name=STYK1; Synonyms=NOK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
RC   TISSUE=Fetal brain;
RX   PubMed=12841579; DOI=10.1023/A:1023934017174;
RA   Ye X., Ji C., Huang Q., Cheng C., Tang R., Xu J., Zeng L., Dai J.,
RA   Wu Q., Gu S., Xie Y., Mao Y.;
RT   "Isolation and characterization of a human putative receptor protein
RT   kinase cDNA STYK1.";
RL   Mol. Biol. Rep. 30:91-96(2003).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA], TISSUE SPECIFICITY, AND VARIANT SER-204.
RC   TISSUE=Amygdala;
RX   PubMed=15150103; DOI=10.1158/0008-5472.CAN-03-2106;
RA   Liu L., Yu X.-Z., Li T.-S., Song L.-X., Chen P.-L., Suo T.-L.,
RA   Li Y.-H., Wang S.-D., Chen Y., Ren Y.-M., Zhang S.-P., Chang Z.-J.,
RA   Fu X.-Y.;
RT   "A novel protein tyrosine kinase NOK that shares homology with
RT   platelet-derived growth factor/fibroblast growth factor receptors
RT   induces tumorigenesis and metastasis in nude mice.";
RL   Cancer Res. 64:3491-3499(2004).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Amygdala;
RG   The German cDNA consortium;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Probable tyrosine protein-kinase, which has strong
CC       transforming capabilities on a variety of cell lines. When
CC       overexpressed, it can also induce tumor cell invasion as well as
CC       metastasis in distant organs. May act by activating both MAP
CC       kinase and phosphatidylinositol 3'-kinases (PI3K) pathways (By
CC       similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC   -!- TISSUE SPECIFICITY: Widely expressed. Highly expressed in brain,
CC       placenta and prostate. Expressed in tumor cells such as hepatoma
CC       cells LO2, cervix carcinoma cells HeLa, ovary cancer cells Ho8910
CC       and chronic myelogenous leukemia cells K562, but not in other
CC       tumor cells such as epidermoid carcinoma (A431).
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF251059; AAK34949.1; -; mRNA.
DR   EMBL; AY563054; AAT01226.1; -; mRNA.
DR   EMBL; AL353940; CAB89250.1; -; mRNA.
DR   PIR; T48680; T48680.
DR   HSSP; P08581; 1R1W.
DR   HGNC; HGNC:18889; STYK1.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   ATP-binding; Kinase; Membrane; Nucleotide-binding; Polymorphism;
KW   Proto-oncogene; Transferase; Transmembrane; Tyrosine-protein kinase.
FT   CHAIN         1    422       Tyrosine protein-kinase STYK1.
FT                                /FTId=PRO_0000088163.
FT   TRANSMEM     26     46       Potential.
FT   DOMAIN      114    384       Protein kinase.
FT   NP_BIND     120    128       ATP (By similarity).
FT   ACT_SITE    251    251       Proton acceptor (By similarity).
FT   BINDING     147    147       ATP (By similarity).
FT   VARIANT     204    204       G -> S (in dbSNP:3759259).
FT                                /FTId=VAR_022245.
FT   CONFLICT    192    192       V -> M (in Ref. 3).
FT   CONFLICT    304    304       R -> S (in Ref. 3).
SQ   SEQUENCE   422 AA;  47584 MW;  81D1F676DC6F2E26 CRC64;

  Query Match             100.0%;  Score 49;  DB 1;  Length 422;
  Best Local Similarity   100.0%;  Pred. No. 4.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        308 DVWSFGILL 316


RESULT 25
Q52LR3_HUMAN
ID   Q52LR3_HUMAN   PRELIMINARY;   PRT;   422 AA.
AC   Q52LR3;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   21-FEB-2006, entry version 12.
DE   Serine/threonine/tyrosine kinase 1.
GN   Name=STYK1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RG   NIH MGC Project;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC093824; AAH93824.1; -; mRNA.
DR   EMBL; BC093822; AAH93822.1; -; mRNA.
DR   Ensembl; ENSG00000060140; Homo sapiens.
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DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
KW   ATP-binding; Kinase; Membrane; Nucleotide-binding; Receptor;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
SQ   SEQUENCE   422 AA;  47547 MW;  B7CD8BC006029D3B CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 422;
  Best Local Similarity   100.0%;  Pred. No. 4.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        308 DVWSFGILL 316


RESULT 26
Q53EL3_HUMAN
ID   Q53EL3_HUMAN   PRELIMINARY;   PRT;   449 AA.
AC   Q53EL3;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   C-src tyrosine kinase variant (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
RA   Maruyama K., Sugano S.;
RT   "Oligo-capping : a simple method to replace the cap structure of
RT   eucaryotic mRNAs with oligoribonucleotides.";
RL   Gene 138:171-174(1994).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=98038986; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
RA   Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
RT   "Construction and characterization of a full length-enriched and a 5'-
RT   end-enriched cDNA library.";
RL   Gene 200:149-156(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RA   Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK223626; BAD97346.1; -; mRNA.
DR   SMR; Q53EL3; 4-449.
DR   Ensembl; ENSG00000103653; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   449 AA;  50617 MW;  45BD3B64B8ABB05E CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 449;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        367 DVWSFGILL 375


RESULT 27
Q80UI3_MOUSE
ID   Q80UI3_MOUSE   PRELIMINARY;   PRT;   449 AA.
AC   Q80UI3;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 23.
DE   Fert2 protein (Fragment).
GN   Name=Fert2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N-3; TISSUE=Mammary tumor. MMTV-LTR/INT3 model. 5 month old
RC   mouse. Taken by biopsy.;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
```

```
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N-3; TISSUE=Mammary tumor. MMTV-LTR/INT3 model. 5 month old
RC   mouse. Taken by biopsy.;
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC051249; AAH51249.1; -; mRNA.
DR   HSSP; P11362; 1FGK.
DR   Ensembl; ENSMUSG00000000127; Mus musculus.
DR   MGI; MGI:105917; Fert2.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.
DR   GO; GO:0007155; P:cell adhesion; IMP.
DR   GO; GO:0006935; P:chemotaxis; IMP.
DR   GO; GO:0007242; P:intracellular signaling cascade; RCA.
DR   GO; GO:0046777; P:protein amino acid autophosphorylation; IDA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   449 AA;  51136 MW;  5463C70B41B1FFC7 CRC64;

  Query Match             100.0%;  Score 49;  DB 2;  Length 449;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
              |||||||||
Db        369 DVWSFGILL 377


RESULT 28
CSK_CHICK
ID   CSK_CHICK      STANDARD;      PRT;   450 AA.
AC   P41239;
DT   01-FEB-1995, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1995, sequence version 1.
DT   07-MAR-2006, entry version 45.
DE   Tyrosine-protein kinase CSK (EC 2.7.1.112) (C-SRC kinase).
GN   Name=CSK;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Brain;
RX   MEDLINE=92196083; PubMed=1372437;
RA   Sabe H., Knudsen B., Okada M., Nada S., Nakagawa H., Hanafusa H.;
RT   "Molecular cloning and expression of chicken C-terminal Src kinase:
RT   lack of stable association with c-Src protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:2190-2194(1992).
CC   -!- FUNCTION: Specifically phosphorylates a tyrosine on the SRC
CC       kinase. This tyrosine acts as a negative regulatory site. Can also
CC       act on the LYN and FYN kinases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Interacts with PTPN8 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (Probable).
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSK
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; M85039; AAA51436.1; -; mRNA.
DR   PIR; A41973; A41973.
DR   HSSP; P41240; 1BYG.
DR   SMR; P41239; 4-450.
DR   Ensembl; ENSGALG00000001318; Gallus gallus.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation; SH2 domain;
KW   SH3 domain; Transferase; Tyrosine-protein kinase.
FT   CHAIN         1    450       Tyrosine-protein kinase CSK.
FT                                /FTId=PRO_0000088069.
FT   DOMAIN        9     70       SH3.
FT   DOMAIN       82    171       SH2.
FT   DOMAIN      195    450       Protein kinase.
FT   NP_BIND     201    209       ATP (By similarity).
FT   REGION        9     70       Interaction with PTPN8 (By similarity).
FT   ACT_SITE    314    314       Proton acceptor (By similarity).
FT   BINDING     222    222       ATP (By similarity).
FT   MOD_RES     416    416       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
SQ   SEQUENCE   450 AA;  50751 MW;  5AA3C406AA4F246F CRC64;

  Query Match             100.0%;  Score 49;  DB 1;  Length 450;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
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Db        368 DVWSFGILL 376


RESULT 29
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CSK_HUMAN
ID   CSK_HUMAN      STANDARD;      PRT;   450 AA.
AC   P41240; Q6FGZ6;
DT   01-FEB-1995, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1995, sequence version 1.
DT   07-MAR-2006, entry version 62.
DE   Tyrosine-protein kinase CSK (EC 2.7.1.112) (C-SRC kinase) (Protein-
DE   tyrosine kinase CYL).
GN   Name=CSK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=92050797; PubMed=1945408;
RA   Partanen J., Armstrong E., Bergman M., Maekelae T.P., Hirvonen H.,
RA   Huebner K., Alitalo K.;
RT   "CYL encodes a putative cytoplasmic tyrosine kinase lacking the
RT   conserved tyrosine autophosphorylation site (Y416src).";
RL   Oncogene 6:2013-2018(1991).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Lung;
RX   MEDLINE=92073297; PubMed=1720539;
RA   Braeuninger A., Holtrich U., Strebhardt K., Ruebsamen-Waigmann H.;
RT   "Two additional protein-tyrosine kinases expressed in human lung:
RT   fourth member of the fibroblast growth factor receptor family and an
RT   intracellular protein-tyrosine kinase.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:10411-10415(1991).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND TISSUE SPECIFICITY.
RX   PubMed=1371489; DOI=10.1016/0378-1119(92)90649-A;
RA   Brauninger A., Holtrich U., Strebhardt K., Rubsamen-Waigmann H.;
RT   "Isolation and characterization of a human gene that encodes a new
RT   subclass of protein tyrosine kinases.";
RL   Gene 110:205-211(1992).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=93241739; PubMed=7683131;
RA   Braeuninger A., Karn T., Strebhardt K., Ruebsamen-Waigmann H.;
RT   "Characterization of the human CSK locus.";
RL   Oncogene 8:1365-1369(1993).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA   Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
RA   Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA   Korn B., Zuo D., Hu Y., LaBaer J.;
RT   "Cloning of human full open reading frames in Gateway(TM) system entry
RT   vector (pDONR201).";
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS ASP-287; GLN-398 AND
RP   ARG-442.
RA   Livingston R.J., Rieder M.J., Shaffer T., Bertucci C., Baier C.N.,
RA   Rajkumar N., Willa H.T., Daniels M., Downing T.K., Stanaway I.B.,
RA   Nguyen C.P., Gildersleeve H., Cassidy C.M., Johnson E.J.,
RA   Swanson J.E., McFarland I., Yool B., Park C., Nickerson D.A.;
RT   "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT   of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Uterus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   PHOSPHORYLATION SITES TYR-184 AND TYR-304, AND MUTAGENESIS OF TYR-184
RP   AND TYR-304.
RX   MEDLINE=97220407; PubMed=9148770;
RA   Joukov V., Vihinen M., Vainikka S., Sowadski J.M., Alitalo K.,
RA   Bergman M.;
RT   "Identification of csk tyrosine phosphorylation sites and a tyrosine
RT   residue important for kinase domain structure.";
RL   Biochem. J. 322:927-935(1997).
RN   [9]
RP   INTERACTION WITH PAG1.
RX   MEDLINE=20253245; PubMed=10790433; DOI=10.1084/jem.191.9.1591;
RA   Brdicka T., Pavlistova D., Bruyns E., Leo A., Korinek V.,
RA   Angelisova P., Scherer J., Shevchenko A., Shevchenko A., Hilgert I.,
RA   Cerny J., Drbal K., Kuramitsu Y., Horejsi V., Schraven B.;
RT   "Phosphoprotein associated with glycosphingolipid-enriched
RT   microdomains (PAG), a novel ubiquitously expressed transmembrane
RT   adaptor protein, binds the protein tyrosine kinase csk and is involved
RT   in regulation of T cell activation.";
RL   J. Exp. Med. 191:1591-1604(2000).
RN   [10]
RP   INTERACTION WITH SIT1.
RX   PubMed=11433379;
RX   DOI=10.1002/1521-4141(200106)31:6<1825::AID-IMMU1825>3.0.CO;2-V;
RA   Pfrepper K.-I., Marie-Cardine A., Simeoni L., Kuramitsu Y., Leo A.,
RA   Spicka J., Hilgert I., Scherer J., Schraven B.;
RT   "Structural and functional dissection of the cytoplasmic domain of the
RT   transmembrane adaptor protein SIT (SHP2-interacting transmembrane
RT   adaptor protein).";
RL   Eur. J. Immunol. 31:1825-1836(2001).
RN   [11]
RP   INTERACTION WITH LIME1.
RX   PubMed=14610046; DOI=10.1084/jem.20031484;
RA   Brdickova N., Brdicka T., Angelisova P., Horvath O., Spicka J.,
RA   Hilgert I., Paces J., Simeoni L., Kliche S., Merten C., Schraven B.,
RA   Horejsi V.;
RT   "LIME: a new membrane raft-associated adaptor protein involved in CD4
RT   and CD8 coreceptor signaling.";
RL   J. Exp. Med. 198:1453-1462(2003).
RN   [12]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 1-71.
RX   MEDLINE=94185778; PubMed=7511113; DOI=10.1016/0014-5793(94)80244-0;
RA   Borchert T.V., Mathieu M., Zeelen J.P., Courtneidge S.A.,
RA   Wierenga R.K.;
RT   "The crystal structure of human CskSH3: structural diversity near the
RT   RT-Src and n-Src loop.";
RL   FEBS Lett. 341:79-85(1994).
CC   -!- FUNCTION: Specifically phosphorylates Tyr-504 on LCK, which acts
CC       as a negative regulatory site. Can also act on the LYN and FYN
CC       kinases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Interacts with PTPN8 (By similarity). Interacts with
CC       phosphorylated SIT1, PAG1 and LIME1.
CC   -!- SUBCELLULAR LOCATION: Mainly cytoplasmic. Also present in lipid
CC       rafts (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed in lung and macrophages.
CC   -!- PTM: Autophosphorylation of Tyr-304 occurs only at abnormally high
CC       CSK concentrations in vitro.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSK
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CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X60114; CAA42713.1; -; mRNA.
DR   EMBL; X59932; CAA42556.1; -; mRNA.
DR   EMBL; X74765; CAB58562.1; -; Genomic_DNA.
DR   EMBL; CR541960; CAG46758.1; -; mRNA.
DR   EMBL; DQ075211; AAY57329.1; -; Genomic_DNA.
DR   EMBL; BC106073; AAI06074.1; -; mRNA.
DR   PIR; JH0559; JH0559.
DR   PDB; 1BYG; X-ray; A=173-450.
DR   PDB; 1CSK; X-ray; A/B/C/D=1-71.
DR   SMR; P41240; 4-450.
DR   OGP; P41240; -.
DR   Ensembl; ENSG00000103653; Homo sapiens.
DR   HGNC; HGNC:2444; CSK.
DR   MIM; 124095; gene.
DR   LinkHub; P41240; -.
DR   GO; GO:0005886; C:plasma membrane; IPI.
DR   GO; GO:0008022; F:protein C-terminus binding; TAS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; TAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF07714; Pkinase_Tyr; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   3D-structure; ATP-binding; Kinase; Nucleotide-binding;
KW   Phosphorylation; Polymorphism; SH2 domain; SH3 domain; Transferase;
KW   Tyrosine-protein kinase.
FT   CHAIN         1    450       Tyrosine-protein kinase CSK.
FT                                /FTId=PRO_0000088070.

  Query Match             100.0%;  Score 49;  DB 1;  Length 450;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
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Db        368 DVWSFGILL 376


RESULT 30
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ID   CSK_MOUSE      STANDARD;      PRT;   450 AA.
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DT   01-FEB-1995, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1995, sequence version 1.
DT   07-MAR-2006, entry version 55.
DE   Tyrosine-protein kinase CSK (EC 2.7.1.112) (C-SRC kinase) (Protein-
DE   tyrosine kinase MPK-2) (p50CSK).
GN   Name=Csk;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Brain;
RX   MEDLINE=94195789; PubMed=7511815;
RA   Klages S., Adam D., Class K., Fargnoli J., Bolen J.B., Penhallow R.C.;
RT   "Ctk: a protein-tyrosine kinase related to Csk that defines an enzyme
RT   family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:2597-2601(1994).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 316-367.
RC   STRAIN=C57BL/6; TISSUE=Embryonic brain;
RX   MEDLINE=93096484; PubMed=1281307;
RA   Gilardi-Hebenstreit P., Nieto M.A., Frain M., Mattei M.-G.,
RA   Chestier A., Wilkinson D.G., Charnay P.;
RT   "An Eph-related receptor protein tyrosine kinase gene segmentally
RT   expressed in the developing mouse hindbrain.";
RL   Oncogene 7:2499-2506(1992).
RN   [3]
RP   INTERACTION WITH PTPN8.
RX   PubMed=8890164;
RA   Cloutier J.-F., Veillette A.;
RT   "Association of inhibitory tyrosine protein kinase p50csk with protein
RT   tyrosine phosphatase PEP in T cells and other hemopoietic cells.";
RL   EMBO J. 15:4909-4918(1996).
RN   [4]
RP   INTERACTION WITH PAG1.
RX   PubMed=12218089;
RA   Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,
RA   Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;
RT   "Fyn is essential for tyrosine phosphorylation of Csk-binding
RT   protein/phosphoprotein associated with glycolipid-enriched
RT   microdomains in lipid rafts in resting T cells.";
RL   J. Immunol. 169:2813-2817(2002).
RN   [5]
RP   INTERACTION WITH PAG1.
RX   PubMed=12612075; DOI=10.1128/MCB.23.6.2017-2028.2003;
RA   Davidson D., Bakinowski M., Thomas M.L., Horejsi V., Veillette A.;
RT   "Phosphorylation-dependent regulation of T-cell activation by PAG/Cbp,
RT   a lipid raft-associated transmembrane adaptor.";
RL   Mol. Cell. Biol. 23:2017-2028(2003).
RN   [6]
RP   INTERACTION WITH PAG1, AND SUBCELLULAR LOCATION.
RX   PubMed=16166631; DOI=10.1128/MCB.25.19.8486-8495.2005;
RA   Xu S., Huo J., Tan J.E.-L., Lam K.-P.;
RT   "Cbp deficiency alters Csk localization in lipid rafts but does not
RT   affect T-cell development.";
RL   Mol. Cell. Biol. 25:8486-8495(2005).
CC   -!- FUNCTION: Specifically phosphorylates Tyr-504 on LCK, which acts
CC       as a negative regulatory site. Can also act on the LYN and FYN
CC       kinases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Interacts with phosphorylated SIT1 and LIME1 (By
CC       similarity). Interacts with PTPN8. Interacts with phosphorylated
CC       PAG1.
CC   -!- SUBCELLULAR LOCATION: Mainly cytoplasmic. Also present in lipid
CC       rafts.
CC   -!- TISSUE SPECIFICITY: Ubiquitous, but most abundant in thymus and
CC       spleen, as well as in neonatal brain.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSK
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 SH2 domain.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
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DR   EMBL; U05247; AAA18766.1; -; mRNA.
DR   EMBL; X57242; CAA40518.1; -; mRNA.
DR   PIR; I48929; I48929.
DR   PDB; 1JEG; NMR; A=1-83.
DR   SMR; P41241; 4-450.
DR   Ensembl; ENSMUSG00000032312; Mus musculus.
DR   MGI; MGI:88537; Csk.
DR   GO; GO:0005886; C:plasma membrane; TAS.
DR   GO; GO:0005524; F:ATP binding; TAS.
DR   GO; GO:0005515; F:protein binding; IC.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; TAS.
DR   GO; GO:0016740; F:transferase activity; TAS.
DR   GO; GO:0007242; P:intracellular signaling cascade; TAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   GO; GO:0050863; P:regulation of T cell activation; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
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DR   Pfam; PF00018; SH3_1; 1.
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DR   PRINTS; PR00452; SH3DOMAIN.
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DR   ProDom; PD000066; SH3; 1.
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DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
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DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   3D-structure; ATP-binding; Kinase; Nucleotide-binding;
KW   Phosphorylation; SH2 domain; SH3 domain; Transferase;
KW   Tyrosine-protein kinase.
FT   CHAIN         1    450       Tyrosine-protein kinase CSK.
FT                                /FTId=PRO_0000088071.
FT   DOMAIN        9     70       SH3.
FT   DOMAIN       82    171       SH2.
FT   DOMAIN      195    449       Protein kinase.
FT   NP_BIND     201    209       ATP (By similarity).
FT   REGION        9     70       Interaction with PTPN8.
FT   ACT_SITE    314    314       Proton acceptor (By similarity).
FT   BINDING     222    222       ATP (By similarity).
FT   MOD_RES     184    184       Phosphotyrosine (By similarity).
FT   MOD_RES     416    416       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
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FT   STRAND       24     24
FT   TURN         25     26
FT   STRAND       27     27
FT   TURN         32     33
FT   STRAND       35     41
FT   STRAND       43     51
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FT   STRAND       55     55
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  Query Match             100.0%;  Score 49;  DB 1;  Length 450;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DVWSFGILL 9
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Db        368 DVWSFGILL 376

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